

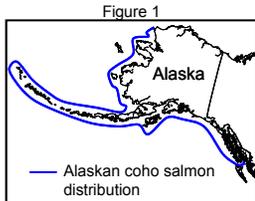
# Microsatellites reveal unique patterns of fine- and broad-scale population structure in Alaskan coho salmon

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## 1. Introduction

Coho salmon in Alaska are distributed from the Dixon Entrance in southeast Alaska, north to Point Hope in the Chukchi sea (Figure 1). Little is known about the population structure of coho salmon in this region, although Alaska represents half of the species' North American range.



## 2. Objectives

Estimates of population structure will provide an important genetic foundation on which to develop and evaluate conservation and management plans for Alaskan coho salmon. This study has two objectives:

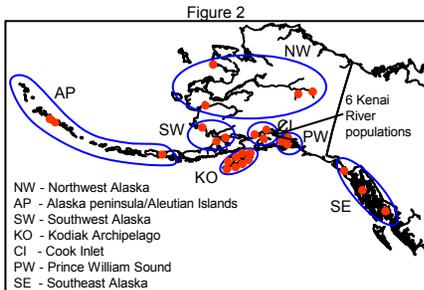
1. Estimate and evaluate the degree of population structure.
2. Evaluate the spatial distribution of population structure.



## 3. Methods

### Sample collection

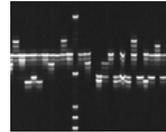
- 32 populations were sampled from seven regions (Figure 2).
- Opportunistic sampling in Kenai River and Kodiak Archipelago allowed for detailed intra-regional analysis for objective 2.



## 3. Methods (con't)

### Sample collection

- Fin tissue was collected for DNA analysis.
- All samples were genotyped using microsatellite DNA.

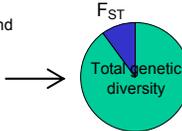


### Data analysis

#### Objective 1:

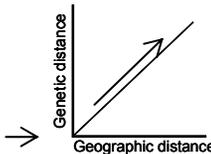
- Estimate  $F_{ST}$  over all populations and within each region.

- $F_{ST}$  is a measure of population structure. It is the proportion of the total genetic diversity from all populations that is due to variation between populations ( $0 \leq F_{ST} \leq 1$ ).



#### Objective 2:

- Evaluate the spatial distribution by testing for genetic isolation by distance (IBD) over all populations and within the Kodiak Archipelago and Kenai River.

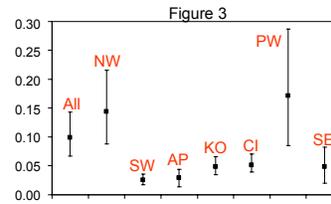


- IBD exists if the genetic distance between populations increases (is correlated) with geographic distance.

## 4. Results

### Objective 1

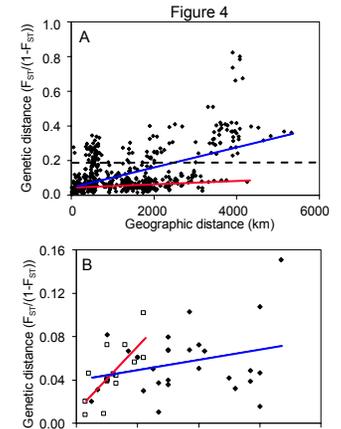
- The  $F_{ST}$  value for all 32 populations is 0.099 (Figure 3).
- The  $F_{ST}$  values for the seven regions vary greatly. The values for the NW and PW populations are surprisingly high.
- The 95% confidence intervals do not include zero, indicating significant population structure within each region and overall.



## 4. Results (con't)

### Objective 2

- Genetic and geographic distance are strongly correlated for all pairs of populations (Figure 4A – blue line).
- However, when the NW and PW populations are removed (above dashed line), the correlation is no longer significant (Figure 4A – red line).
- Genetic and geographic distance are strongly correlated for the Kenai River populations ( $\square$ , red line) but are not correlated for the Kodiak Archipelago populations ( $\blacklozenge$ , blue line).



## 5. Summary and Discussion

### Objective 1

- The  $F_{ST}$  value (0.099) is large among Pacific salmon species in Alaska, indicating a relatively high degree of population structure in coho salmon.
- The degree of population structure varies greatly among regions.

### Objective 2

- Strong support for IBD appears only at the finest geographic scale (within the Kenai River).
- The general lack of IBD suggests that the influence of gene flow on the spatial distribution of population structure is very weak except for geographically proximate populations within rivers.

### Conservation and management implications

- Important genetic diversity exists within Alaskan coho salmon populations.
- Genetic markers should play an integral role in defining conservation units for Alaskan coho salmon.
- More intensive intra-regional sampling is needed for conservation and management applications.

## 6. Acknowledgements

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