

## WASHINGTON SEA GRANT PROJECT COMPLETION SUMMARY REPORT

**INSTRUCTIONS:** Please provide a lay summary for your completed project that includes the following project elements:

- objectives
- methodology
- rationale
- major findings
- significance of results

If relevant, also include:

- students supported (number and degree level)
- partnerships
- outreach activities

Please note that this summary will be submitted in the Washington Sea Grant annual report to the National Sea Grant Office and will be available to the public via the NIMS database and the Washington Sea Grant website.

---

WSG Project Number:       **R/B-41**  
Project Title:               Genome Mapping of Growth and Growth-Related Traits in  
                                      Coho Salmon: Implications for Conservation

Project period:               2/1/2004 – 1/31/2008

Principal Investigator(s) and Affiliation:  
**Kerry Naish**                 School of Aquatic and Fishery Sciences, University of  
                                      Washington

### PROJECT COMPLETION SUMMARY REPORT

*(Please provide your summary here. Character limit: 5,000 characters, including spaces):*

#### **OBJECTIVES**

Our aim is to develop genetically characterized salmon pedigrees in which we will link important characters such as size, weight and age at maturity, to one or more genetic markers. These characters are related to the long-term survivorship (or fitness) of salmon populations, and linked genetic markers can be used in conservation research to evaluate the genetic consequences of mixing populations, rearing populations in culture and supplementation of wild populations. Our specific objectives were:

1. To study the inheritance of associations between DNA markers and genes encoding growth characters in experimental populations
2. To survey the genetic diversity of these markers in wild populations of coho salmon, in order to detect whether the markers are indicative of adaptation at the genes involved in growth characters.

These goals were achieved through creating a map of the coho genome, identifying markers linked to growth-related genes, and surveying the diversity of the markers in wild populations of coho.

## **METHODOLOGY**

We mated individuals from different populations of coho - one derived from aquaculture and selected for rapid development and growth, the other a wild population. Using families from these populations, we created a reference map of the coho genome which correlates with the maps of other salmon species. We then studied the inheritance of both neutral genetic markers on the map and genes coding for the growth traits. Co-inheritance between the growth genes and the markers were used to identify some of the genetic regions responsible for the growth-related characters. Markers linked to the genes underlying these characters were then used in genetic surveys in four populations that were separated over different time scales, in order to determine whether these genes played a role in the evolution of coho salmon populations.

## **RATIONALE**

Fisheries genetics has been very effective at determining how populations are structured, estimating the number of populations that comprise a high seas fishery and estimating family relationships. However, some of the key challenges remaining in the conservation and management of fishes concern understanding and predicting genetic responses in fish populations to a variety of evolutionary pressures. Specifically, we need to be able to identify natural environmental influences on the evolution of growth characters, and then to anticipate how populations might respond to human activities such as fishing, global environmental change, habitat changes and conservation actions such as supplementation by hatcheries. Genomic methods will provide a basis for such goals, and it is important to start building the resources before new sequencing and gene expression technologies become widely available. The development of fundamental scientific approaches, in which molecular techniques play a central role, will provide the basis for understanding the complex interaction between genes and the environment and between characters such as growth, smolting and age at maturity. The results of this study will broaden our understanding both of the genetic basis of growth traits. Such work will form the foundation for more complex studies into the long-term monitoring of conservation-based mitigation programs in the Pacific Northwest.

## **MAJOR FINDINGS**

We initiated a genomic-based resource for the measurement and tracking of growth characters. We created reference maps describing the coho salmon genome, and were able to identify the sex chromosomes and molecular markers linked to the region of the genome that encodes sex. The coho maps were aligned with other, more intensively studied, Pacific salmon species. This result means that genetic tools developed in the

intensively studied salmon can be applied to coho. We identified fifty-three regions of the genome that are involved in hatch timing, and growth rate, length and weight at eight time periods. We found many regions of the genome encode more than one character. In wild populations, we found that four DNA regions involved in growth-related traits and seven uncharacterized regions of the genome were involved in the evolution of populations in the wild.

### **SIGNIFICANCE**

Researchers in academic and government agencies will use the research populations and molecular tools for further characterization of the coho genomes.

We have significantly contributed to knowledge on how the genomes of all salmon species are organized, and have identified conserved regions of the salmonid genomes. Markers linked to growth characters can be used in to improve the performance of coho in aquaculture and in conservation applications such as population restoration.

### **INTERACTIONS**

One PhD and one MS student were supported. Our collaborations included three government agencies (one in Canada) and two academic institutions (one in Canada) and one aquaculture firm. We have published three papers and will publish five further papers.