Genetic Diversity In U.S. Hatchery Stocks Of Crassostrea Ariakensis (Fujita, 1913) And Comparison With Natural Populations In Asia

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GENETIC DIVERSITY IN U.S. HATCHERY STOCKS OF *CRASSOSTREA ARIAKENSIS* (FUJITA, 1913) AND COMPARISON WITH NATURAL POPULATIONS IN ASIA

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**ABSTRACT** Although several different U.S. hatchery stocks of the Asian Suminoe oyster *Crassostrea ariakensis* were used in laboratory and field trials assessing performance, and in comparative studies with the native oyster *Crassostrea virginica*, the genetic composition of these hatchery stocks has not yet been examined comprehensively. Using eight microsatellite markers we investigated the genetic variability among five hatchery stocks and compared the genetic makeup of these stocks with 8 wild populations from Asia. Results showed significant genetic differentiation among the 5 hatchery stocks that was 6-fold larger than that observed among wild populations. A significant reduction in genetic diversity was observed in hatchery stocks compared with wild source populations, indicating a genetic bottleneck. Two long-established stocks showed significant decreases in both allelic diversity and heterozygosity compared with the wild, Japanese source population, whereas three recently established stocks showed less severe reductions in allelic diversity and a nonsignificant change in levels of heterozygosity compared with their source Chinese populations. These microsatellite markers also proved useful for assignment of hatchery individuals back to their source stocks with a high degree of confidence. Although assignment of wild individuals back to their population of origin proved less reliable, approximately 70% of wild individuals could be assigned either to their source population or to geographically proximal populations. Our results suggest that results obtained from experiments that used hatchery animals of a single *C. ariakensis* stock for biological and ecological studies should be interpreted cautiously, because they may not always accurately reflect the behavior of wild populations or of other hatchery stocks.

**KEY WORDS:** Suminoe oyster, *Crassostrea ariakensis*, microsatellites, hatchery stocks, genetic diversity, genetic bottleneck

**INTRODUCTION**

The Suminoe oyster *Crassostrea ariakensis* naturally occurs along the coast of the northwest Pacific, and is a commercially important oyster species for aquaculture in both China and Japan (Langdon & Robinson 1996, Guo et al. 1999, Zhou & Allen 2003). In the 1970s, it was accidentally introduced to the west coast of the United States along with a shipment of *Crassostrea gigas* and *Crassostrea sikamea* oyster seed from the Kumamoto Prefecture in Japan (Breese & Malouf 1977). The introduced stocks of *C. ariakensis* have been spawned in hatcheries and raised in culture in the coastal waters of Oregon and Washington, but to date no wild populations are known to have established in the region, possibly because of the low water temperatures in the northeast Pacific (Breese & Malouf 1977, Perdue & Erickson 1984, Langdon & Robinson 1996). Recently, proposals to introduce a nonnative oyster species to the Chesapeake Bay region of the U.S. east coast led to research on nonnative oyster species, including *C. gigas* and *C. ariakensis* (Mann et al. 1991). Based on preliminary studies, *C. ariakensis* appeared to grow faster and be more tolerant to local oyster parasites in some locations of Chesapeake Bay compared with the native eastern oyster *Crassostrea virginica* and the other nonnative species tested, *C. gigas* (Calvo et al. 1999, Calvo et al. 2001, Grabowski et al. 2004). Therefore, focus shifted to *C. ariakensis* and, during the late 1990s, *C. ariakensis* broodstocks were imported from Oregon to Rutgers University and to the Virginia Institute of Marine Science (VIMS). Two other stocks of oysters, imported from the Yellow River basin, Shandong Province in northern China, and Beihai, Guangxi Province in southern China, have been maintained at VIMS since 1999 (NRC 2004, Zhang et al. 2005). Although no reproductively capable *C. ariakensis* were ever approved for in-water testing along the U.S. east coast, sterile triploid *C. ariakensis* derived from these hatchery stocks (Calvo et al. 2000, Allen et al. 2003) were used in field trials, and both triploid and diploid hatchery animals were used for laboratory experiments conducted under quarantine conditions for comparative taste (Grabowski et al. 2003), biological and ecological studies (Calvo et al. 2001, Grabowski et al. 2004, Bishop & Hooper 2005, Hudson et al. 2005, Alexander et al. 2008, Kingsley-Smith & Luckenbach 2008, McGhee et al. 2008, Paynter et al. 2008, Tamburri et al. 2008), as well as for testing disease tolerance (Calvo et al. 2001, Grabowski et al. 2004, Moss et al. 2006).

