



NOAA CHESAPEAKE BAY OFFICE Non-native Oyster Research

Research
Topic:

*Understanding
Crassostrea
ariakensis within
its native range
in Asia*



Quarterly Review
Fall 2006



Background

Decline in abundance of the native oyster, *Crassostrea virginica*, in the Chesapeake Bay has led to the collapse of a formerly productive fishery and the loss of significant ecological services. Two oyster diseases, MSX and Dermo, have contributed at least in part to the decline, and continue to challenge oyster restoration efforts. In response to this situation the State of Maryland and Commonwealth of Virginia have proposed to intentionally introduce a non-native oyster species, *Crassostrea ariakensis*, which has greater resistance to the pathogens responsible for MSX and Dermo. Considerable controversy exists over the proposed course of action and many questions remain about the implications of such an introduction.

In 2003 the U.S. Congress authorized the Army Corps of Engineers to prepare an Environmental Impact Statement (EIS) to examine both the risks and benefits of introducing this species to the Chesapeake Bay. The EIS is being conducted by the Corps as the lead federal agency, with the Maryland Department of Natural Resources (MDNR) and the Virginia Marine Resources Commission (VMRC) serving as lead state agencies. The U.S. Environmental Protection Agency (EPA), National Oceanic and Atmospheric Administration (NOAA), and Fish & Wildlife Service (FWS) are cooperating agencies on the EIS.

In 2004 the NOAA Chesapeake Bay Office (NCBO) initiated a 3-year Non-native Oyster Research program funded at \$2M annually to obtain the scientific information needed to evaluate the proposed Asian oyster introduction. The program is aimed at research priorities recently identified by the National Research Council (NRC) and the Scientific and Technical Advisory Committee of the Chesapeake Bay Program (STAC), as well as guidance from the International Code of Practice on the Introductions and Transfers of Marine Organisms.

Research findings are reviewed quarterly at meetings or web conferences sponsored by NCBO and hosted by the Chesapeake Research Consortium. Invitees include scientists conducting research relevant to the EIS, representatives from federal and state agencies, and other interested management groups. These quarterly review sessions are designed to facilitate timely discussions of research results among scientists and managers, and speed the transfer of information to the EIS evaluation process. It must be emphasized that the findings of ongoing research are preliminary. Additional time will be required for the projects to be completed, and the results to be peer reviewed.

Summary reports of all Quarterly Reviews and additional information on NOAA's Non-native Oyster Research initiative are available at <http://chesapeakebay.noaa.gov/>.

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| Spring 2005 | Overview of research topics: Taxonomy, genetics, disease, human health, ecology, interspecific interactions, ecosystem services and functions |
| Summer 2005 | Aquaculture options: Biological and economic factors affecting aquaculture production of native and non-native oysters in the mid-Atlantic |
| Fall 2005 | Potential for <i>Crassostrea ariakensis</i> - <i>C. virginica</i> interactions: Larval substrate selection, post-settlement competition, and fertilization interference |
| Winter 2006 | Evaluating human health risks: Uptake, depuration, and post-harvest levels of waterborne human pathogens in <i>Crassostrea ariakensis</i> compared with <i>C. virginica</i> . |
| Spring 2006 | Special session on <i>Crassostrea ariakensis</i> at the 98th Annual National Shellfisheries Association meeting |
| Summer 2006 | Comparative growth and mortality of <i>Crassostrea ariakensis</i> and <i>C. virginica</i> : Providing additional data for the oyster demographic model |
| Fall 2006 | Understanding <i>Crassostrea ariakensis</i> within its native range in Asia |

Understanding *Crassostrea ariakensis* within its native range in Asia

Why is this research important for the EIS?

The International Council for Exploration of the Sea (ICES) 2003 *Code of Practice on the Introductions and Transfers of Marine Organisms* includes recommendations for evaluating proposed introductions of non-native species. The United States is a signatory to this international Code of Practice, which calls for understanding the ecology, genetics, and diseases within the native range of a species before reaching a decision to introduce that species elsewhere. Also, the 2004 STAC report, *Identifying and Prioritizing Research Required to Evaluate Ecological Risks and Benefits of Introducing Diploid *C. ariakensis* to Restore Oysters to Chesapeake Bay*, identified research on genetic and phenotypic variation among different strains of *C. ariakensis* as a high priority for the EIS.

