

# Founding events influence genetic population structure of sockeye salmon

Kristina M Ramstad<sup>1\*</sup>, Carol A Woody<sup>2</sup>, George K Sage<sup>2</sup>, Chris Habicht<sup>3</sup>, James E Seeb<sup>3</sup>, and Fred W Allendorf<sup>1</sup>

<sup>1</sup>University of Montana, Missoula, MT, <sup>2</sup>U. S. Geological Survey, Anchorage, AK, <sup>3</sup>Alaska Department of Fish & Game, Anchorage, AK

\*Corresponding author: kristina.ramstad@mso.umt.edu



## INTRODUCTION

- Founder effects are genetic bottleneck effects associated with the founding of a new population.
- Sockeye salmon (*Oncorhynchus nerka*) are vulnerable to founder effects because they have excellent colonizing abilities and often occupy geologically young habitats.
- During a bottleneck event, genetic drift reduces genetic variation within and increases genetic divergence among populations. Thus, sockeye salmon populations may differ genetically because of historical founder effects.
- Sockeye salmon populations may also differ genetically because there is reduced gene flow between populations that spawn in different habitat types (ecological isolation), in geographically distant habitats (spatial isolation), or at different times (temporal isolation; Wood 1995).
- **Objective:** Determine the relative importance of ecological, spatial, and temporal isolation (restricted gene flow) and founder effects (genetic drift) on the genetic population structure of sockeye salmon of Lake Clark, Alaska (Fig. 1).

## METHODS

- Fin tissue was collected from 15 spawning populations throughout Lake Clark, Six-mile Lake and northeast Lake Iliamna (Table 1, Fig. 1).
- Fish were genotyped at 11 microsatellite loci.
- Heart, muscle, liver, and eye tissue were also collected from 7 of the 15 populations and fish were genotyped at 19 allozyme loci.
- RFLP analysis of the ND1/ND2 region resolved mitochondrial DNA (mtDNA) haplotypes for 8 of the 15 populations surveyed.

## RESULTS

### Genetic divergence among populations

- Allele and haplotype frequencies differ significantly in 132 of 154 pair-wise population comparisons.  $F_{ST}$  between populations (Weir and Cockerham 1984) ranges from zero to 0.089, 0.112, and 0.427 for microsatellites, allozymes, and mtDNA.
- Principle component analysis of both microsatellite loci and mtDNA suggests Six-mile & Iliamna Lake populations are similar genetically but highly divergent from Lake Clark populations (Fig. 2).
- The Sucker Bay Lake population is highly divergent from all other populations at microsatellite loci but similar to other Lake Clark populations at mtDNA (Fig. 2).

### Genetic variation within populations

- Relative to Six-mile & Iliamna Lake populations, Lake Clark populations have:
  - reduced mean allelic richness at all three markers types, and
  - a lower proportion of rare (frequency <0.1) microsatellite and allozyme alleles ( $P \leq 0.03$ ; Table 1).
- In addition, Lake Clark populations exhibit greater heterozygosity than expected at mutation-drift equilibrium at microsatellite and allozyme loci (Fig. 3).
- The Sucker Bay Lake population of Lake Clark has the greatest genetic bottleneck signals of all populations surveyed (Table 1; Fig. 3).

### Correlation between genetic divergence and diversity

- Genetic divergence ( $F_{ST}$ ) is correlated with difference in allelic richness and spawning time ( $P < 0.01$ ) but not with differences in spawning habitat type ( $P = 0.97$ ) or geographic distance ( $P = 0.21$ ) between populations.

## ABSTRACT

Bottlenecks can have lasting effects on genetic population structure that obscure patterns of contemporary gene flow and drift. Founder effects are genetic bottleneck effects associated with the founding of a new population. Sockeye salmon are vulnerable to bottleneck effects because the species is highly structured, has excellent colonizing abilities, and often occupies geologically young habitats. We assessed nuclear (microsatellite and allozyme) and mitochondrial DNA variation of sockeye salmon populations throughout the Lake Clark area of Alaska. Six-mile Lake populations are genetically similar to Lake Iliamna populations and divergent from Lake Clark populations. Reduced allelic and haplotypic diversity and strong divergence of Lake Clark populations relative to Six-mile Lake and Lake Iliamna populations suggest a bottleneck associated with the colonization of Lake Clark. Geographic distance and spawning habitat differences do not contribute to isolation and divergence among populations. However, temporal isolation based on spawning time and a common founder effect associated with colonization contribute to the genetic population structure of Lake Clark sockeye salmon.