Little is known, however, about the genetic makeup of the hatchery stocks and their genetic differentiation from wild populations, which might be associated with differences in biology, behavior, and performance under various environmental conditions. Studies on some marine bivalves show that allelic reduction is quite common in hatchery lines, and it is often associated with deviations in allelic or genotypic frequencies compared with the natural source populations (Hedgecock & Sly 1990, Gaffney et al. 1996, Yu & Guo 2005, Carlsson et al. 2006). This drift is thought to arise as a result of bottleneck effects from the small effective number of parents typically contributing to spawns in hatcheries, and nonrandom selection that often occurs during breeding and larval recruitment in the hatchery (Hedgecock & Sly 1990, Gaffney et al. 1996, Boudry et al. 2002, Yu & Guo 2005). Consequently, inbreeding is common in hatchery stocks, and sometimes a concomitant decrease in various performance measures can occur (Hedgecock et al. 1995, Bierne et al. 1998, Ermande et al. 2003). Studies have shown that there is a small but significant genetic heterogeneity among wild *C. ariakensis* populations in Asia, and the genetic differentiation increases with geographic distance among populations, indicating a genetic pattern of isolation by distance.
(Xiao et al. 2010). Although an initial study showed reduced genetic diversity in 5 VIMS hatchery stocks compared with wild populations (Zhang et al. 2005), this previous study did not provide detailed information on the genetic structuring within and among C. ariakensis hatchery stocks and wild populations.

Because of concerns over the social, economic, and ecological risks of introducing the nonnative C. ariakensis into the Chesapeake Bay ecosystem, the proposed introduction of C. ariakensis for helping restore the Eastern oyster population in Chesapeake Bay is no longer being considered (http://www.nao.usace.army.mil/OysterEIS/FINAL_PEIS/homepage.asp). However, accidental release or intentional, illegal introduction of reproductively capable C. ariakensis is still possible through various means (Simberloff 2005). Some triploid C. ariakensis have been found by local farmers in the waters of North Carolina and Chesapeake Bay (K. Reece unpubl. data). The highly polymorphic microsatellite markers used here have proved useful for differentiating among natural populations of C. ariakensis in Asia (Xiao et al. 2010). The current study tested further the utility of these markers to differentiate among U.S. hatchery stocks, to assess the relationship among these stocks and their natural source populations, and to assign C. ariakensis of unknown origin back to their source domestic stocks or wild populations.

MATERIALS AND METHODS

Samples

A total of 245 individuals from 5 hatchery stocks were collected in 2002 (Table 1) and confirmed to be C. ariakensis by PCR-RFLP analysis (Zhang et al. 2005, Cordes et al. 2008). Forty-eight C. ariakensis oysters were shipped from Taylor Shellfish Farms, Inc. (TUI), and genomic DNA was extracted directly from the tissues of these oysters for genotyping. TUI was derived from the “Oregon strain,” which was inadvertently introduced to the west coast of the United States in the 1970s from Japan, and has been spawned and reared in hatcheries for several generations (Breese & Malouf 1977). In comparison with TUI, a west coast C. ariakensis (WCA) sample, also derived from the “Oregon Strain,” was comprised of the offspring of a C. ariakensis stock imported from the coastal waters of Washington state to VIMS in 1999. A north China C. ariakensis stock (NCA) was derived directly from wild broodstock brought to VIMS from the Yellow River Basin, Shandong Province, northern China, and spawned in 1999 at the VIMS Aquaculture and Breeding Technology Center (ABC). Similarly, two south China C. ariakensis stocks (SCA99 and SCA00) were derived from a wild broodstock collected in Beihai, Guangxi Province, southern China, and spawned by ABC in 1999 and 2000, respectively. For the purpose of this study, TUI and WCA were considered to be long-established stocks because of the long separation time (around 30 y) from their natural source populations in Japan (Breese & Malouf 1977). NCA, SCA99, and SCA00 were considered recent stocks because the broodstocks were transported into the United States quite recently, and each stock had undergone only 1 generation of hatchery propagation at the time of sampling.

As inferred by the population genetic structure analysis of Xiao et al. (2010), samples from eight genetically heterogeneous natural populations in Asia were also included in the analyses (Table 1). They were used for comparisons of genetic variability and diversity among hatchery stocks and wild populations, and as reference populations for assignment tests. Two additional wild samples, which were not included in the wild population genetic structure analysis, were genotyped and used as test

