

**Summary of OSM Final Report No. FIS 01-042,
Lake Clark Population Assessment Research**

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Final Report Summary Page

Title: Population Assessment of Lake Clark Sockeye Salmon

Study Number: FIS 01-042

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Geographic Area: Bristol Bay, Kvichak watershed; Lake Clark National Park and Preserve

Information Type: Stock Status and Trends

Issue(s) Addressed: Lack of information regarding sockeye salmon spawning distributions in Lake Clark. Lack of information regarding genetic diversity within and among Lake Clark sockeye salmon populations, and between Lake Clark and Iliamna originating populations.

Study Cost: \$228,000

Study Duration: June 2000 to December 2002

**Part I. Summary of Radiotelemetry Study Results: Identification and Mapping of Lake
Clark Sockeye Salmon Spawning Habitats**

Abstract:

Radio telemetry was used to identify and map sockeye salmon spawning habitats in glacially influenced Lake Clark, Kvichak River watershed (Figure 1). Two hundred eighty two of 332 radio tagged adult sockeye salmon were tracked to spawning grounds. Thirty five spawning areas were identified, including 18 previously unidentified. Previous routine aerial surveys have greatly underestimated spawning habitats used by sockeye salmon in Lake Clark. Sockeye salmon spawned in both glacial and clear water habitats, but two thirds of radio tagged fish spawned in glacial waters. More than half of identified spawning areas were located along the shores of Lake Clark and Little Lake Clark. Most spawning areas are adjacent to private land; proposed development on these lands could negatively impact critical spawning habitats if protective measures are not in place.

Objectives of the Study

- 1) Locate Lake Clark sockeye salmon spawning habitats using radio telemetry.
- 2) Map spawning habitats in a Geographic Information System (GIS) database.
- 3) Determine spawner distribution by water clarity: glacial (> 5 NTUs) or clear (≤ 5 NTUs).
- 4) Determine spawner distribution by land ownership: federal - National Park Service or private ownership.

Results of the Study

Tagging

Three hundred thirty-two adult sockeye salmon were tagged with radio transmitters as they entered Lake Clark: 175 in 2000, 157 in 2001. Spawning areas were determined for 282 of 332 radio tagged sockeye salmon (Figure 2). Thirty-five spawning locations were identified, including three sites downstream of the tagging area and five sites identified by means other than radio telemetry (Figure 2, Appendix 1). Radio tagged fish returned to 20 spawning areas in 2000 and 27 in 2001 (Appendix 1). Eighteen spawning sites had tagged fish return in both years of the study.

Radio tagged fish returned to three primary spawning areas within the Lake Clark watershed: Tlikakila River, Kijik Lake, and beach spawning areas along the shores of Lake Clark and Little Lake Clark (Figure 3, Appendix 1). Each year about half of the tagged fish returned to the 19 beach spawning habitats in Lake Clark and Little Lake Clark (Figure 3, Appendix 1). No tagged fish were tracked into 22 Creek, the Tanalian River, or the Chulitna River.

Spawning Habitat Distribution: Glacial vs. Clear

Spawning activity was observed in both glacial and clear water, which included areas of beaches and rivers. (Figure 2 Figure 5, Appendix 1). However, during both years of study, more fish returned to glacial habitats than clear habitats (Figure 4).

Fish entered the system from July to September and peak spawning times varied among habitats. The earliest peak spawning activity was observed in Sucker Bay Lake (August – early September; Appendix 1).

Spawning Habitat Distribution: Public vs. Private Land

Approximately 60% of the Lake Clark shoreline is privately owned (National Park Service 2001). Seventy-five percent of the identified spawning areas are adjacent to private land (Figure 6), though only 50% of the radio tagged fish spawned in areas adjacent to private land (Table 3). More tagged fish returned to pristine areas as compared to developed areas (Table 3, Appendix 1). Spawning grounds were located near the town of Port Alsworth, which has the greatest concentration of development.

Comparison to Historic Aerial Surveys

Historic aerial survey data identified 12 spawning areas in the Lake Clark watershed; our radiotagging study identified 33 spawning areas including 11 of the areas identified by aerial surveys (Figure 7, Appendix 1, Appendix 2). Historic aerial survey data identified spawning areas along the shores of Lake Clark however, specific spawning sites were not identified or mapped and little or no spawning activity was attributed to these sites (Figure 3, Appendix 2). The radio tagging study identified and mapped 22 beach spawning habitats along the shores of Lake Clark (Figure 2, Appendix 1). Historic aerial surveys identified less spawning in glacial rivers than recent aerial surveys; the radio tagging study indicated that 26% of tagged fish spawned in glacial river systems (Appendix 2).

Aerial surveys identified the Kijik Lake drainage as the most important spawning area within Lake Clark, attributing about 70% of spawning to that area (Figure 3, Appendix 2). In the radiotagging study, fewer than 30% of fish spawned in the Kijik system.

Conclusion

Sockeye salmon spawning habitats in the Lake Clark watershed have historically been underestimated because high glacial turbidity makes identification difficult to impossible to see spawning fish. This study provides the first comprehensive survey of the spawning areas within the drainage, particularly in glacially obscured waters. Radio telemetry and visual observations were used to identify and map 33 spawning areas within the Lake Clark watershed, including 18 previously unidentified sites. Sockeye salmon spawned in both glacial and clear water habitats, but most radio tagged fish spawned in glacial waters (>65%). More than half of the spawning habitats were along beaches of Lake Clark and Little Lake Clark.

More than 65% of spawning areas identified were adjacent to private lands. Identification of spawning habitats in this study will allow the National Park Service and private landowners to employ proactive measures to protect spawning habitats and thereby protect future subsistence, sport, and commercial harvests. It is critical that fisheries resource managers take proactive measures to enforce responsible development and prevent degradation to critical spawning habitats.

Recommendations

- Further research is required to more precisely define and map extent of beach spawning habitats, particularly along beaches. Fish may spawn in deep waters (>15m).
- Research should be repeated in years of greater salmon abundance, which may allow for identification of additional spawning habitats.

- The current results should be compared with traditional ecological knowledge, which may allow identification of undocumented populations or may provide insight into populations that may no longer exist.

