

## Update Report

Period: 2/1/2014 - 1/31/2015

**Project: R/HCE-4 - Measuring what matters: linking life history traits and disease resistance with genomic variation in Chinook salmon conservation hatcheries**

### STUDENTS SUPPORTED

**Waters, Charles**, cwaters8@uw.edu, University of Washington, School of Aquatic and Fishery Sciences, status: cont, field of study: Genetics, advisor: Kerry Naish, degree type: PhD, degree date: 2016-06-01, degree completed this period: No  
Student Project Title:

Reducing Genetic Risks to Wild Populations: Evaluating the Effectiveness of Integrated Management in Captive Breeding Programs

Involvement with Sea Grant This Period:

Graduate student

Post-Graduation Plans: *none*

### CONFERENCES / PRESENTATIONS

Naish KA, Briec MSO, Drinan DP, Kodama M, Ostberg CO (2014) "An overview of our understanding on the location and frequency of recombination between homeologs in Pacific salmon ", "Homeolog Hell" workshop, American Genetics Association, Seattle, WA, June 30 - July 1., public/profession presentation, 30 attendees, 2014-06-30

c. Waters, C.D, J.J. Hard, M.S.O. Briec, D.E. Fast, K.I. Warheit, C.M. Knudsen, W.J. Bosch, K.A. Naish. "Managed gene flow reduces adaptation to captivity in supportive breeding programs: A multi-generational analysis of a Chinook salmon hatchery." Yakima Basin Science and Management Conference, Ellensburg, Washington, June 18-19, 2014., public/profession presentation, 150 attendees, 2014-06-18

b. Waters, C.D, J.J. Hard, M.S.O. Briec, D.E. Fast, K.I. Warheit, C.M. Knudsen, W.J. Bosch, K.A. Naish. "Managed gene flow reduces adaptation to captivity in supportive breeding programs: A multi-generational analysis of a Chinook salmon hatchery." 2nd International Conference on Integrative Salmonid Biology, Vancouver, British Columbia, Canada, June 10-12, 2014., public/profession presentation, 400 attendees, 2014-06-10

a. Waters, C.D, J.J. Hard, M.S.O. Briec, D.E. Fast, K.I. Warheit, C.M. Knudsen, W.J. Bosch, K.A. Naish. "Managed gene flow reduces adaptation to captivity in supportive breeding programs: A multi-generational analysis of a Chinook salmon hatchery." Coastwide Salmonid Genetics Meeting, Juneau, Alaska, June 3-5, 2014., public/profession presentation, 80 attendees, 2014-06-03

### ADDITIONAL METRICS

**P-12 Students**

Reached:

100

**P-12 Educators**

Trained:

0

Approximately 100 students visited our educational booth on fisheries genetics at the Discover Science Weekend at the Seattle Aquarium

**Participants in Informal Education Programs:**

0

**Volunteer Hours:**

6

Trevor Eakes, undergraduate at School of aquatic and Fishery Sciences, spawning and setting up crosses.

**Acres of coastal habitat protected, enhanced or restored:**

0

**Resource Managers who use Ecosystem-Based Approaches to Management:**

0

**Annual Clean Marina Program - certifications:**

0

**HACCP - Number of people with new certifications:**

0

## ECONOMIC IMPACTS

Description	Patents	Market	Non-	Business	Business	Jobs	Jobs
		Impact	Market				
		ts (\$)	Impact	es	es	ed	ed
			ts (\$)	Created	Retained	ed	ed
Our research will improve the longevity of hatchery programs, which support sustainable fisheries and conservation activities.	0	0	0	0	0	0	0

## SEA GRANT PRODUCTS

Description	Developed?	Used?	ELWD?	Number	Names of
				of Managers	
				s	
Genomic	Yes	Yes	No	0	

dataset of  
over  
10,000  
variable  
genetic  
markers in  
two  
hatchery  
population  
s of  
Chinook  
salmon