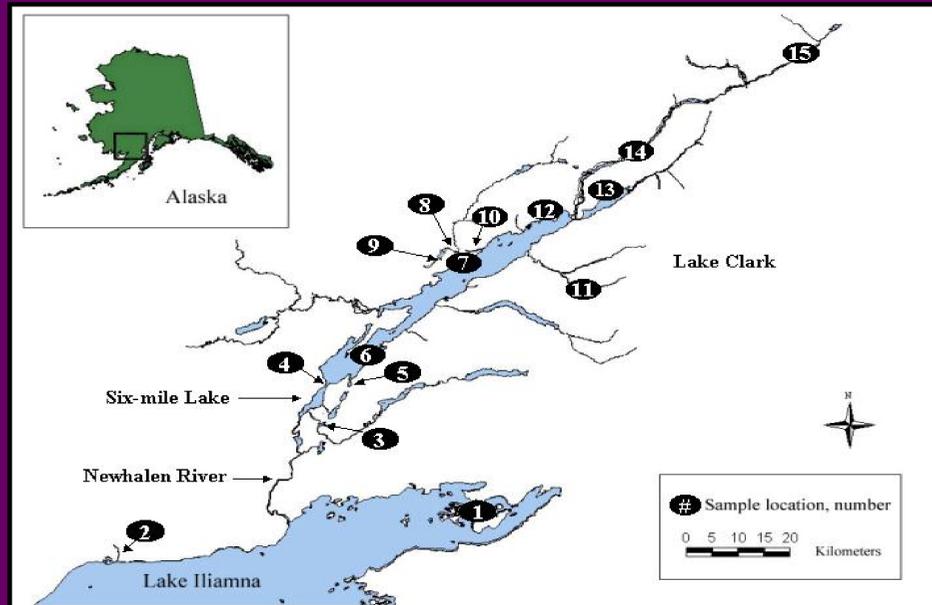


Figure 1. Sample sites in Lake Clark, Six-mile Lake, and Lake Iliamna, Alaska. See Table 1 for site names, sites are numbered in downstream to upstream direction.

Table 1. Genetic variation of Lake Clark, Six-mile Lake and Lake Iliamna sockeye salmon. Sample size ( $N$ ), mean expected heterozygosity ( $H_E$ ), and allelic richness ( $A$ ) are given for 11 microsatellite loci, 19 allozyme loci, and mtDNA.

Site	Lake	Microsatellites			Allozymes			MtDNA		
		$N$	$H_E$	$A$	$N$	$H_E$	$A$	$N$	$H_E$	$A$
1 Fuel Dump Island	Iliamna	87	0.48	6.5	99	0.10	1.7	30	0.66	3.9
2 Talarik Creek	Iliamna	97	0.50	6.0	100	0.10	1.7	24	0.75	4.0
3 Tazimina River	Six-mile	99	0.51	5.8	100	0.10	1.7	23	0.71	4.0
4 Lake Clark Outlet	Six-mile	100	0.52	5.7	---	---	---	---	---	---
5 Sucker Bay Lake	Clark	100	0.50	4.2	---	---	---	23	0.61	3.0
6 Chi Point	Clark	99	0.48	5.4	---	---	---	---	---	---
7 Kijik River	Clark	99	0.48	4.9	100	0.12	1.5	23	0.24	2.0
8 Little Kijik River	Clark	98	0.46	4.6	100	0.11	1.5	26	0.54	3.0
9 Kijik Lake South Beach	Clark	100	0.45	4.6	100	0.11	1.6	26	0.52	2.0
10 Priest Rock Creek	Clark	65	0.48	4.9	---	---	---	---	---	---
11 Currant Creek	Clark	100	0.48	5.0	---	---	---	---	---	---
12 Hatchet Point Beach	Clark	99	0.50	5.3	---	---	---	---	---	---
13 Little Lake Clark Beach	Clark	100	0.47	5.1	---	---	---	---	---	---
14 Lower Tlikakila	Clark	100	0.46	4.9	---	---	---	---	---	---
15 Upper Tlikakila	Clark	100	0.48	4.8	100	0.12	1.5	28	0.36	3.0

## DISCUSSION

- Reduced allelic richness, fewer rare alleles, and heterozygosity excess in Lake Clark populations suggest a bottleneck associated with the colonization of Lake Clark by sockeye salmon.
- The severe reduction in microsatellite diversity but not mtDNA diversity suggests the Sucker Bay Lake population has experienced smaller effective population size than other Lake Clark populations since their common founding.
- Early spawning time and large inter-annual variation in numbers of spawners contribute to the continued isolation and low  $N_e$  of the Sucker Bay Lake population.
- Correlation between genetic divergence and differences in allelic richness between populations suggests that founder effects have deeply affected the genetic population structure of Lake Clark sockeye salmon.