Figures:

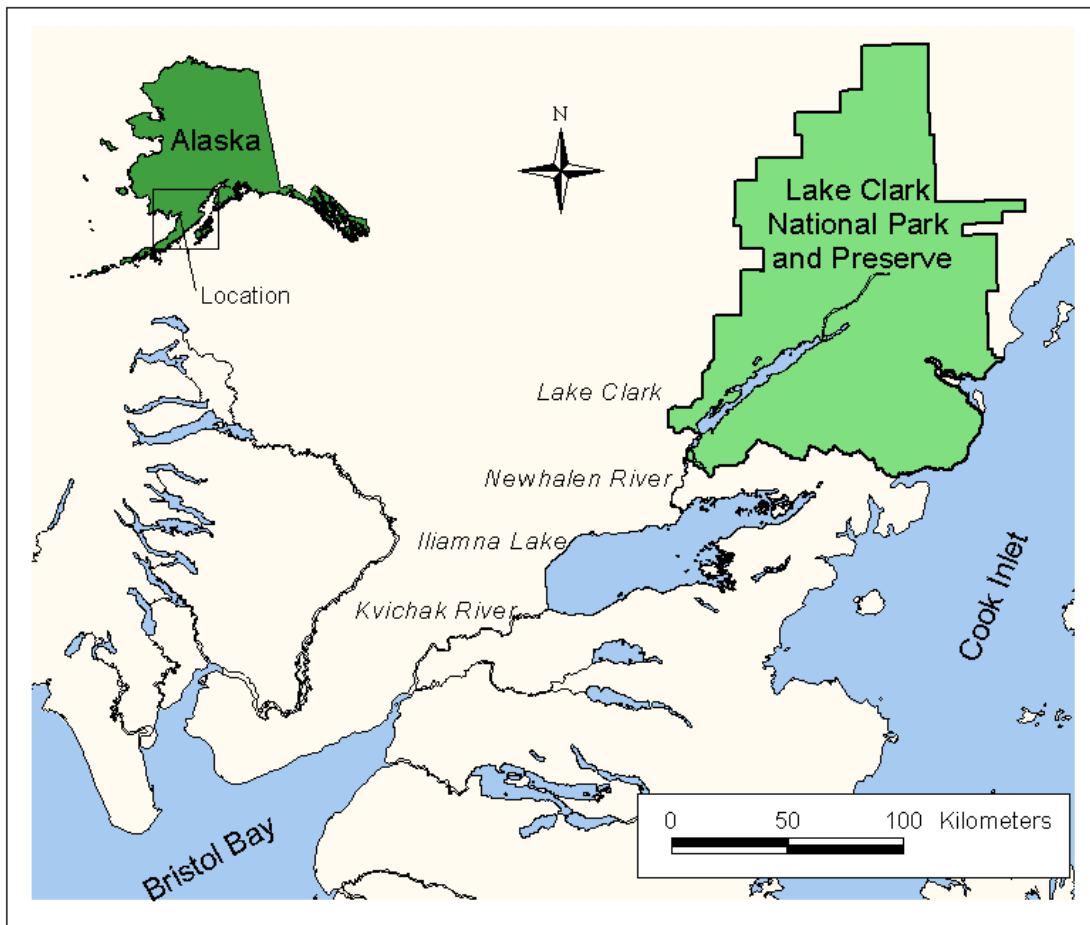


Figure 1. Location of Lake Clark relative to Bristol Bay, Alaska.

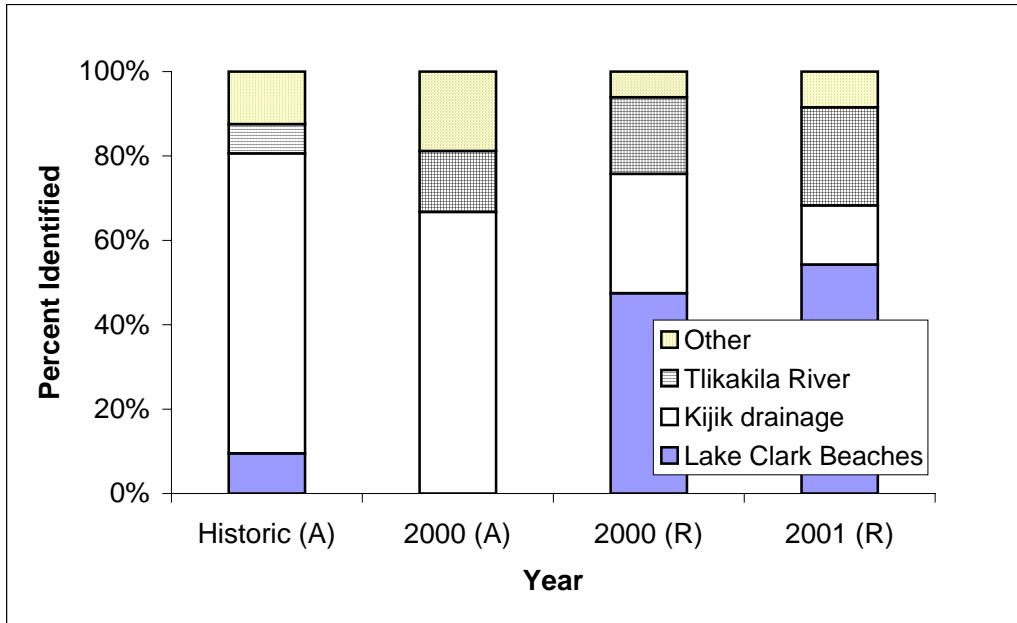


Figure 3. Four main spawning areas identified in Lake Clark by radio telemetry (R) and aerial surveys (A), historic, 2000, and 2001. Historic aerial survey data are from 1968 – 1983 (Regnart 1998). The aerial survey in 2000 was flown by ADF&G (unpublished data ADF&G, King Salmon, Alaska). Note the large percentage of glacially influenced beach spawning areas identified by radio telemetry (R) but missing, or extremely underestimated, by aerial surveys (A).