Crosses of Chinook salmon population s, used for measuring genetic basis of disease resistance and growth	Yes	Yes	No	0
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## HAZARD RESILIENCE IN COASTAL COMMUNITIES

*No Communities Reported This Period*

### ADDITIONAL MEASURES

Number of stakeholders modifying  
practices: 0

Sustainable Coastal Development

**# of coastal communities: 0**

a. Number of aquaculture personnel who modify  
their practices: None at this point in time.  
However, our findings could potentially affect  
hatcheries and aquaculture personnel along the  
entire West Coast once published, because our  
research is directly relevant to hatchery rearing  
and breeding practices.

### PARTNERS

Partner Name: University of Washington

Partner Name: USGS Western Fisheries Research Center, type: Government, scale:  
Federal or National

Partner Name: Washington Department of Fish and Wildlife

Partner Name: Yakama Nation, Cle Elum Supplementation and Research Facility,  
type: Other, scale: Tribal

## **IMPACTS AND ACCOMPLISHMENTS**

**Title: Washington Sea Grant research investigates genetic basis for managing conservation hatcheries for Chinook salmon and strategies for reforming hatchery practices**

Type: accomplishment

Description:

Relevance: Conservation hatcheries are an important component of strategies for restoring endangered and threatened salmon runs in the Pacific Northwest. The hatcheries' goal is to produce healthy fish with attributes of wild fish that are necessary for rebuilding depleted stocks and that maintain long-term fitness traits. Facilities must determine optimal levels of gene flow between hatchery and wild fish to prevent hatchery fish from diverging from wild fish and reduce fish health risks.

Response: Washington Sea Grant-supported research identified fitness traits in Chinook salmon using segregated and integrated hatchery lines. The two approaches were used to compare rates of genetic change attributable to selection and to identify fitness traits for monitoring changes in other hatchery populations. Genetically transmitted fitness traits such as return timing and disease resistance were measured over several generations. Both lines are being compared to wild populations.

Results: Researchers compiled phenotypic data on 413 adult Chinook salmon, collected data on 72 adults returning in 2014, and created 34 families from the segregated hatchery line and 42 families from the integrated line. Early developmental traits such as average weight and survival were measured. Disease resistance was successfully tested using the pathogen *Vibrio anguillarum*. Results will be used to develop strategies for maximizing benefits from conservation hatcheries and may ultimately refine the hatcheries' role.

Recap:

Recap:

Washington Sea Grant research is testing best hatchery practices for salmon conservation and recovery, focusing on maintenance of genetically transmitted fitness traits and reduction of fish health risks.

Comments:

Primary Focus Area: HCE

Secondary Focus Area: SFA

Associated Goals: Ocean and coastal resources are managed using ecosystem-based approaches. (HCE)

Fisheries are safe, responsibly managed and economically and culturally vibrant. (SFA)

Partners:

USGS Western Fisheries Research Center  
Washington Department of Fish and Wildlife  
Yakama Nation, Cle Elum Supplementation and Research Facility  
Related Partners: University of Washington, USGS Western Fisheries Research Center, USGS Western Fisheries Research Center, Washington Department of Fish and Wildlife

### **PUBLICATIONS**

*No Publications Reported This Period*

### **OTHER DOCUMENTS**

*No Documents Reported This Period*

### **LEVERAGED FUNDS**

Type: influenced Period: 2014-05-30: : 2015-07-30 Amount: \$5943

Purpose:

Funding for additional DNA sequencing.