Prior to recent genetic work, several oyster species in Asia were frequently misidentified as *C. ariakensis* – a reflection on the general state of taxonomic confusion for *Crassostrea* species identification in Asia. The ability to distinguish *C. ariakensis* from other oyster species is a necessary foundation for understanding many aspects of *C. ariakensis* biology such as its range, distribution, population structure, and ecology. Resolving the taxonomy of *C. ariakensis* is also necessary to determine how much of the existing scientific literature on “*C. ariakensis*” can be reliably utilized as representing this species as opposed to other species.

Crassostrea ariakensis first arrived in the U.S. when a small number of individuals were accidentally imported to Oregon with a shipment of *C. sikamea* and *C. gigas* seed from Japan around 1970. Broodstock of this “Oregon Strain” of *C. ariakensis* were brought to research hatcheries in New Jersey (Rutgers) and Virginia (VIMS) in the 1990s. Progeny from the Japan-Oregon shipment were the sole source of *C. ariakensis* broodstock in the U.S. until VIMS brought back *C. ariakensis* from a single location in northern China and another location in southern China in 1999 and 2000.

Due to the limited nature of the original gene pool and subsequent generations of hatchery propagation, genetic bottlenecks and reduced genetic diversity are major concerns currently under investigation. The genetic composition of the *C. ariakensis* broodstock that would be propagated by hatcheries to implement the proposed introduction may be a significant factor in determining the long-term success of this species in novel environments outside of its native range where *C. ariakensis* evolved. The “Oregon Strain” proposed for introduction may or may not be the one best suited for introduction into the Chesapeake Bay. For these reasons, it is important to understand the population genetic structure of *C. ariakensis* wild populations and relative levels of genetic diversity between the wild and hatchery stocks.

Finally, information on whether *C. ariakensis* co-exists with other oyster species, what its environmental tolerances and growth forms are, and how it is cultivated is necessary in order to better understand the potential risks and benefits of a possible introduction into the Chesapeake Bay. Research presented at this Quarterly Review has made great progress towards answering many of these important questions.

Presentations:

Jan Cordes and Kim Reece (VIMS) – Understanding *C. ariakensis* within its native range in Asia: Taxonomy, genetic variation, and population genetic structure (PIs: Cordes, Xiao, Stubbs, Reece)

Ximing Guo (Rutgers) – Distribution and abundance of *C. ariakensis* in China (PIs: Guo, Wan, Zhang, Liu, Qian, Wang)

Heather Harwell (VIMS) – *C. ariakensis* in the Seomjin River, South Korea (PIs: Harwell, Allen)

Some preliminary findings:

Identification of C. ariakensis in its Native Range

- At least 7 different *Crassostrea* species are frequently misidentified as *C. ariakensis* within its native range in Asia.
- In China alone – the apparent center of *C. ariakensis* distribution in Asia – *C. ariakensis* is often confused with 3 other *Crassostrea* species. There are over 18 oyster species in China, several of which remain unidentified at this time.
- *Crassostrea ariakensis* has commonly been reported as *C. rivularis* in China, where two forms (red and white) are recognized on the basis of their meat color. Recent molecular data and phylogenetic analysis show that the red meat form of *C. rivularis* is the true *C. ariakensis*, while the white meat form is actually *C. hongkongensis*.
- A genetic identification key has now been developed for Indo-Pacific *Crassostrea* species, and significant progress has been made in reclassifying many oyster species that were previously misidentified based on morphology.
- In light of new knowledge from genetic studies on Asian oyster species identification, all previously published information on *C. ariakensis* (e.g., range, life history, ecology, environmental tolerances) should be viewed with caution given the likelihood of misidentification.
- It is important that proper species identification be performed for any live oysters brought into the U.S., whether for resale, aquaculture, or introduction.