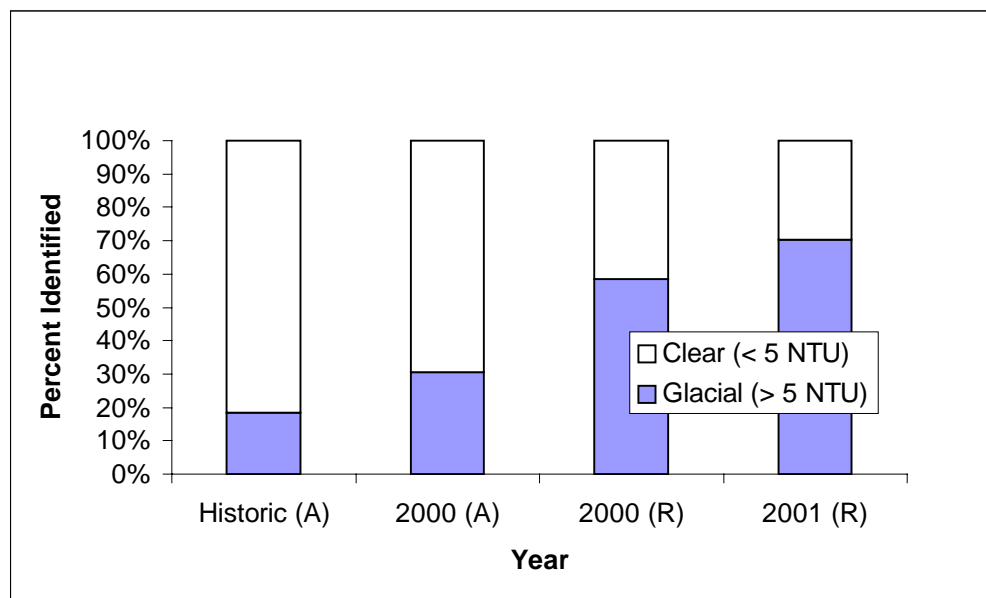


Figure 4. Proportion of glacial (> 5 NTUs) and clear (\leq 5 NTUs) spawning habitats identified by aerial surveys (A) and radio telemetry (R), historic, 2000, and 2001. Historic aerial survey data are from 1968 – 1983 (Regnart 1998). The aerial survey in 2000 was flown by ADF&G (unpublished data, ADF&G, King Salmon, Alaska).

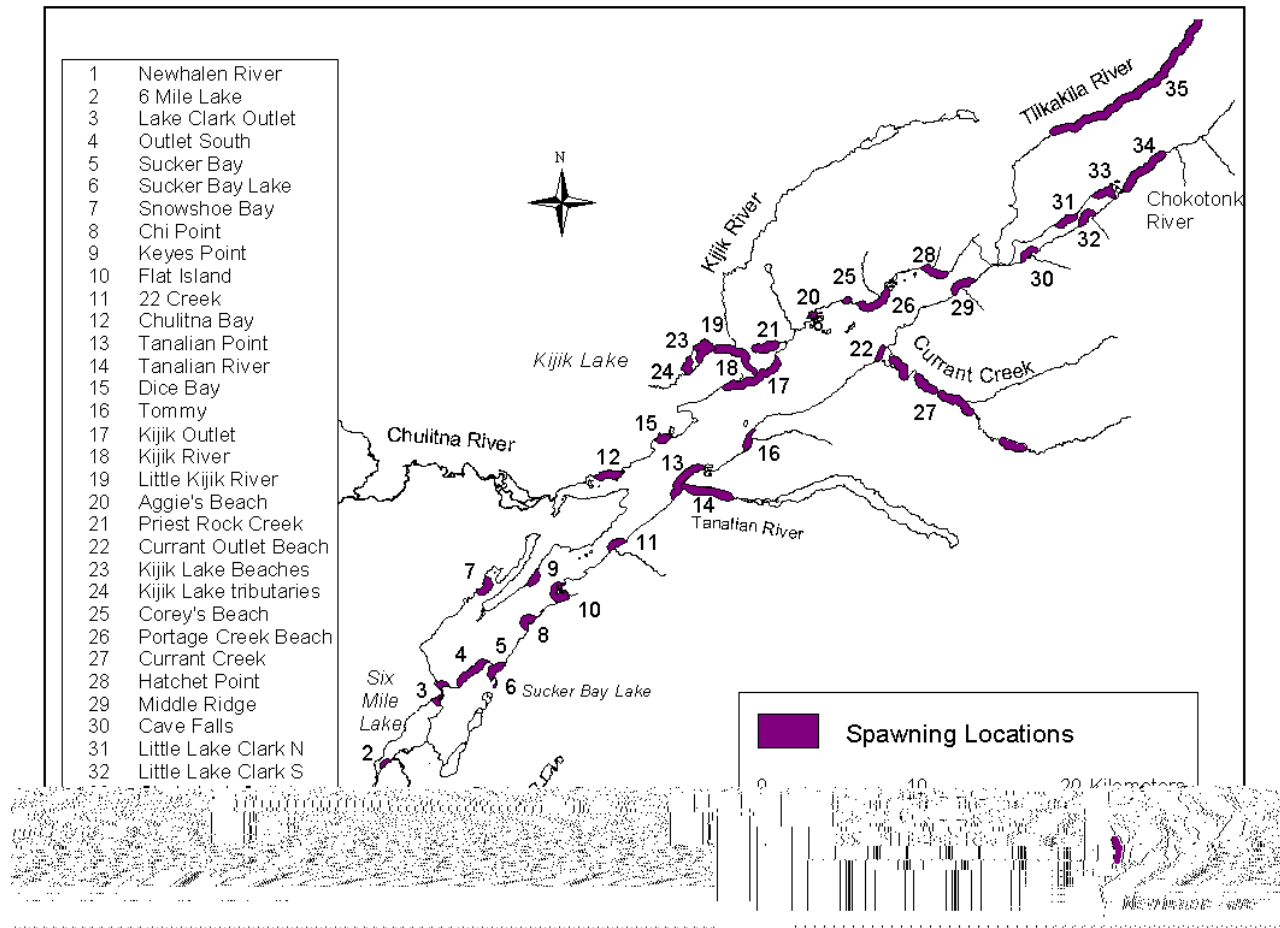


Figure 5. Key to spawning areas identified by visual observation and radio tagging in Lake Clark, 2000 and 2001.

