

**NONPAREIL DAM ADULT TRAP AND
COHO GENETIC PEDIGREE PROJECT**

2006

FINAL

~~PROGRESS REPORT~~

FOR

NONPAREIL TRAP

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**OREGON WATERSHED ENHANCEMENT BOARD
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The last progress report was submitted to the Oregon Watershed Enhancement Board (OWEB) in August 2005. This progress report is an update to the August report and summarizes the activities that occurred from September – January 2006.

I. Project Background

The Nonpareil Dam and Adult Trap and Coho Genetic Pedigree Project was undertaken as a Conservation Hatchery Incentive Project (CHIP project) to study experimental supplementation of coho. The ongoing CHIP project is being conducted at Calapooya Creek (Figure 1) within the Umpqua watershed. Overall the project is composed of three phases to evaluate the effectiveness and impact of using hatchery coho to speed the recovery of wild coho populations. The basic hatchery scenarios being tested are the survival of: 1) hatchery progeny released as smolts; and 2) hatchery progeny released as unfed fry. The broodstock utilized for these hatchery scenarios included wild type (W x W) crosses and hatchery type (H x H) crosses. The project could therefore test: W x W progeny released as smolts, H x H progeny released as smolts; W x W progeny released as unfed fry and H x H progeny released as unfed fry. This project was started in 2001 and will continue to 2009 to follow three complete generations of coho salmon and their progeny replicated within three consecutive years. In partnership with Oregon State University (OSU), DNA fingerprinting is being used to form a genetic pedigree of the Calapooya coho population for multiple generations. This will provide direct evidence of the success or failure of hatchery supplementation to recover the coho population. The multi-generational genetic pedigree will also provide data on some of the risks to wild coho as predicted by genetic theory.

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II. Project Activities

Phase I

Phase I of the CHIP project involved annually capturing an adequate number of hatchery and wild coho to use for the parent generation for the study and the initial supplemental releases. The project used 100 pair each of W x W and H x H coho during three consecutive brood years (2001 – 2003). Genetic samples were taken from each pair of fish so their subsequent progeny could be genetically identified and linked back to the parent generation. Progeny from brood years 2001, 2002, and 2003 were released as unfed fry in 2002, 2003, and 2004. Smolts require one-year for rearing, thus they were released in 2003, 2004, and 2005.

Phase I was completed in April of 2005. The project successfully collected 100 pairs of both hatchery and wild-type coho to use for the H x H and W x W crosses each brood year. This provided enough brood to produce an adequate number of eggs each year to fulfill the smolt and unfed fry requirements of the study. The project released approximately 1.3 million unfed fry from 2002 - 2004 (~200,000 per year for both the hatchery-type and wild-type releases). Additionally the project released approximately 66,000 smolts from 2003 – 2005 (~10,000 each per year for both H x H and W x W-types) (Figure 1). OSU was able to genotype the genetic samples collected from the initial brood fish to discern hatchery versus wild backgrounds. Thus OSU can identify the parentage (H x H or W x W) of the progeny with 95 – 99% confidence.

Phase II

The CHIP program is currently in Phase II. This involves capturing adult and jack coho salmon as they return to the Calapooya Nonpareil trap. Coho progeny from Phase I are part of the first generation (F1) of the supplementation program. Genetic samples are collected from each returning coho. Pedigree analysis is then used to trace the F1 fish back to its parent generation as progeny from a H x H, W x W, or native wild cross. All smolts released as part of the supplementation portion of this study had their adipose fin (AD) removed and were maxillary clipped to allow visual identification of H x H or W x W crosses. The left maxillary (ADLM) was clipped for the hatchery-type stock while the right maxillary (ADRM) was clipped for the wild-type stock smolts. Pedigree analysis is still conducted on these fish to test survival and have parent genetic material for mapping the second generation (F2) of this project. Progeny released as unfed fry were not fin or maxillary clipped thus cannot be visually separated from returning native wild coho. Thus, genetic fingerprinting is used to identify the parentage of unmarked fish and have parent material for the F2 generation.

To date, the Nonpareil trap has been successfully operated from 2003 to the present to collect genetic samples from coho returning from brood year 2001 (jacks in 2003 and adults in 2004) and brood year 2002 (jacks in 2004 and adults in 2005). In spring 2005,

OSU successfully identified the parentage of the coho returning to the Nonpareil trap from the 1,311 samples collected in brood year 2004.

As part of Phase II, from September 2005 to January 17, 2005, the CHIP program has accomplished the following tasks.

Task 1. The first task undertaken this fall was annual maintenance and new modifications for the Nonpareil adult trap. Annual repairs included new dam boards for the ladder, repairing trap hinges, rocking the access road, and renting a porta-potty. Additionally the block-logs were installed above the ladder intake to reduce the amount of debris flowing into the trap.