<table>
<thead>
<tr>
<th>Sample Code</th>
<th>Collecting Date</th>
<th>Sample Type</th>
<th>Sample Size</th>
<th>Source</th>
</tr>
</thead>
<tbody>
<tr>
<td>TU1</td>
<td>2002</td>
<td>Hatchery</td>
<td>48</td>
<td>Taylor Shellfish Farms, Inc., derived from the ‘Oregon Strain’ on west coast of United States</td>
</tr>
<tr>
<td>WCA</td>
<td>2002</td>
<td>Hatchery</td>
<td>50</td>
<td>ABC, derived from the ‘Oregon Strain’ on west coast of United States</td>
</tr>
<tr>
<td>NCA</td>
<td>2002</td>
<td>Hatchery</td>
<td>50</td>
<td>ABC, F1 generation of Yellow River stock (YR) from northern China, spawned in 1999</td>
</tr>
<tr>
<td>SCA99</td>
<td>2002</td>
<td>Hatchery</td>
<td>50</td>
<td>ABC, F1 generation of Beihai stock (BH) from southern China, spawned in 1999</td>
</tr>
<tr>
<td>SCA00</td>
<td>2002</td>
<td>Hatchery</td>
<td>47</td>
<td>ABC, F1 generation of Beihai stock (BH) from southern China, spawned in 2000</td>
</tr>
<tr>
<td>IR*</td>
<td>1999, 2005</td>
<td>Wild</td>
<td>99</td>
<td>Ariake Sea, Saga Prefecture, Kyushu, Japan</td>
</tr>
<tr>
<td>KR*</td>
<td>2004</td>
<td>Wild</td>
<td>33</td>
<td>Kawha River, South Korea</td>
</tr>
<tr>
<td>SR*</td>
<td>2004</td>
<td>Wild</td>
<td>20</td>
<td>Sunjin River, South Korea</td>
</tr>
<tr>
<td>KI*</td>
<td>2004</td>
<td>Wild</td>
<td>20</td>
<td>Kanghwa Island, Incheon, South Korea</td>
</tr>
<tr>
<td>YzR*</td>
<td>2005, 2006, 2006</td>
<td>Wild</td>
<td>137</td>
<td>Yangzi River estuary, China</td>
</tr>
<tr>
<td>HC*</td>
<td>2005, 2006</td>
<td>Wild</td>
<td>95</td>
<td>Haicheng, Fujian Province, China</td>
</tr>
<tr>
<td>BH*</td>
<td>1999, 2005</td>
<td>Wild</td>
<td>69</td>
<td>Dafeng River, Beihai, Guangxi Zhuang, China</td>
</tr>
<tr>
<td>IR05a</td>
<td>2005</td>
<td>Wild</td>
<td>50</td>
<td>Ariake Sea, Saga Prefecture, Kyushu, Japan</td>
</tr>
<tr>
<td>YR05a</td>
<td>2005</td>
<td>Wild</td>
<td>36</td>
<td>Yellow River, Weifang, Shandong Province, China</td>
</tr>
</tbody>
</table>

* The eight wild populations were from Xiao et al. (2010). Sixteen wild samples originally used for the study in Xiao et al. (2010) were grouped into 8 genetically distinguished populations based on the results of the genetic analysis in that study.
samples for the assignment analyses conducted here. These test samples were composed of 50 individuals collected from the Itoki River in Japan (IR05a) and 36 individuals from the Yellow River in China (YR05a) in 2005. These additional samples were confirmed to be *C. ariakensis* using the PCR-RFLP molecular identification key of Cordes et al. (2008).

**DNA Extraction, Microsatellite Amplification, and Data Analysis**

Genomic DNA extraction, PCR amplifications of 8 microsatellite markers (*Car11*-70, *Car115*-d0, *Car119*-6a, *Car130*-08, *CarG1*-0b, *CarG4*-60, *CarG12*-; GenBank accession nos.: EU241319-EU241322, EU241324-EU241327), and separation of PCR products on a PRISM ABI 3130 genetic analyzer (Applied Biosystems, Foster City, CA) followed the protocols described in Xiao et al. (2008). Allele sizes in base pairs (bp) were called based on comparisons with the panels generated by scoring 605 wild individuals of *C. ariakensis* from Japan, South Korea, and China (Xiao et al. 2010), using the software package GeneMarker (SoftGenetics, State College, PA).

Based on multilocus genotype data, inter- and intrapopulation variation were measured by various parameters. Observed and expected heterozygosity (*H*<sub>O</sub> and *H*<sub>E</sub>, respectively) were calculated using the program GENETIX (Belkhir et al. 1996–2004). Unbiased F statistics (*F*<sub>IS</sub> and *F*<sub>ST</sub>) were calculated using GENEPOP 3.4 (Raymond & Rousset 1995), and the significance levels of *F*<sub>IS</sub> and *F*<sub>ST</sub> values were assessed by bootstrapping with 10,000 iterations at each locus and over all loci in GENETIX. Allelic richness (*A*) was computed by FSTAT 2.9.3 (Goudet 2001) and adjusted to a sample size of 47 diploid individuals by a rarefaction method (Petit et al. 1998). The genetic relationship between hatchery stocks and natural populations, as well as among all samples was visualized through construction of a neighbor-joining (NJ) tree using the software package PHYLIP 3.67 (Felsenstein 1989) based on Cavalli-Sforza and Edwards’ (1967) genetic distances.

In the assignment analyses, 8 wild populations (IR, KR, SR, K1, YR, YzR, HC, and BH) and the 5 hatchery stocks were used as the reference samples. To assess the ability of the markers to assign individuals correctly back to their source populations, self-assignment tests were first conducted (during which the population of origin for a sampled individual was considered the source) for the eight natural populations and 5 hatchery populations by a “leave-one-out” procedure that excluded the individual to be assigned from the population during computation (Piry et al. 2004). To assign “unknown” individuals to a natural population or hatchery stock, 10 individuals from each of the 5 hatchery samples (named TUIa, WCAa, NCAa, SCA99a, and SCA00a) were drawn randomly and removed from the “reference” database. These 50 hatchery individuals, along with 86 test individuals (total *n* = 136) from two additional natural samples (IR05a and YR05a), were assigned to a population or stock based on their multilocus genotype profiles. A Bayesian method (Rannala & Mountain 1997) implemented in the program GeneClass 2 (Piry et al. 2004) was used to compute the probability of an individual being classified to each reference population. The reference population with the highest assignment probability was chosen as the assigned source for each individual, and compared with the known information from sampling.