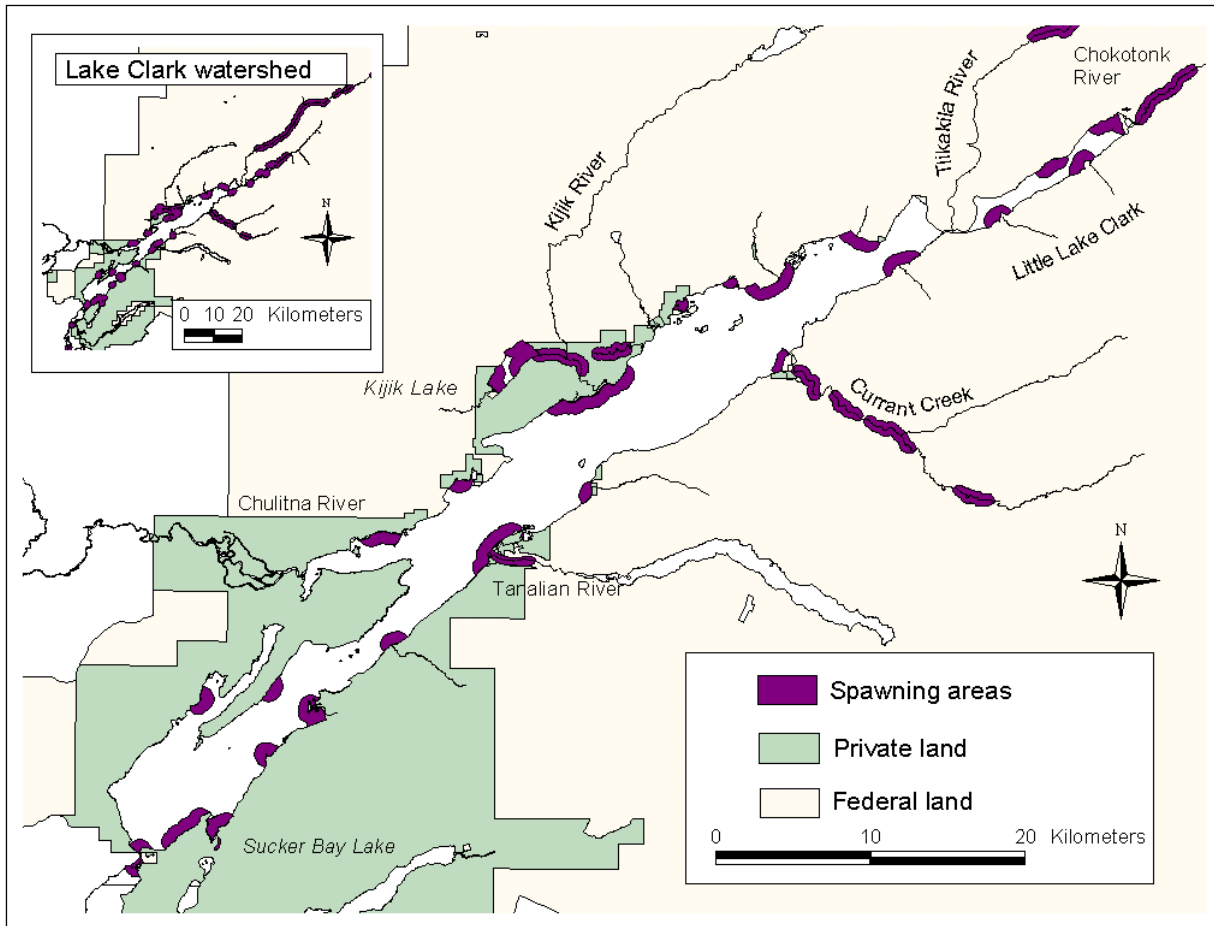


Figure 6. Spawning areas identified by radio telemetry and visual observation relative to land ownership in Lake Clark, 2000 and 2001.