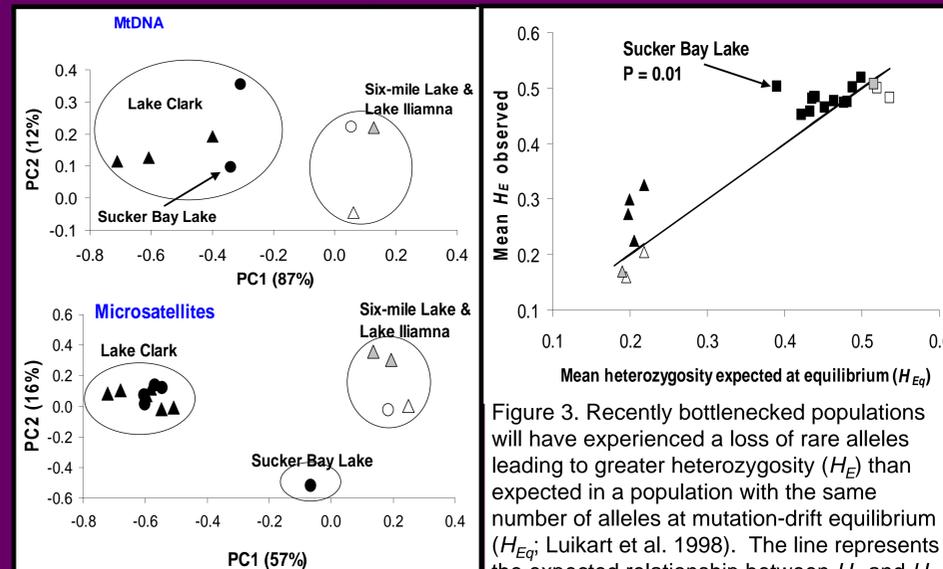


Figure 2. Principal components analysis of mtDNA and microsatellite loci. Circles enclose major population groups. Points are coded by habitat type (triangles = tributaries, circles = beaches) and lake (Clark = black, Six-mile Lake (grey), and Lake Iliamna (open) sockeye salmon populations).

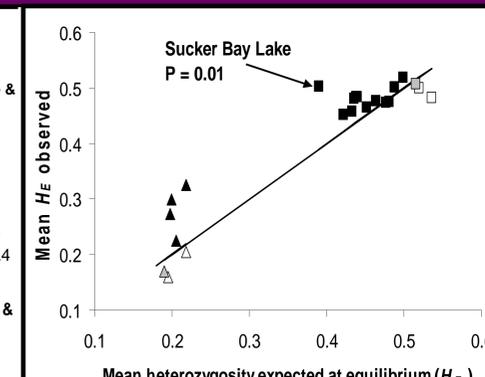


Figure 3. Recently bottlenecked populations will have experienced a loss of rare alleles leading to greater heterozygosity ( $H_E$ ) than expected in a population with the same number of alleles at mutation-drift equilibrium ( $H_{Eq}$ ; Luikart et al. 1998). The line represents the expected relationship between  $H_E$  and  $H_{Eq}$  under the Infinite Alleles Model of mutation. Points represent 11 microsatellite loci (squares) and 13 allozyme loci (triangles) in Lake Clark (black), Six-mile Lake (grey), and Lake Iliamna (open) sockeye salmon populations.

## LITERATURE CITED

- Luikart, G. and J-M Cornuet. 1998. Conservation Biology 12:228-233.  
 Weir, B. S., and C. C. Cockerham. 1984. Evolution 38:1358-1370.  
 Wood, C. C. 1995. American Fisheries Society Symposium 17:195-216.

## ACKNOWLEDGMENTS

Funded by the U.S. Geological Survey and the U.S. Fish and Wildlife Service. The National Park Service provided logistical support. Iliamna Lake samples were provided by the Alaska Salmon Program at the University of Washington. Special thanks to all who assisted in fieldwork, G. Ataian and F. Gardipee for genetic data collection, and A. Gray, J. Olsen, D. Churikov, and C. Kondzela for advice on mtDNA analyses.