

## **Description**

Data, pedigrees, reports and manuscripts herein are from an investigation conducted with coho salmon of the Umpqua River in southern Oregon from 2001-2009. They relate to a study investigating several areas of uncertainty about the use of salmon hatcheries to increase the abundance of wild populations. At that time, there was considerable interest in using hatcheries to speed the recovery of wild populations. However the value of such an approach was untested. Substantial literature indicated that hatchery programs may pose high risks to wild populations, rather than aid them (see the following reviews: Hindar et al 1991, Waples 1991, Waples 1999, and Lichatowich 1999 and literature cited therein). If these risks were real, hatcheries may interfere with recovery, rather than speed it up. Until the early 2000s, analytical methods to explore the critical questions and risks associated with hatchery programs were unavailable because we were not able to track lineages in streams once hatchery and wild fish were allowed to spawn together. New molecular genetics methods, however, allowed the use of DNA fingerprints to pedigree entire populations under some circumstances and develop lineages that continue for multiple generations under natural spawning conditions.

The objective of the study was to conduct an experimental supplementation project for coho salmon in Calapooya Creek, a tributary of the Umpqua River, using the following hatchery scenarios:

- a. Rock Creek hatchery stock released as smolts (a "conventional hatchery program");
- b. Rock Creek hatchery stock released as unfed fry (a low-intervention hatchery program);
- c. First-generation wild-type hatchery stock released as smolts; and
- d. First-generation wild-type hatchery stock released as unfed fry.

Success and genetic implications of these alternative hatchery scenarios were evaluated using DNA pedigree reconstruction for parents over three consecutive years (2001,2&3), their returns and subsequent mating success as inferred from grand-offspring returns through 2009.

Primary tasks of the project were to assess:

Task 1. What is the relative success of using a first generation, wild-type broodstock in a supplementation program compared to a broodstock that has been captive for multiple generations?

Task 2. What is the relative success of unfed fry releases compared to smolt releases in producing returning adults?

Task 3. What is the reproductive success in the wild of adult fish from the following treatments:

- a. First-generation hatchery fish from unfed fry releases;
- b. First-generation hatchery fish from smolt releases;
- c. Multi-generation hatchery fish from unfed fry releases;
- d. Multi-generation hatchery fish from smolt releases; and
- e. Wild fish.

Task 4: How does the supplementation program modify the effective population size of the population in Calapooya Creek (termed the "Ryman-Laikre Effect" (Ryman and Laikre 1991, Ryman et al 1995)

Task 5: What is the level of inbreeding that results from the supplementation program?

Task 6: What is the incidence of natural crossing between adults from the different treatment groups while on the natural spawning grounds and the consequences of mate choice to the relative production of offspring by individuals;

Task 7: What differences in reproductive success occur by treatment by age (males), by gender, by adult run time, and by adult body size (length)?

Task 8: Does the size of the naturally produced population increase due to successful natural reproduction by hatchery fish? Does the contribution to this increase vary by treatment group?

Data and findings archived herein are the outcome of these endeavors.

## **Methodology**

### Sampling

Oregon Department of Fish and Wildlife (ODFW) biologists collected adult wild and hatchery-reared coho returning to the Umpqua River in 2001, 2002, and 2003 to create single pair crosses. Offspring were reared in the hatchery and released into Calapooya Creek, a tributary of the Umpqua River, as unfed fry and smolts. ODFW biologists monitored a fish trap at the base of Nonpareil Dam in Calapooya Creek from 2002 – 2009 and sampled all returning adults. After a fin clip (for genetic identification), fork length, and run data were taken, adult fish were passed above the dam to spawn in the river.

#### Parentage Analysis

DNA was extracted using Qiagen DNA extraction kits and amplified at ten putatively neutral microsatellites (*OTS519*, *OTS520*, *ONE111*, *P53*, *OTS3*, *ONE $\mu$ 2*, *OCL8*, *OTS215*, *ONE $\mu$ 13*, *OMY1011*) using PCR. Amplicons were visualized with an ABI 3730xl Prism (Applied Biosystems) using fluorescently labeled forward primers and analyzed using GeneMapper Software v3.7 (Applied Biosystems) (see Moyer *et al.* 2007 for further details). Parentage analysis was conducted with the software PAPA 2.0 and PASOS 1.0, which use a maximum likelihood allocation approach and a combination of a maximum likelihood allocation approach and exclusion respectively (see Thériault *et al.* 2010,2011 for further details).

#### Relevant Theses, Publications, and Reports

- Moyer, G. R., M. S. Blouin, and M. A. Banks. 2007. The influence of family-correlated survival on *Nb/N* for progeny from integrated multi- and single-generation hatchery stocks of coho salmon (*Oncorhynchus kisutch*). *Canadian Journal of Fisheries and Aquatic Science*. 64: 1258-1265.
- Johnson, M.A., and M. A. Banks. 2008. Genetic structure, migration and patterns of allelic richness among coho salmon (*Oncorhynchus kisutch*) populations of the Oregon Coast. *Canadian Journal of Fisheries and Aquatic Science* 75(7): 1274-1285.
- Marc A. Johnson. 2009. Patterns of Natural Selection and demography in Coastal Oregon Coho salmon (*Oncorhynchus kisutch*) Populations: Evidence from Neutral and Olfactory receptor Gene-linked Markers. PhD thesis. <http://ir.library.oregonstate.edu/jspui/handle/1957/11595>
- Johnson, M.A. and M.A. Banks. 2009. Interlocus variance of *Fst* provides evidence for directional selection over an olfactory receptor gene in Coho salmon (*Oncorhynchus kisutch*) populations *Marine Genomics* 2(2):127-131.

- Thériault, V., G. R. Moyer, and M.A. Banks. 2010. Survival and life history characteristics among wild and hatchery coho salmon (*Oncorhynchus kisutch*) returns: how do unfed fry differ from smolt releases? *Canadian Journal of Fisheries and Aquatic Sciences*. 67:486-497.
- Thériault, V., G. R. Moyer, L.S. Jackson, M.S. Blouin, and M.A. Banks. 2011. Reduced reproductive success of hatchery coho salmon in the wild: insights into most likely mechanisms. *Molecular Ecology*. 20(9):1860–1869.
- Johnson M.A., and M.A. Banks. 2011. Sequence conservation among orthologous vomeronasal type 1 receptor-like (Ora) genes does not support the differential tuning hypothesis in Salmonidae. *Gene*. 485(1):16-21.
- Amelia C. Whitcomb 2012. Mate choice of wild spawning coho salmon (*Oncorhynchus kisutch*) in the Umpqua River, Oregon. MS thesis. <http://ir.library.oregonstate.edu/xmlui/handle/1957/35596?show=full>
- Banks M.A. (2013) OWEB Completion Report of OSU Component for Nonpareil Dam Adult Trap and Genetic Pedigree – contract 209-904. Oregon State University.

### **Comments**

Blanks for a field in data sheets are a result of an inability to calculate that field (typically because the field does not apply) or a lack of information.