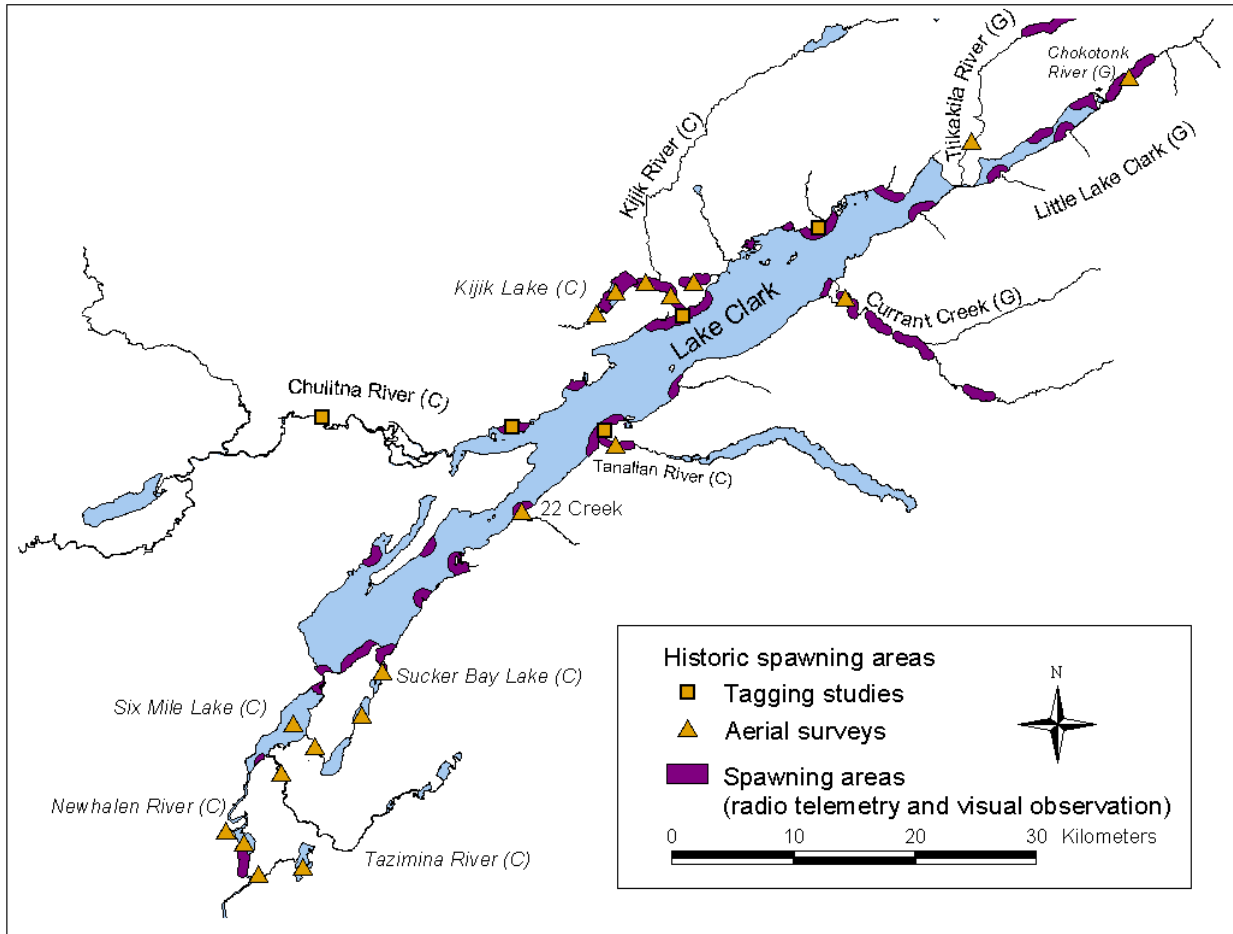


Figure 7. Comparison of spawning areas identified in Lake Clark by radio telemetry and visual observation in this study and spawning areas identified during historic aerial surveys (Parker and Blair 1987, Regnart 1998) and tagging studies (Smith 1964, Jensen and Mathisen 1987).

Tables

Table 1. Mid-eye to hypural length (mm) of tagged and untagged adult sockeye salmon captured at the outlet of Lake Clark, 2000 and 2001.

	2000		2001	
	Male		Female	
	Tagged	Untagged	Tagged	Untagged
Mean	510	510	484	479
Range	404-592	409-583	404-552	377-546
Standard error	4.1	5.0	4.0	4.0
N	93	81	82	187

	2000		2001	
	Male		Female	
	Tagged	Untagged	Tagged	Untagged
Mean	0	546	526	522
Range	0	409-616	415-591	411-511
Standard error	0	1.3	2.0	2.1
N	0	474	157	187

Table 2. Tagging and tracking summary for radio tagged adult sockeye salmon in Lake Clark, 2000 and 2001.

Category	Number of salmon		
	2000	2001	Total
Tagged	175	157	332
Never located	8 (5%)	0	8 (2%)
Lost / no determination	33 (19%)	9 (6%)	42 (13%)
Tracked to spawning area	134 (76%)	148 (94%)	282 (85%)

Spawning Distribution			
Downstream spawning areas*	35 (26%)	6 (4%)	41 (15%)
Lake Clark spawning areas	99 (74%)	142 (96%)	241 (85%)

* Includes spawning areas at the outlet of Lake Clark, in Six Mile Lake, and in the Newhalen River.

Table 3. Number and percent distribution of spawning radio tagged fish relative to land ownership and development in Lake Clark, Alaska, 2000 and 2001.

Land Category	2000	2001	Total
Private	75 (76%)	73 (51%)	148 (61%)
Federal	24 (24%)	69 (49)	93 (39%)
Development	34 (34%)	29 (20%)	63 (26%)
No Development	65 (66%)	113 (80%)	178 (74%)

Appendix 1. Spawning locations identified by radio telemetry and visual observation in Lake Clark, 2000 and 2001. Water type (glacial > 5 NTUs; clear < 5 NTUs) was determined at time of peak spawning activity. Distance was calculated from the tagging site at the outlet of Lake Clark. Historic data was collected during aerial surveys by Fisheries Research Institute from 1968 to 1983 (Regnart 1998). Private land and Development were recorded adjacent to a spawning area as present (Yes = Y) or not present (No = N).

ID	Spawning location	Specific location	Habitat type	Water type	Peak spawning	Distance (km)	Historic	Private land	Development	Number of tagged fish		
										2000	2001	Total
35	Tlikakila River		Stream	Glacial	9/15-10/15	98	Y	N	N	18 (18.2%)	33 (23.2%)	51 (21.2%)
34	Chokotonk River		Stream	Glacial	9/15-10/15	86	Y	N	N	1 (1.0%)	6 (4.2%)	7 (2.9%)
27	Currant Creek		Stream	Glacial	9/15-9/30	57	Y	N	N	2 (2.0%)	3 (2.1%)	5 (2.1%)
1	Newhalen River*		Stream	Clear		19	Y	-	-	0	1 *	1 *
3	Lake Clark Outlet*		Stream	Clear	8/25-9/15	1	N	N	N	35 *	4 *	39 *
14	Tanalian River ¹		Stream	Clear	9/15-10/1	31	Y	Y	N	0	0	0
21	Priest Rock Creek		Stream	Clear	9/25-10/15	52	Y	Y	N	0	1 (0.7%)	1 (0.4%)
18	Kijik River		Stream	Clear	9/15-10/15	45	Y	Y	N	2 (2.0%)	0	2 (0.8%)
19	Little Kijik River		Stream	Clear	9/15-10/15	49	Y	Y	N	5 (5.1%)	1 (0.7%)	6 (2.5%)
24	Kijik Lake Tributaries		Stream	Clear	9/25-10/15	53	Y	Y	N	0	0	0
23	Kijik Lake Beaches		Beach	Clear	9/15-10/30	52	Y	Y	N	21 (21.2%)	19 (13.4%)	40 (16.6%)
6	Sucker Bay Lake		Beach	Clear	8/25-9/15	9	Y	Y	N	3 (3.0%)	2 (1.4%)	5 (2.1%)
2	6 Mile Lake*		Beach	Clear		8	Y	-	-	0	1 *	1 *
13	Lake Clark Beaches	Tanalian Point	Beach	Glacial	9/15-10/15	31	Y	Y	Y	17 (17.2%)	17 (12%)	34 (14.1%)
33	Lake Clark Beaches	Chokotonk Outlet	Beach	Glacial	9/15-10/30	80	N	N	N	2 (2.0%)	16 (11.3%)	18 (7.5%)
17	Lake Clark Beaches	Kijik Outlet	Beach	Glacial	9/15-10/15	41	Y	Y	Y	12 (12.1%)	7 (4.9%)	19 (7.9%)
26	Lake Clark Beaches	Portage Creek	Beach	Glacial	9/15-10/15	54	Y	Y	N	3 (3.0%)	3 (2.1%)	6 (2.5%)
31	Lake Clark Beaches	Little Lake Clark N	Beach	Glacial	9/15-10/15	76	N	N	N	0	5 (3.5%)	5 (2.1%)
28	Lake Clark Beaches	Hatchet Point	Beach	Glacial	9/15-10/15	62	N	Y	Y	0	3 (2.1%)	3 (1.2%)
29	Lake Clark Beaches	Middle Ridge	Beach	Glacial	9/15-10/15	64	N	N	N	1 (1.0%)	2 (1.4%)	3 (1.2%)
16	Lake Clark Beaches	Tommy	Beach	Glacial	9/15-10/15	38	N	Y	Y	2 (2.0%)	0	2 (0.8%)
29	Lake Clark Beaches	Cave Falls	Beach	Glacial	9/15-10/15	71	N	N	N	0	2 (1.4%)	2 (0.8%)
32	Lake Clark Beaches	Little Lake Clark S	Beach	Glacial	9/15-10/15	77	N	N	N	0	2 (1.4%)	2 (0.8%)
15	Lake Clark Beaches	Dice Bay	Beach	Glacial	9/1-9/30	33	N	Y	N	0	1 (0.7%)	1 (0.4%)
20	Lake Clark Beaches	Aggie's Beach ¹	Beach	Glacial	9/15-10/15	49	N	Y	Y	0	0	0
22	Lake Clark Beaches	Currant Outlet Beach ¹	Beach	Glacial	9/15-10/15	52	N	Y	N	0	0	0

