Sea Grant
California

Saving San Francisco Bay-Delta native fishes: hatchery management and reintroduction strategies

Katie Fisch, Delta Science Fellow

BACKGROUND

Several native fish species in the San Francisco Bay-Delta and Central Valley have experienced dramatic population declines and could realistically go extinct in the wild.

As a conservation measure, scientists have proposed establishing refugial populations – modern Noah's Arks – that could help rebuild or re-establish populations should their numbers continue to slide.

The longfin smelt, Sacramento splittail, Sacramento perch, green sturgeon, delta smelt, Chinook salmon and steelhead trout are among the region's imperiled species that could potentially benefit from population management techniques used at zoos.
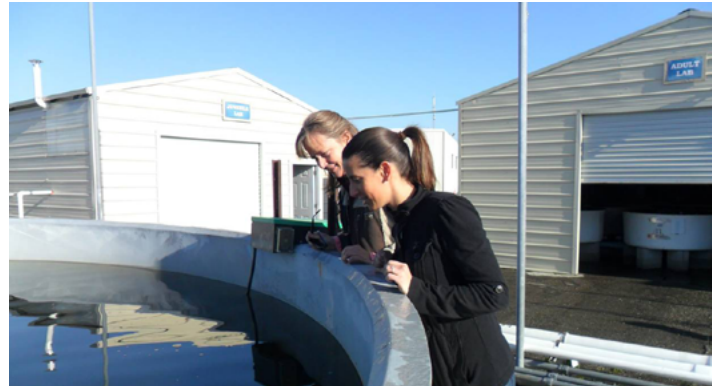
Researcher Katie Fisch explored strategies for protecting the wild gene pools of endangered, native fishes in the San Francisco Bay-Delta and Central Valley.
PHOTO: UC Davis

PROJECT

The overarching purpose of this project is to identify hatchery management strategies for minimizing the genetic impacts of artificial propagation on wild fish.

To this end, the fellow has been surveying and reviewing management practices currently in use at salmon and trout hatcheries along the West Coast and in Idaho.

She has been documenting:

- Options for managing the genetics of fish at conservation hatcheries
- Approaches currently in use, and
- Individual hatcheries goals

Fisch is also developing a computer simulation model that can be "tuned" to the life history characteristics of any species of interest, by inputting life history parameters such as fecundity and lifespan.

The model simulates the effects of different mating strategies on the genetics of hatchery, wild and supplemented fish populations. The relative performances of the different mating strategies are then ranked according to genetic diversity parameters at different points in time, measured in generations.

The output will be used to evaluate the effects of different hatchery management plans on species of management concern in the Bay-Delta and Central Valley.

The delta smelt is one of several native fish species in the San Francisco Bay-Delta that scientists say could go extinct. PHOTO: California Dept. of Water Resources

PROGRESS TO DATE

Based on survey responses from 36 hatchery programs, the currently available options for managing the genetics of fish include:

- Factorial mating – a female is mated to several males; and a male is mated to several females, basically at random.

- Equalizing family size – the number of offspring from each pair of breeding fish is equalized.

- Reconstructing pedigrees – a multi-generational family tree is constructed for each fish, and only unrelated individuals are mated.

- Estimating molecular relatedness – in the absence of information on who was mated with whom, researchers look at the genetics of each fish to estimate relatedness among individuals (e.g., are two fish siblings or cousins) and then avoid mating closely related pairs.

- Selecting minimal or mean kinship – pedigrees are used to identify relatedness among individuals and only the least related individuals, with the most desired genes, are mated. This is the strategy employed often at zoos for species such as the giant panda.

Most of the hatcheries that responded to the fellow's questionnaire use random factorial mating to breed fish, which basically means that fish are spawned at random, the fellow explained. A few hatcheries use molecular relatedness estimation, and one uses a modified version of mean kinship selection.

Even though the majority of hatcheries are not incorporating molecular data into their spawning and release programs, hatchery managers widely recognize the value of conserving wild genetics, she said. The reasons for random mating are mostly logistical, somewhat cultural, and somewhat knowledge-based.

When finalized, the computer model mentioned previously will simulate a hatchery population managed in each of the five available genetic management techniques. The simulation output will provide estimates of the effects of each breeding strategy, at the end of each generation, on genetic diversity, levels of inbreeding and effective population size for hatchery fish and wild fish supplemented with hatchery releases. These results will then be analyzed to determine, for example, the value of minimal kinship selection breeding methods versus less intensive management programs. The analysis will ultimately be compiled into a guide for hatchery managers that will let them weigh different options for conserving wild fish genetics.

PRESENTATIONS

Fisch, K., C. Kozfkay, J. Ivy, O. Ryder, & R. Waples. (2013) Genetic Management and Monitoring of Conservation Hatcheries: Part I. Hatcheries and Management of Aquatic Resources Symposium, American Fisheries Society Annual Meeting, Little Rock, Ark.

Fisch, K., J. Ivy, O. Ryder, & R. Waples. (2012) Saving San Francisco Bay-Delta native fishes: Hatchery management and reintroduction strategy modeling. Bay-Delta Science Conference, Sacramento, Calif.

PUBLICATION

Fisch, K., C. Kozfkay, J. Ivy, O. Ryder, & R. Waples. In Review. Fish hatchery genetic management techniques: Lessons from zoo population management. Submitted to Journal of Heredity in July 2013.

RESEARCH MENTORS
Oliver Ryder, UC San Diego/San Diego Zoo Institute for Conservation Research
Robin Waples, NOAA Northwest Fisheries Science Center

COMMUNITY MENTORS
Ted Sommer, California Department of Water Resources
Louise Conrad, California Department of Water Resources

CONTACT
Kathleen Fisch, Ph.D.
Research Associate
The Scripps Research Institute
858-784-2112
kmfisch@ucdavis.edu

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