**RESULTS**

**Genetic Diversities Within the Hatchery Stocks and Comparisons with Natural Populations**

A total of 152 different alleles were amplified at 8 microsatellite loci in 246 individuals from 5 hatchery stocks. Only 52.6% of the alleles that amplified in wild samples (Xiao et al. 2010) were observed in the hatchery stocks. In addition, 3 alleles (from loci *CarG4*-60, *Car130*-08, and *Car115*-d0) that were not observed in the wild samples were amplified from hatchery stocks. One of these unique alleles was only found in the Japanese-derived hatchery stocks TUI and WCA; the other two were found only in stocks SCA99 and SCA00, which were derived from southern Chinese populations.

Adjusted allelic richness (*A*) across all loci in hatchery stocks ranged from an average of 3.8 (TUI)–12.2 (SCA99) alleles per locus per stock (Table 2). There was a significant difference in *A* values among these 5 hatchery stocks, and the long-established stocks (TUI and WCA) had much lower *A* values compared with the recently derived stocks (*P* < 0.001, 2-tailed Mann-Whitney test).

Multilocus analysis of the hatchery stocks indicated that the TUI stock showed a significant negative *F*<sub>IS</sub> (−0.226), which is an indication of an excess of observed heterozygotes compared with expected. However, individual tests of HWE for each stock at every locus (Table 2) revealed that 15 of 40 tests were significantly out of HWE after a sequential Bonferroni correction (*P* < 0.05, *K* = 5, initial *α* = 0.01), and 11 (69%) of them were the result of an excess of heterozygotes. TUI had the highest number (5 of 8) of deviations from HWE, all resulting from *H*<sub>O</sub> > *H*<sub>E</sub>.

We compared further the genetic diversity in terms of allelic richness (*A*) and heterozygosity (*H*<sub>O</sub>, *H*<sub>E</sub>) of the hatchery stocks with their wild source populations. For the purpose of comparison, *A* values of hatchery stocks were adjusted to a sample size of *n* = 14, which was the adjusted sample size for the wild samples in the previous study (Xiao et al. 2010). The values for all three parameters were decreased significantly (all *P* values < 0.05) in the two long-established stocks TUI and WCA compared with those parameters in their source population (IR; Figs. 1 and 2); whereas the three recent stocks (NCA, SCA99, and SCA00) had reduced values of *A* (*P* = 0.009; Fig. 1), but not of *H*<sub>E</sub> and *H*<sub>O</sub> (*P* = 0.615 and 0.105, respectively; Fig. 2) compared with their source populations (YR and BH, respectively). The average *A*, *H*<sub>O</sub>, and *H*<sub>E</sub> values of the two long-established stocks (TUI and WCA) were decreased by 60.4%, 10.9%, and 26.4%, respectively, compared with their wild source population (IR). In comparison, the average reduction in *A* in the three recent hatchery stocks, although significantly lower than in the wild populations, was much smaller, and *H*<sub>E</sub> and *H*<sub>O</sub> values did not decrease significantly. Allelic richness was 17.7% lower for NCA compared with its source population YR, and 29.5% lower for the SCA99 and SCA00 stocks compared with the wild BH population.

**Genetic Differentiation Among Hatchery Stocks and Wild Populations**

Population pairwise *θ*<sub>ST</sub> values among hatchery samples (Table 3) ranged from 0.054 (SCA99 vs. SCA00)–0.238 (TUI vs. SCA00; *global θ*<sub>ST</sub> = 0.132), and were clearly larger than those previously observed among 8 natural populations.
and Korean populations (KR, SR, and KI), but without
strong bootstrap support values (<0.001). Likewise, the
NCA stock (derived from broodstock source population (BH),
but with lower bootstrap support value (75%). SCA99 and SCA00
also grouped with their wild source population (IR), with a
moderate bootstrap support value (50%). Similarly, the
NCA stock (derived from broodstock source population
(3R), but with lower bootstrap support value (75%).

Overall

Assignment Tests

The results of all assignment tests are shown in Table 4,
including two groups of self-assignments and the assignments of
some additional and/or random samples to natural and/or hatchery origins. The self-assignment tests correctly assigned
84.0%–97.9% of hatchery individuals back to their hatchery
stocks, whereas variable percentages (20.0%–72.7%) of wild
individuals were assigned back to their specific wild source
populations. The three Korean populations, which had small
sample sizes (20–33), had quite a low incidence of correct
assignments (20.0%–30.0%). Nevertheless, results (Table 4)
indicate that a large portion of wild individuals were assigned
either correctly to their source or to a geographically proximal population. For example, 15.0%–40.0% of individual oysters from the 3 Korean populations (KR, SR, and KI) were

assigned to the Yellow River basin population (YR), and an additional 20.0% and 35.0% of individuals from the SR and KI populations, respectively, were assigned to the Yangzi River population (YzR). Similarly, a substantial proportion of oysters (14.7%) from Haicheng (HC) were classified to the other southern Chinese population (BH), and vice versa (i.e., 29.0% from BH assigned to HC).