Source: UW College of the Environment Hall Conservation Genetics Research Award

Type: influenced Period: 2014-04-30: : 2014-06-05 Amount: \$150

Purpose:

Travel award for graduate student to attend Coastwide Salmonid Genetics Meeting

Source: Fisheries Interdisciplinary Network of Students (FINS)

### **UPDATE NARRATIVE**

Uploaded File: [Naish\\_6485\\_update\\_narr....2.pdf](#), 14 kb

## **Progress Report 2/1/2014-1/31/2015**

### **Measuring what matters: linking life history traits and disease resistance with genomic variation in Chinook salmon conservation hatcheries, R/HCE-4**

**Kerry Naish**, University of Washington, **Kenneth Warheit**, Washington Department of Fish and Wildlife, **David Fast**, Yakama Nation Fisheries, **Maureen Purcell** and **Diane Elliott**, Western Fisheries Research Center, USGS

#### **Activities carried out**

The aim of our project is to identify fitness traits that have responded to genetic adaptation in captivity in a segregated and an integrated hatchery line, so that we can compare rates of genetic change attributable to selection since founding and identify traits that can be used to monitor changes in other hatchery populations. This aim will be attained by:

1. Linking key fitness traits that have been measured in returning adult Chinook salmon to molecular markers using Genome Wide Association Studies (GWAS).
2. Measuring early development and disease resistance in families created within the hatchery lines, and linking these traits to molecular markers.
3. Determining which traits have responded to selection in the hatchery environment by linking variation in fitness traits to divergence in genetic markers.

Our activities to date for each of these tasks are as follows:

Task 1: We compiled all phenotypic data on the 413 adult Chinook salmon (from 1998, 2002, 2006, 2010) for which we have DNA sequence information. In addition, we collected data on 72 adults that returned in 2014, which will be added to the project once we sequence their DNA. We are now beginning GWAS analyses.

Task 2. We created 42 families from the integrated hatchery line and 34 families from the segregated line in September 2014. Early development traits, including average weights at eyed and ponding stages, survival to eyed stage and ponding, and individual hatch timing, were measured in all 76 families. We are continuing to raise 56 families for disease challenges, which will be used to assess disease resistance. In addition, we are rearing 32 groups of fish, comprising individuals from all families, to measure early growth rate.

Task 3. This task depends on the results of Tasks 1 and 2, which are still underway.

#### **Participants**

We collaborated with the Cle Elum Supplementation and Research Facility, managed by the Yakama Nation, and the Washington Department of Fish and Wildlife to obtain phenotypic data from the adult Chinook and to collect gametes for the experimental families created in Task 2. We are working with the USGS Western Fisheries Research Center to carry out the disease challenge and growth rate study.

## **Results**

We are beginning analyses for Task 1 and are still collecting data for Task 2. Thus, we have no results to report at this time.

## **Challenges Encountered**

We proposed to measure disease resistance using the bacterium *Aeromonas salmonicida*, the causative agent of salmonid furunculosis, which impacts all life stages and contributes to pre-spawning mortality of Chinook salmon. However, we were unsuccessful in growing the bacteria to sufficient, reliable concentrations for use in our experimental challenges. This could prevent us from achieving the optimal dose for the protocol (50% mortality) and could lead to unequal exposure of individual families to the pathogen. For this reason, we were approved by Animal Care to change the pathogen from *Aeromonas salmonicida* to *Vibrio anguillarum*.

The pathogen *Vibrio anguillarum* is a suitable replacement for multiple reasons. First, this pathogen causes Vibriosis, a disease that is also prevalent among salmonids, particularly those raised in hatcheries. Second, like *A. salmonicida*, *V. anguillarum* serves as a model bacterial pathogen. Pathogen challenge leads to rapid onset of disease, and survival is dependent on the rapidly responding innate immune system, which is 'non-specific.' The innate immune system relies on molecular patterns that distinguish broad classes of pathogens such as distinguishing among viruses, bacteria, or fungi. Thus, the innate host response mounted against *V. anguillarum* would be similar to the response mounted against a broad range of bacterial pathogens. Third, the culture and growth of *V. anguillarum* has proven reliable in previous research, thus enabling us to conduct our disease challenges efficiently and effectively.

## **Changes in Project Direction**

We have the same project direction despite the change in bacterial pathogen.