ID	Spawning location	Specific location	Habitat type	Water type	Peak spawning	Distance (km)	Historic	Private land	Develop-ment	Number of tagged fish		
										2000	2001	Total
25	Lake Clark Beaches	Corey's Beach ¹	Beach	Glacial	9/15 - 10/15	53	N	Y	Y	0	0	0
10	Lake Clark Beaches	Flat Island	Beach	Clear	9/1-10/15	16	N	Y	N	3 (3.0%)	7 (4.9%)	10 (4.1%)
12	Lake Clark Beaches	Chulitna Bay	Beach	Clear	9/15-10/15	30	Y	Y	N	2 (2.0%)	5 (3.5%)	7 (2.9%)
4	Lake Clark Beaches	Outlet South	Beach	Clear	9/1-10/1	4	N	Y	N	1 (1.0%)	3 (2.1%)	4 (1.7%)
8	Lake Clark Beaches	Chi Point	Beach	Clear	9/1-9/30	12	N	Y	Y	2 (2.0%)	1 (0.7%)	3 (1.2%)
5	Lake Clark Beaches	Sucker Bay	Beach	Clear	9/1-10/1	8	Y	Y	N	1 (1.0%)	1 (0.7%)	2 (0.8%)
7	Lake Clark Beaches	Snowshoe Bay	Beach	Clear	9/1-9/30	11	N	Y	N	0	1 (0.7%)	1 (0.4%)
9	Lake Clark Beaches	Keyes Point	Beach	Clear	9/1-10/1	15	N	Y	Y	0	1 (0.7%)	1 (0.4%)
11	Lake Clark Beaches	22 Creek	Beach	Clear	9/15-10/1	22	Y	Y	Y	1 (1.0%)	0	1 (0.4%)

* identified by radio telemetry but not included in estimates of spawning distribution

¹ identified by visual observation or seining - no radio tags were tracked to this location

Appendix 2. Comparison of percent spawning distribution among habitats of Lake Clark sockeye salmon identified by aerial survey¹ (A) and radio telemetry² (R).

Spawning Location	Habitat Type	Water Type	Peak Spawning	Historic (A)	Percent spawning distribution by location			
					2000 (A)	2000 (R)	2001 (R)	Total (R)
Tlikakila River	Stream	Glacial	9/15-10/15	7	14	18	23	21
Chokotonk River	Stream	Glacial	9/15-10/15	2	3	1	4	3
Currant Creek	Stream	Glacial	9/15-9/30	0	13	2	2	2
Priest Rock Creek	Stream	Clear	9/25-10/15	5	0	0	1	0
Tanalian River	Stream	Clear	9/15-9/30	1	0	0	0	0
22 Creek	Stream	Clear	9/15-9/30	0	0	0	0	0
Little Kijik River	Stream	Clear	9/15-10/15	18	15	5	1	2
Kijik River	Stream	Clear	9/15-10/15	9	5	2	0	1
Kijik Lake Tributaries	Stream	Clear	9/25-10/15	3	3	0	0	0
Kijik Lake Beaches	Beach	Clear	9/15-10/15	41	44	21	13	17
Sucker Bay Lake	Beach	Clear	9/1-9/15	5	3	3	1	2
Lake Clark Beaches	Beach	Both	9/1-11/1	9	0	47	54	51

¹ Aerial survey data from 1968 - 1983 was used as it was the most comprehensive and flown by the same observer (e.g. Pat Poe, present address: Bonneville Power Association, Portland, OR).

² Aerial survey data for 2000 was flown by the Alaska Department of Fish and Game (unpublished data, ADF&G, King Salmon, Alaska).

Part II. Summary of Genetic Study Results

Abstract:

Lake Clark, Alaska contributes 6 to 80 percent of the Kvichak return of sockeye salmon. In this study we describe the genetic divergence among and genetic variation within spawning populations of sockeye salmon throughout the Lake Clark system, information that is critical for effective management. Fin tissue was collected from 1,442 sockeye salmon representing 15 spawning populations of Lake Clark and northeastern Lake Iliamna. Allele frequencies differed significantly across 11 microsatellite loci in 94 of 105 pair-wise population comparisons. Pair-wise estimates of F_{ST} ranged from zero to 0.089. **There is significant genetic divergence between populations of Lake Clark and Six-Mile Lake, the latter being more similar to fish of Lake Iliamna.** The reduced numbers of alleles and strong divergence of most Lake Clark populations relative to Lake Iliamna/Six-mile Lake populations suggest a bottleneck associated with the colonization of Lake Clark by sockeye salmon. The greatest bottleneck effect detected and the most genetically distinct population was Sucker Bay Lake. Possible causes of these bottlenecks include reductions in effective population size associate with recent poor returns or colonization of new spawning habitats.