Trap modifications including installing iron channel brackets across the top of the ladder so that 2" x 12" boards could be installed. This allowed the ladder to withstand an additional 12 inches of water during flood conditions. Installation included having the channel brackets and attachment plates created at a welding shop, then drilling screws into the concrete walls of the ladder to attach the brackets. Screws were secured with concrete binding glue. While the concrete work was being conducted, the overflow notch in the fish ladder was also repaired. During flood conditions this notch allows water to escape the fish ladder to reduce the probability of water flowing over the top of the trap.

Task 2. To have adequate field staff to operate the trap this year, the ODFW hired three seasonal Experimental Biological Aids (EBAs) and one Student Conservation Aid (SCA) intern. Additionally, an ODFW NRS 2 biologist helped oversee the field work and data entry of the project and was available to help at the trap during peak run times. Two vehicles were used by the ODFW CHIP staff. Annual field supplies such as vials, preservatives, labels, data sheets, fish nets, waders, and rain gear were also purchased.

Task 3. Trapping this year (brood year 2005) began at the Nonpareil trap in October and continued through January. The first coho was captured on 4 November. A total of 1,686 coho have been captured to date during 2005. The number of jacks captured is similar to 2004. There was an increase in the number of smolts captured and a smaller percentage of unmarked fish were captured in 2005 (Table 1).

Table 1. Coho captured at the Nonpareil Trap, Calapooya Creek.

Mark/Age	2002 No F1	2003 Only BY01 jacks return marked	2004 BY01 adult BY02 jack	2005 BY02 adult BY03 jack
Total Jacks*	62 (5.7%)	161 (19.5%)	131 (10%)	165 (9.7%)
ADLM		39 (24.2%)	213 (16.2%)	408 (24.2%)
ADRM		22 (13.7)	178 (13.6%)	343 (20.3%)
AD		4 (2.5%)	9 (0.69%)	7 (0.4%)
Poor fin clip			None	4 (0.2%)
Unmarked		96 (59.6)	911 (69.5%)	924 (54.8%)
Total Coho	1,093	824	1,311	1,686

*Jacks are included within mark categories to represent the total number of coho.

Phase III of the CHIP program will be completed after trapping at Nonpareil in 2006. Coho captured in 2006 will be the F1 adults from brood year 2003. The program will then move into Phase III.

Phase III

Since genetic material will be collected from all coho passing the trap from 2003 - 2006, the genetic pedigree can be continued to look at the F2 generation of Calapooya coho. As the F2 coho return from 2006 - 2009 the genetic pedigree of the fish can be tested to determine the success of H x H, W x W, Native x Native, H x W, H x Native, W x Native crosses. This will provide valuable management information for the ODFW regarding supplementation programs to aid coho recovery. The ODFW and OSU can also examine the following genetic risks that could occur if a substantial number of hatchery-based coho spawn:

- Risk 1) Population Bottleneck: This risk occurs when a small number of parents (those taken into a hatchery) produce a substantial proportion of the fish in the supplementation population (those left in the wild). Since they share so few parents, the hatchery fish in the supplementation population are more likely to be related to each other, thus increasing the incident of inbreeding.
- Risk 2) Increased Inbreeding: This risk occurs when only a small number of parents (those taken into the hatchery) produce a substantial proportion of the fish in the supplemented population. Since they share so few parents, the hatchery fish in the supplemented population are more likely to be related to each other, thus increasing the incidence of inbreeding.
- Risk 3) Increased Genetic Load: This risk results from the increased reproductive success and survival that occurs while fish are in the captive environment. Increase reproductive success and survival in captivity occurs because natural selection pressures are intensely relaxed which leads to an increase in the level of genetic load.
- Risk 4) Genetic Variation is Lost: When offspring population is smaller than its parent population genetic variation is lost. This is due to reproductive failure by some parents and the loss of the genetic material they carry. Additional random loss of genetic variation may occur when populations are very small.
- Risk 5) Accumulative Genetic Variation: If the hatchery program continues over multiple generations the impacts of the risks will accumulate in the wild populations due to the nature of the genetic mechanisms involved.

III. Conclusions

The CHIP project will provide valuable information on the use of supplementation programs. This project will evaluate the survival of supplementation fish released as smolts versus unfed fry, plus look at differences in the survival of F1 fish produced from hatchery-type and wild-type parent brood. Because these fish can be genetically followed through the F2 generation, survival rates can be tested to determine if supplementation programs contribute to the long-term survival of a population, or if F1 hatchery fish fail to contribute to future generations. This project will also provide valuable information on the potential risks of using hatchery fish to recovery native populations. Information on population bottlenecks, inbreeding, genetic load, and loss of genetic variation can be tested.

The ongoing CHIP project has successfully completed Phase I of the study and will complete Phase II after trapping in 2006. The long-term impacts of supplementation and genetic risks will be studied during Phase III of the study which is planned to continue through 2010.

Figure 1. Release sites for fry and smolts, 2002 - 2005