Genetic Variation in Wild and Hatchery Stocks

- Microsatellite markers have shown promise as a tool for characterizing the genetic structure of wild *C. ariakensis* populations, evaluating genetic variation in hatchery stocks, and assigning hatchery individuals back to their source populations in the wild. These markers could also be used to monitor the success of, and genetically track, any *C. ariakensis* introductions in the U.S.
- There is genetic structure among wild *C. ariakensis* populations across their native range in Asia. The magnitude of genetic differences indicates little or no gene flow among populations, suggesting the potential for local adaptation to the specific suite

of environmental conditions experienced by each population. *Crassostrea ariakensis* derived from locally adapted populations in Asia may differ in their performance and utility for either introduction or aquaculture in Chesapeake Bay.

- Hatchery stocks of *C. ariakensis* in the U.S. show evidence of reduced genetic variation relative to wild populations in Asia. Reduction in genetic diversity initially occurs when a small number of individuals are collected from the wild, and genetic diversity is further reduced in subsequent generations when relatively few individuals typically contribute to successful reproduction during the hatchery spawning process. Thus, hatchery stocks show reduced genetic variation even after a single generation in the hatchery setting, and evidence of accelerated genetic drift from their source populations in the wild.

Range and Environmental Tolerances

- Occurrence of *C. ariakensis* has now been confirmed from southern Japan, South Korea, and throughout coastal China, spanning latitudes from 41° N to 21° N. The corresponding latitudes in North America are from Connecticut to the Yucatan Peninsula – roughly the range of *C. virginica*. This broad latitudinal distribution may be an indication that *C. ariakensis* has wide temperature tolerance, and could spread across a range similar to that of *C. virginica* if introduced into the Chesapeake Bay.
- Although *C. ariakensis* has a broad geographic range, its distribution within that range is patchy. The species was found at only 12 of 70 sampled sites in China, and in low abundances at most sites. Major populations were found only in or near major river systems such as the Yellow, Yangtze, and Jiulong Rivers. Despite the input of fresh water from these river systems, sites where *C. ariakensis* are found typically have intermediately salinities (20-28 ppt). The patchy, river-dependent distribution of *C. ariakensis* may indicate a requirement for specific salinity regimes provided by large river systems for successful recruitment.
- In China *C. ariakensis* is limited to subtidal habitats below the low-tide line, and does not occur in the intertidal zone or in open shore areas away from rivers. In the Seomjin River in Korea *C. ariakensis* inhabits subtidal and lower intertidal areas. These observations from China and Korea parallel the results of recent experimental studies conducted with *C. ariakensis* in the Chesapeake Bay region (reported in the Summer 2006 Quarterly Review), reinforcing the conclusion that this species does not thrive in the intertidal zone as does *C. virginica*.

Growth Forms and Co-occurrence with Other Oyster Species

- There is clear evidence from sites studied in China and Korea that *C. ariakensis* is a reef-builder. *C. ariakensis* is also sometimes found as individual oysters not associated with a reef.
- Throughout its range in China, *C. ariakensis* co-occurs with other oyster species in mixed species assemblages. In the north, it is the dominant oyster in reefs with *C.*

gigas. In the south, it coexists in reefs with *C. sikamea*, *C. hongkongensis*, and *C. angulata*, but is not the dominant species in these reefs.

- Large *C. ariakensis* are often found on the bottom layers of mixed species reefs, while smaller oysters of other species comprise the upper layers. It is not known why small size classes of *C. ariakensis* are so rare in these reefs, but it could be due to environmental factors such as changes in the local salinity regime that may be affecting recruitment.

Aquaculture of C. ariakensis in Asia

- Farmers in China actively select against the red meat of *C. ariakensis* in favor of the white meat of *C. hongkongensis*, which grows faster, tastes better, and has a higher market price. *C. hongkongensis* is the most commonly grown oyster in China, followed by *C. angulata* and *C. gigas*.
- In Korea, *C. gigas* is the predominant species used in oyster aquaculture; however, commercial harvest of *C. ariakensis* in the Seomjin River is increasing and interest in aquaculture of *C. ariakensis* has been growing.
- *C. ariakensis* populations in China are actually in decline due to intense selection against this species in commercial aquaculture, pollution, and habitat destruction. There is a growing awareness of the need to protect *C. ariakensis* in its native range.

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