Introduction

Understanding the pattern of genetic variation among and within populations is critical for effective management of species. The genetic population structure of a species provides a basis for defining management units, can identify populations of unusual genetic composition, and may identify populations at risk of extinction due to low genetic diversity. Population structure is positively associated with genetic diversity and resilience to disturbance such that large, highly structured populations have high genetic diversity and probability of persistence. In contrast, small, panmictic (homogeneous) populations are vulnerable to inbreeding, demographic stochasticity, genetic drift and thus, reduced evolutionary potential, and increased probability of extinction.

Sockeye salmon are a highly structured species due to their homing tendencies and ability to colonize new habitats. Because they home to and spawn in specific natal habitats, populations

can be reproductively isolated from each other and this promotes genetic structuring among populations of sockeye. Lakes are focal points of homing and genetic divergence is typically greater among populations spawning in different lakes than among spawning populations within lakes. However, there is often significant genetic divergence between spawning populations within lakes due to isolation among fish spawning in different habitat types or differing in their time or return or spawning.

Sockeye salmon are vulnerable to bottleneck effects (loss of genetic variation due to severe reductions in effective population size; because they are excellent colonizers that can quickly establish spawning populations with few individuals. Genetic drift (random changes in allele frequencies due to imperfect sampling of the allele frequencies between generations) causes loss of genetic variation during a bottleneck and promotes genetic divergence among populations while reducing genetic diversity within them. Thus genetic drift may drive the genetic population structure of sockeye salmon through bottleneck effects associated with colonization events.

Objectives

1. Test for genetic divergence among spawning populations of sockeye salmon in Lake Clark and between Lake Clark and Lake Iliamna.
2. Test for reduced genetic variation (bottlenecks) within spawning populations of sockeye salmon in Lake Clark and relative to populations in Lake Iliamna.

Results of the Study

Genetic divergence between major population groups

Estimates of F_{ST} ranged from 0 to 0.089 and were greatest between Lake Iliamna and Lake Clark populations. Lake Clark populations were divergent from Six-mile Lake populations, the latter being more similar to Lake Iliamna fish. The Sucker Bay Lake population was highly divergent from all other populations surveyed.

Principal component analysis supported this pattern (Figure 2). The first principal component explained 57% of the total genetic variation and differentiated between three major groups of populations: 1) Lake Iliamna and Six-mile Lake, 2) Sucker Bay Lake, and 3) Lake Clark. The second principal component explained 16% of the total genetic variation, further differentiated the Sucker Bay Lake population, and explained the difference between populations of Iliamna and Six-mile Lakes. Iliamna/Six-mile Lake populations had a pair-wise F_{ST} of 0.048 (95% CI 0.018 – 0.082) with Sucker Bay Lake and 0.054 (95% CI 0.023 – 0.086) with Lake Clark. Between Sucker Bay Lake and Lake Clark populations, F_{ST} was 0.060 (95% CI 0.021 – 0.111). Thus there was significant and similar genetic divergence between these three major population groups.

Genetic divergence within the Lake Clark group

First, the data suggest major genetic divergence between fish spawning in Sucker Bay Lake, and the remaining Lake Clark populations (Figure 2). There was also significant genetic structuring within the Lake Clark group (all populations spawning above the outlet of Lake Clark, not including Sucker Bay Lake). There was no difference in allele frequencies between the two Kijik Lake populations sampled (Little Kijik River, Kijik Lake South Beach) and pair-wise F_{ST} within Lake Clark was greatest between Kijik Lake and other populations (range from 0.008 to 0.024). Priest Rock Creek differed in allele frequencies from all other populations sampled (Table 3). This pattern of divergence within Lake Clark was supported by principal component analysis (Figure 3). The first principal component explained 44% of the genetic variation within Lake Clark and separated the Kijik Lake populations from all others. The second principal component explained 19% of the genetic variation and differentiated the Priest Rock Creek population.

Genetic diversity and bottleneck effects

A significant bottleneck effect was detected in Sucker Bay Lake (Figure 4, $P < 0.005$). The mean expected heterozygosity calculated from observed allele frequencies (0.502) was far in excess of that expected if this population were in mutation – drift equilibrium (0.388). In addition, the Sucker Bay Lake sample had less than half the number of alleles found in the Iliamna/Six-mile Lake samples (48 versus 105). Allelic richness among Sucker Bay Lake fish was 4.17 and significantly lower than that of Iliamna/Six-mile Lake (5.55, $P < 0.001$). Allelic richness within Lake Clark fish was 4.68 and also greater than that of the Sucker Bay Lake population, though the difference is not statistically significant ($P = 0.167$). A lower proportion of rare alleles relative to Iliamna/Six-mile Lake also suggests a bottleneck in Sucker Bay Lake. Fish in Sucker Bay Lake possess approximately 37% fewer rare alleles than fish in Iliamna/Six-mile Lake (Figure 5).

The data also suggest a bottleneck among fish of Lake Clark relative to Iliamna/Six-mile Lake. Eight of the 10 populations in Lake Clark have an excess of heterozygosity relative to that expected at mutation-drift equilibrium though these differences are not statistically significant ($P = 0.517$, Figure 4). However, there is a significant reduction in allelic richness ($P < 0.001$) of Lake Clark populations (4.96) relative Iliamna/Six-mile Lake populations (5.99). We found a total of 105 alleles in Iliamna/Six-mile Lake (383 fish sampled) and only 92 alleles in fish of Lake Clark (959 fish sampled) despite the fact that our sample sizes greatly favored finding more alleles in the Lake Clark populations. In addition, Lake Clark populations have significantly lower proportions of rare alleles than populations of Iliamna/Six-mile Lake ($U_{4,10} = 37$, $P = 0.01$) with 8 of 10 Lake Clark populations having a lower proportion of rare alleles than all four

Iliamna/Six-mile Lake populations (Figure 5). While this difference is not dramatic (Lake Clark mean 0.585, SE 0.010, Iliamna/Six-mile Lake mean 0.641, SE 0.010), it is consistent with our prediction that a bottleneck occurred among fish of Lake Clark relative to Iliamna/Six-mile Lake.