Tests using both hatchery stocks and natural populations as references for 136 putatively “unknown” individuals from 7 different samples resulted in relatively accurate assignment of the hatchery animals to either the correct stock, a closely related stock, or to the source populations, and likewise, assignment of the wild animals to either the correct population or to geographically proximal populations. Interestingly, although 70% of the animals from the NCAa hatchery sample were assigned to the NCA stock, the other 30% were assigned to wild populations (YR and YzR) in northern China, which was either the source population for the NCA stock or near the source. In addition, although 90% of the animals from the hatchery SCA99a sample were assigned to the SCA99 stock, one animal (10%) was assigned to a wild population from southern China (HC). Ninety percent of the individuals in the TUIa sample were assigned to the TUI stock, and 10% were assigned to the WCA stock, which was derived from the same Japanese source population. Although 90% of the animals from SCA00a were assigned correctly to SCA00, 10% were assigned to the other hatchery stock from the same southern Chinese broodstock (SCA99). Only one individual (2%) from the wild Japanese IR05a sample was assigned to an unrelated hatchery stock (SCA99), whereas 68% were assigned to the natural IR population and 22% were assigned to Korean or northern Chinese populations. Approximately 64% of the wild YR05a sample were correctly assigned to the YR population, and another 22% of the individuals were assigned to the geographically proximal YzR population.

DISCUSSION

Genetic Makeup of the Hatchery Stocks

In a hatchery setting, reductions in allelic diversity are believed to be caused by small effective population sizes \( (N_e) \) resulting from few animals being used as broodstock, as well as nonequal gametic viability and/or differential spawning conditions of the potential parents (Hedgecock & Sly 1990, Hedgecock 1994). Reductions in heterozygosity, however, do not always respond immediately to these conditions, depending on the number and severity of the bottlenecks, the original

<table>
<thead>
<tr>
<th>TABLE 3. Pairwise ( \theta_{ST} ) (above diagonal) and ( P ) values (below diagonal) among 5 hatchery stocks of C. ariakensis.</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
</tr>
<tr>
<td>TUI</td>
</tr>
<tr>
<td>NCA —</td>
</tr>
<tr>
<td>WCA &lt;0.001</td>
</tr>
<tr>
<td>SCA99 &lt;0.001</td>
</tr>
<tr>
<td>SCA00 &lt;0.001</td>
</tr>
</tbody>
</table>

All comparisons were highly significant after a sequential Bonferroni correction \( (P < 0.05, K = 10, \text{ initial adjusted } \alpha = 0.005) \). See Table 1 for sample abbreviations.
demonstrated significantly reduced allelic richness, and allelic which the recent stocks (NCA, SCA99, and SCA00) only diversity continues to decrease, heterozygosity eventually de-
breeding is continued over several generations so that allelic 
the effective number of alleles reached 10. However, if in-
& Avise 2000) showed that heterozygosity changed little after 
relation curve based on studies of 78 animal species (DeWoody 
Hedgecock & Sly 1990, Leberg 1992, Petit et al. 1998,). A 
bottleneck events and that a time lag exists before measurable 
previous reports that allelic diversity is more sensitive to 
one generation of hatchery propagation, showed reductions 
recently domesticated stocks, which were analyzed after only 
This is not surprising because these stocks have been domes-
ticated for more than 30 y and have undergone multiple 
generations of hatchery spawning. In contrast, the more 
recently domesticated stocks, which were analyzed after only 
one generation of hatchery propagation, showed reductions in 
allelic diversity but not in heterozygosity, consistent with 
previous reports that allelic diversity is more sensitive to 
bottleneck events and that a time lag exists before measurable 
decreases in heterozygosity are observed (Nei et al. 1975, 
Hedgecock & Sly 1990, Leberg 1992, Petit et al. 1998,). A 
relation curve based on studies of 78 animal species (DeWoody 
& Avise 2000) showed that heterozygosity changed little after 
the effective number of alleles reached 10. However, if in-
breeding is continued over several generations so that allelic 
diversity continues to decrease, heterozygosity eventually de-
creases correspondingly, as indicated by the current study in 
which the recent stocks (NCA, SCA99, and SCA00) only 
demonstrated significantly reduced allelic richness, and allelic 
richness, as well as the observed and expected heterozygosity 
values, were all significantly lower in the long-established 
hatchery stocks (TUI and WCA) compared with their wild 
source population (Figs. 1 and 2).

