

Quantifying and Minimizing the Risk that Hatchery Enhancement Will Reduce Genetic Diversity of White Seabass

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Background

With many of the world's fisheries in decline, some fishery biologists have begun actively pursuing the idea of restocking the sea with hatchery-born fish. Some of the most aggressive of these programs are in Japan, where literally trillions of cultured scallops and hundreds of millions of cultured shrimp are routinely set free in coastal waters.

There is also a growing national interest in using hatcheries to offset effects of overfishing, dams, clear-cutting, water pollution, wetlands destruction and "dead zones." There are, for example, pilot studies and ongoing hatchery-enhancement projects for red drum and red snapper in the Gulf of Mexico, sturgeon and blue crab in the Chesapeake Bay, Atlantic cod in the Northeast, flounder in the Southeast and white seabass in California.

White Seabass Stocking Program

White seabass (*Atractoscion nobilis*) are a popular sport fish (also fished commercially) whose numbers have declined dramatically since the early 1950s.

Prompted by the stock's troubles, the California Department of Fish and Game established the Ocean Resources Enhancement and Hatchery Program in the 1980s. Since 1986, Hubbs-SeaWorld Research Institute's seabass hatchery in Carlsbad, California has released about 744,000 fish.

Issue

While stocking can potentially help rebuild stocks, it may also create new challenges. One such challenge is "swamping." Swamping occurs when released fish "swamp" or dilute the genetic diversity of wild



When a single female can have a million babies, the sea can be stocked with the offspring of a very few individuals, but at a cost to genetic diversity. Photo: Mark Drawbridge, ©Hubbs-SeaWorld Research Institute

fish. Loss of genetic diversity invites a host of potentially serious problems, including reduced reproductive success, increased vulnerability to disease and higher mortality rates.

Sea Grant Project

The goal of this project is to assess the genetic ramifications of California's white seabass stocking program and to develop a set of protocols for helping the hatchery monitor and minimize risks to biodiversity. Dennis Hedgecock, a professor of genetics at the University of Southern California, is leading the three-year project with Sea Grant trainee Katharine Coykendall. The project is part of her doctoral thesis.

The project's cornerstone is quantifying the "effective sizes" of the released and wild fish. Roughly speaking, effective size is the genetic size of a population. It is of fundamental importance because it gives an immediate estimate of the rate of inbreeding within a population: the rate of inbreeding is inversely proportional to a population's effective size. Put another way, the larger a population's effective size, the slower the loss of genetic diversity within that population. Cast in terms of the seabass program, estimates of effective

size will let biologists evaluate the pace at which stocking erodes—or enhances—genetic diversity.

For the project, scientists are looking at changes in the effective size of the seabass population on two time scales: historical and present. To determine the historical effective size of the female population, the scientists mapped the frequency of various mitochondrial DNA (mtDNA) polymorphisms in wild adults.

To calculate the present effective size, Coykendall is analyzing changes in the frequencies of nuclear DNA micro-satellites. This will provide an estimate of genetic drift over recent time from which the population's modern-day effective size can be computed.

Findings

The mtDNA analyses showed that there are a few sequences that occur relatively frequently in the seabass population and an excess of sequences that occur very infrequently. The scientists interpret the pattern as suggesting that long ago the effective size of the seabass population was smaller than it is today. They believe the population grew for several hundreds of thou-

sands of years, reaching a modern-day effective size for females in the population of six million.

From the preliminary nuclear DNA micro-satellite analyses of hatchery fish, it seems that only a few brood females and males produce offspring during a single spawn, suggesting the rate of inbreeding among hatchery fish is occurring faster than anticipated. Released fish, however, are the product of many spawns not just one. Hence, it is possible that different females and males produce offspring during different spawns. Hedgecock and Coykendall are currently examining the degree to which this is true by tracing the parentage of 100,000 fish released in 2001. These fish were the product of 46 spawns.

Impacts

The project will result in a predictive model for evaluating the genetic impact of stocking and thus provide a framework for greater resource conservation. Within this framework, the findings will identify practical protocols for minimizing risks to biodiversity. The methods developed in this project will also have

direct applications to other stocking programs.

Based on the scientists' preliminary findings, hatcheries need to monitor spawning to identify which brood members are producing offspring. "The most important thing for a hatchery is to even out contributions from brood stock," Hedgecock explained. "If one female or male repeatedly spawns, you might want to reduce its contribution."

Collaborating Institutions

California Department of Fish and Game
Hubbs-SeaWorld Fish Hatchery,
Carlsbad, California

Trainee

Katharine Coykendall

Presentations

Coykendall, D.K. and D. Hedgecock.

The long-term effective size of the white seabass *Atractoscion nobilis*. Annual meeting of the Society for Conservation Biology, New Orleans, Louisiana, February 1, 2004.

Coykendall, D.K. and D. Hedgecock.

The effect of hatchery supplementation on the genetics of white seabass *Atractoscion nobilis*. Aquaculture 2004, Honolulu, Hawaii, March 4, 2004.



Geneticist Dennis Hedgecock. Photo: Eva Emerson, College of Letters, Arts and Sciences, USC

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