Unlike natural populations in which deviations from HWE 
(mostly at locus Car115-a0) were primarily the result of 
allele deficiencies likely resulting from null alleles (Xiao et al. 2010), an overall high proportion (68.8%) of the signif-
ificant $F_{IS}$ values in these hatchery stocks were the result of 
allele excess. In fact, 83.3% of the deviations observed 
in the TUI stock were the result of an excess of observed 
allele deficiencies. A closer look at the genotype frequencies showed 
that a few genotypes were highly prevalent in this hatchery stock 
(data not shown), which is not an uncommon observation in 
hatchery-propagated inbred oyster families (Saavedra & Guerra 
1996, McGoldrick & Hedgecock 1997, Bierne et al. 1998, Marsic-
Lucic & David 2003). Uneven parental contribution and selection 
against deleterious homozygotes resulting from identical-by-
descent markers might contribute to the distorted genotypic 
frequencies in such hatchery stocks, particularly in the short 
term (McGoldrick & Hedgecock 1997, Bierne et al. 1998, 
Launey & Hedgecock 2001). Furthermore, the distorted geno-
typic frequencies observed here indicate nonequal contributions 
to the progeny genotypes from the parents, and there were 
probably only a few successful breeders at each spawning. This 
“founder effect” can cause shifts in allelic frequencies at 
individual loci by random chance (i.e., drift). Loss of rare alleles 
and a high prevalence of a few common alleles can result in very 
different allelic distributions compared with the parental pop-
ulation. Relatively rapid divergence from source populations 
and from other stocks derived from the same source is often 
oberved in highly fecund species like oysters (Hedgecock 1994, 
Saavedra & Guerra 1996, Vercaemert et al. 2006). This likely 
explains the large genetic distance among hatchery stocks and 
between the hatchery stocks and wild populations in this study.

**Implications for C. ariakensis Stock Management**

Although *C. ariakensis* was seriously considered for in-
troduction into the Chesapeake Bay region for the purpose of 
helping to restore the Chesapeake Bay oyster populations and 
the oyster industry, an alternative that involves only restoration 
of the native Eastern oyster was put forth as the preferred 
option in the final programmatic environmental impact statement 
(http://www.nao.usace.army.mil/OysterEIS/FINAL_PeIS/ 
homepage.asp). As an economically important species in Asia, 
however, *C. ariakensis* has been considered for potential addi-
tional aquaculture development on the west coast of the United 
States (Breese & Malouf 1977, Perdue & Erickson 1984, Langdon & 
Robinson 1996). In France there has been some interest in using 
*C. ariakensis* as an alternative to, or as additional oyster species 
for, the *C. gigas* aquaculture industry (Cochennec et al. 1998). 
Understanding the genetic makeup of these hatchery stocks and 
managing them based on the genetic information is important 
for any oyster industry planning to raise *C. ariakensis* in culture.

Based on the results described here, there are three possible 
effects of genetic bottlenecks on the current U.S. hatchery 
stocks tested. First, loss of genetic diversity over the long term 
may cause inbreeding depression. Although the overall and 
long-term effects of inbreeding depression and its converse, 
heterosis (hybrid vigor), are not completely understood in

![Figure 3. Unrooted neighbor-joining tree based on Cavalli-Sforza and Edwards’ (1967) genetic distances among 5 hatchery stocks (TUI, WCA, NCA, SCA99, and SCA00) and eight wild populations (IR, KR, SR, KI, YR, YzR, HC, and BH) of *C. ariakensis.* See Table 1 for sample abbreviations and source locations. Numbers on internal branches are bootstrap support values greater than 50% after 10,000 iterations.](Image)
**TABLE 4.**

Number and percentage of individuals assigned to various hatchery and wild reference samples using Rannala and Mountain's (1997) Bayesian method.

<table>
<thead>
<tr>
<th>Sample</th>
<th>Size</th>
<th>IR</th>
<th>KR</th>
<th>SR</th>
<th>KI</th>
<th>YR</th>
<th>YzR</th>
<th>HC</th>
<th>BH</th>
<th>TUI</th>
<th>WCA</th>
<th>NCA</th>
<th>SCA99</th>
<th>SCA00</th>
</tr>
</thead>
<tbody>
<tr>
<td>(A) Eight wild populations*</td>
<td>99</td>
<td>72 (72.7)</td>
<td>5 (5.1)</td>
<td>2 (2.0)</td>
<td>3 (3.0)</td>
<td>4 (4.0)</td>
<td>6 (6.1)</td>
<td>4 (4.0)</td>
<td>3 (3.0)</td>
<td>87</td>
<td>35</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>(B) Five hatchery populations*</td>
<td>48</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>TUI</td>
<td>10</td>
<td>0 (0.0)</td>
<td>0 (0.0)</td>
<td>0 (0.0)</td>
<td>0 (0.0)</td>
<td>0 (0.0)</td>
<td>0 (0.0)</td>
<td>1 (1.0)</td>
<td>1 (1.0)</td>
<td>20 (90.0)</td>
<td>35 (50.7)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>WCA</td>
<td>50</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
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<td></td>
<td></td>
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<td></td>
<td></td>
</tr>
<tr>
<td>NCA</td>
<td>50</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>SCA99</td>
<td>50</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>SCA00</td>
<td>47</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
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<td></td>
<td></td>
<td></td>
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<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>(C) Seven putatively unknown samples</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>IR05a</td>
<td>34 (68.0)</td>
<td>3 (6.0)</td>
<td>1 (2.0)</td>
<td>0 (0.0)</td>
<td>3 (6.0)</td>
<td>4 (8.0)</td>
<td>0 (0.0)</td>
<td>4 (8.0)</td>
<td>0 (0.0)</td>
<td>0 (0.0)</td>
<td>0 (0.0)</td>
<td>1 (2.0)</td>
<td>0 (0.0)</td>
<td></td>
</tr>
<tr>
<td>YR05a</td>
<td>36</td>
<td>0 (0.0)</td>
<td>1 (2.8)</td>
<td>0 (0.0)</td>
<td>2 (5.6)</td>
<td>23 (63.9)</td>
<td>8 (22.2)</td>
<td>1 (2.8)</td>
<td>1 (2.8)</td>
<td>0 (0.0)</td>
<td>0 (0.0)</td>
<td>0 (0.0)</td>
<td>0 (0.0)</td>
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</tr>
<tr>
<td>TUIa</td>
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<td>0 (0.0)</td>
<td>0 (0.0)</td>
<td>0 (0.0)</td>
<td>0 (0.0)</td>
<td>0 (0.0)</td>
<td>0 (0.0)</td>
<td>0 (0.0)</td>
<td>9 (90.0)</td>
<td>1 (10.0)</td>
<td>0 (0.0)</td>
<td>0 (0.0)</td>
<td>0 (0.0)</td>
</tr>
<tr>
<td>WCAa</td>
<td>10</td>
<td>0 (0.0)</td>
<td>0 (0.0)</td>
<td>0 (0.0)</td>
<td>0 (0.0)</td>
<td>0 (0.0)</td>
<td>0 (0.0)</td>
<td>0 (0.0)</td>
<td>0 (0.0)</td>
<td>0 (0.0)</td>
<td>9 (90.0)</td>
<td>1 (10.0)</td>
<td>0 (0.0)</td>
<td>0 (0.0)</td>
</tr>
<tr>
<td>NCAa</td>
<td>10</td>
<td>0 (0.0)</td>
<td>0 (0.0)</td>
<td>0 (0.0)</td>
<td>0 (0.0)</td>
<td>0 (0.0)</td>
<td>0 (0.0)</td>
<td>0 (0.0)</td>
<td>0 (0.0)</td>
<td>0 (0.0)</td>
<td>0 (0.0)</td>
<td>7 (70.0)</td>
<td>0 (0.0)</td>
<td>0 (0.0)</td>
</tr>
<tr>
<td>SCA99a</td>
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<td>0 (0.0)</td>
<td>0 (0.0)</td>
<td>0 (0.0)</td>
<td>0 (0.0)</td>
<td>0 (0.0)</td>
<td>0 (0.0)</td>
<td>0 (0.0)</td>
<td>0 (0.0)</td>
<td>0 (0.0)</td>
<td>0 (0.0)</td>
<td>9 (90.0)</td>
<td>0 (0.0)</td>
<td></td>
</tr>
<tr>
<td>SCA00a</td>
<td>10</td>
<td>0 (0.0)</td>
<td>0 (0.0)</td>
<td>0 (0.0)</td>
<td>0 (0.0)</td>
<td>0 (0.0)</td>
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<td>0 (0.0)</td>
<td>0 (0.0)</td>
<td>0 (0.0)</td>
<td>0 (0.0)</td>
<td>9 (90.0)</td>
<td>0 (0.0)</td>
<td></td>
</tr>
</tbody>
</table>

* The eight wild populations were from Xiao et al. (2010).

See Table 1 for sample abbreviations. Numbers in bold type indicate the number of oysters that were correctly classified to sample of origin.

Marine bivalves, positive correlations between multilocus heterozygosity and fitness-related traits were often observed in highly inbred families and populations of bivalves (Gaffney et al. 1990, Hedgecock et al. 1995, McGoldrick & Hedgecock 1997, Bierne et al. 1998, David 1998, Naciri-Graven et al. 2000, Launey & Hedgecock 2001, Hedgecock et al. 2007). Reduction in heterozygosity, although undetectable in the first several generations of inbreeding (Hedgecock & Sly 1990), could become significant after continued use of a small numbers of individuals for spawning, which are drawn from stocks that are already showing reduced allelic diversity. Therefore, successive introduction of broodstock from wild populations is recommended to enrich and maintain healthy genetic pools in existing hatchery stocks, especially for those stocks isolated from their source for the longest times (TUI and WCA). Second, given the high genetic differentiation among the hatchery stocks derived from different source populations, there might be phenotypic divergence among stocks. As the practical basis of selective breeding, phenotypic differences are often intentionally selected to produce broodstock with specific traits; however, this process can be unintentionally associated with a decrease in genetic diversity, and particularly in allelic diversity (Yu & Guo 2005, Carlsson et al. 2006). Third, inadvertent artificial selection pressure resulting from time and energy constraints in the laboratory or hatchery has been shown to cause trait differences from what is observed in wild animals, and to reduce variance in growth and development of domesticated oysters. For example, Taris et al. (2006) reported that by culling C. gigas larvae in early stages, the stocks resulted in individuals that were an average of 10% larger and had a 12% shorter time to settlement than control groups, and the variance in the parameter means was reduced by 30%–40% and 55%, respectively. It is still unclear whether the genetic shifts in the C. ariakensis hatchery stocks compared with their wild source populations is linked to any changes in growth performance, early recruitment, or development, because the results of side-by-side performance trials comparing within and among hatchery stocks and wild populations have not been reported, and there is little information on the basic biology of C. ariakensis in its native region. Differences in larval settlement and swimming, however, were observed among different strains of C. ariakensis (Luckenbach 2004, Tamburri et al. 2008). Numerous comparative studies between C. ariakensis and C. virginica on biological traits such as growth, early development, and disease tolerance were conducted using stocks of C. ariakensis derived from the so-called “Oregon Strain” from the west coast of the United States (Calvo et al. 2001, Hudson et al. 2005, Kingsley-Smith & Luckenbach 2008, Paynter et al. 2008), which correspond to the TUI and WCA stocks used in this study. These stocks showed the greatest genetic bottleneck effects and genetic drift from their natural source populations and the other hatchery stocks. Therefore, interpretations of comparisons among studies conducted in the United States during the past decade might be compromised as a result of the use of stocks that might differ from each other and...
from wild populations not only genetically, but also in performance and fitness parameters.

**Genetic Tracking**

Assignment tests based on an individual’s genotypic profile have been widely used to detect immigrants, identify hybrids, trace the origins of animals and plants, and detect dispersal patterns (Paetkau et al. 1997, Maudet et al. 2002, Castric & Bernatchez 2003, Manel et al. 2005, Vercaemert et al. 2006). Although an introduction of fertile *C. ariakensis* oysters to Chesapeake Bay was not approved, accidental release or intentional, illegal introduction of reproductively capable *C. ariakensis* has been a concern (Simberloff 2005). Some loose triploid *C. ariakensis* have been found in the waters of North Carolina and Chesapeake Bay (K. S. Reece unpubl. data), although biosecurity regulations for the EIS trials required that all *C. ariakensis* animals be contained during, and retrieved at the conclusion of, the scientific studies. Therefore, the ability to trace such introductions of *C. ariakensis* could be important for controlling these nonnative oysters.

In the current study, domesticated oysters could be tracked back to their specific hatchery stock origins with very high accuracy (≥70%), and most of the observed “incorrect assignments” were assigned to stocks derived from the same source population or to the source population itself. The ability to assign wild oysters accurately back to their specific source population, however, was rather low to moderate (20%–73%), probably as a result of reduced genetic differentiation among these natural populations compared with the relatively high differentiation among the hatchery stocks. However, in an analysis including only the larger sample sizes (i.e., excluding the Korean populations with samples sizes, n ≤ 33), more than 70% of the wild animals in this study were assigned either to their specific source population or to that from a geographically proximal location. This is not surprising given a genetic pattern of isolation by distance observed in the wild populations (Xiao et al. 2010). Because the probability of correct assignments largely depends on population genetic differentiations (Cornuet et al. 1999, Manel et al. 2005), relatively smaller genetic differentiation and higher gene flow among populations with shorter geographic distances, compared with populations farther apart, probably resulted in a relatively high number of individuals being misassigned to a population geographically proximate to their sampled populations. It has been reported that a 100% correct assignment could be achieved by scoring 10 microsatellite loci on 30–50 individuals from each of 10 populations with $F_{ST}$ values around 0.1 (Cornuet et al. 1999), which is in the range observed among the hatchery stocks in the current study ($\theta_{ST} = 0.132$). However, for those populations with $F_{ST}$ values approximately 10-fold lower, (e.g., $\approx 0.01$, comparable with the $\theta_{ST}$ value of 0.020 that we observed among the 8 natural populations), the percentage of correct assignments seldom reached 50%, even using 20 loci and 90 individuals per population (Cornuet et al. 1999). Therefore, the low sample sizes of some wild populations in this study, particularly the Korean samples, probably affected the accuracy of these assignment tests. Overall, assignment test results suggest that these microsatellite markers are very powerful for genetic identification of domesticated stocks, and that bolstering the samples sizes and adding more markers could further improve the utility of these markers for identifying animals from wild populations.

**NOTE**

1. Global $\theta_{ST}$ was 0.018 among 16 wild *C. ariakensis* samples originally analyzed. The 16 wild samples were then grouped into eight genetically differentiated populations based on their genetic relationship and after grouping the global $\theta_{ST}$ was 0.020 (Xiao et al. 2010).

**ACKNOWLEDGMENTS**

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**LITERATURE CITED**