Management relevancy of findings

The strong divergence we found between Lake Clark and Lake Iliamna populations provides fishery managers with a tool to differentiate between fish returning to the different lakes and thus the potential to better regulate harvest for Lake Clark and the Kvichak as a whole. Tissue from approximately 1,100 sockeye salmon from 11 Lake Clark spawning populations were shared with ADF&G for use in the Bristol Bay mixed stock fishery analysis. These samples will allow inclusion of Lake Clark sockeye salmon in their microsatellite, allozyme, and mitochondrial DNA baselines and may ultimately provide harvest rate estimates for Lake Clark sockeye salmon. The ability to differentiate between Lake Iliamna and Lake Clark sockeye salmon will also allow for studies of juvenile dynamics within the lakes, determination of the two lakes contribution to the Kvichak smolt outmigration, and distribution of fish while at sea.

These findings provide a valuable foundation for fishery managers of Lake Clark National Park and Preserve to define population units for conservation or fishery management and to identify population groups for long term monitoring. The reduced genetic diversity within most Lake Clark sockeye salmon populations, and in Sucker Bay Lake in particular, suggests that conservation of these populations should be a high priority for Lake Clark and Bristol Bay fishery managers.

CONCLUSIONS

1. The magnitude of genetic differentiation among spawning populations of Lake Clark sockeye salmon is larger than that typically found between populations within the same lake.
2. There is significant genetic divergence between populations of Lake Clark and Six-mile Lake, the latter being more similar to fish of Lake Iliamna.
3. The reduced numbers of alleles and strong divergence of most Lake Clark populations relative to Lake Iliamna/Six-mile Lake populations suggest a bottleneck, or period of reduced populations size, associated with the colonization of Lake Clark by sockeye salmon.
4. The greatest bottleneck effect detected and the most genetically distinct population was Sucker Bay Lake in Lake Clark. This population also appears to be a much reduced abundance (<300 fish, 2002) compared to historical aerial survey data (>1000 fish).
5. Bottleneck effects may exist among other populations within Lake Clark; additional tests with more sensitive markers will be required to resolve these.

Recommendations

The data strongly support managing sockeye salmon of Lake Clark, and the Six-mile and Lake Iliamna sockeye as separate populations. Special consideration should be given to the conservation of the fish of Sucker Bay Lake, Kijik Lake, and Priest Rock Creek because these populations are genetically divergent from other populations surveyed. In addition, the Sucker Bay Lake and Priest Rock Creek populations have very reduced numbers of spawners (< 300) and genetic diversity, which indicate these populations are at risk of extinction.

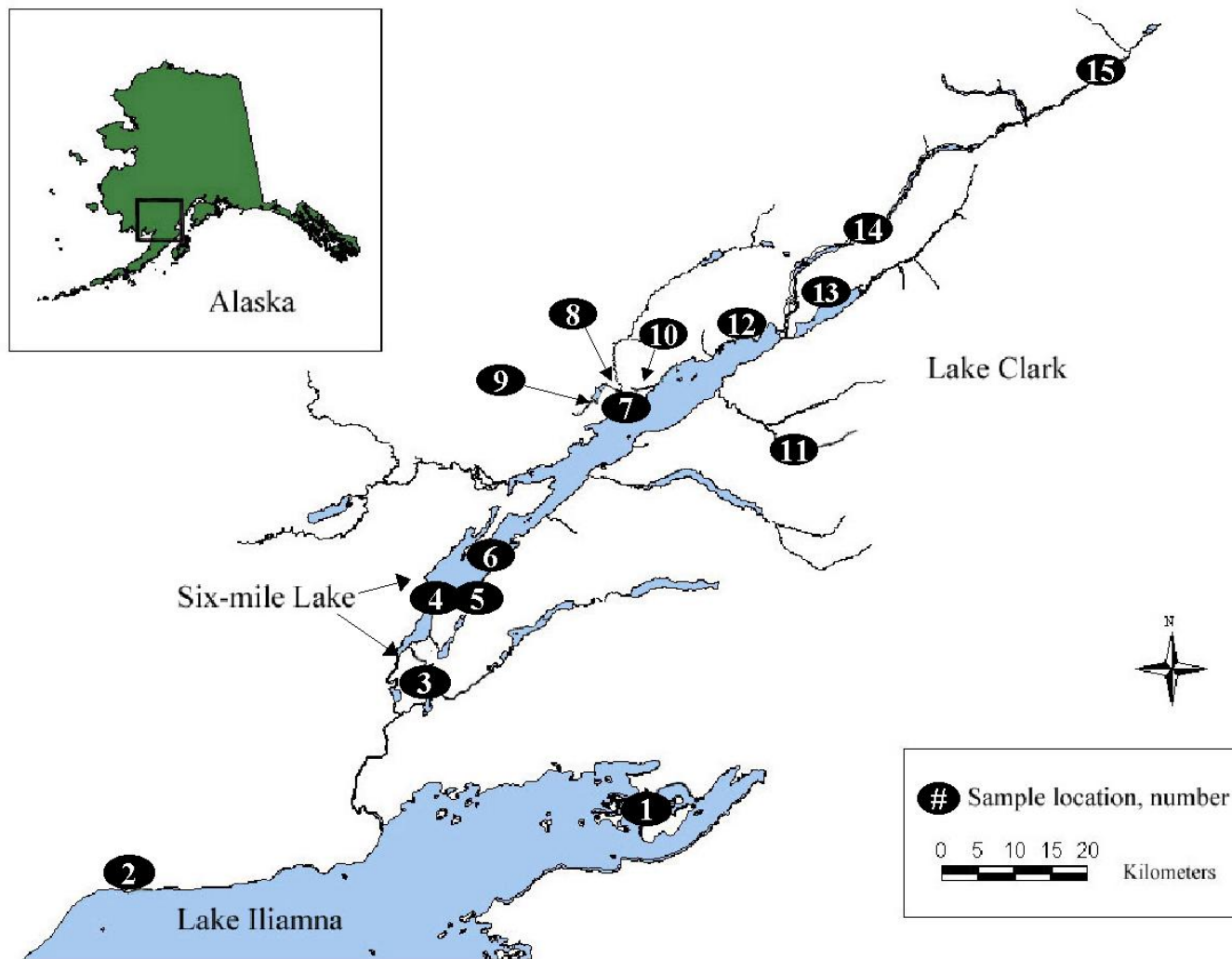


Figure 1. Map of Lake Clark, Six-mile Lake, and Lake Iliamna with sample sites shown. Refer to Table 1 for population numbers.

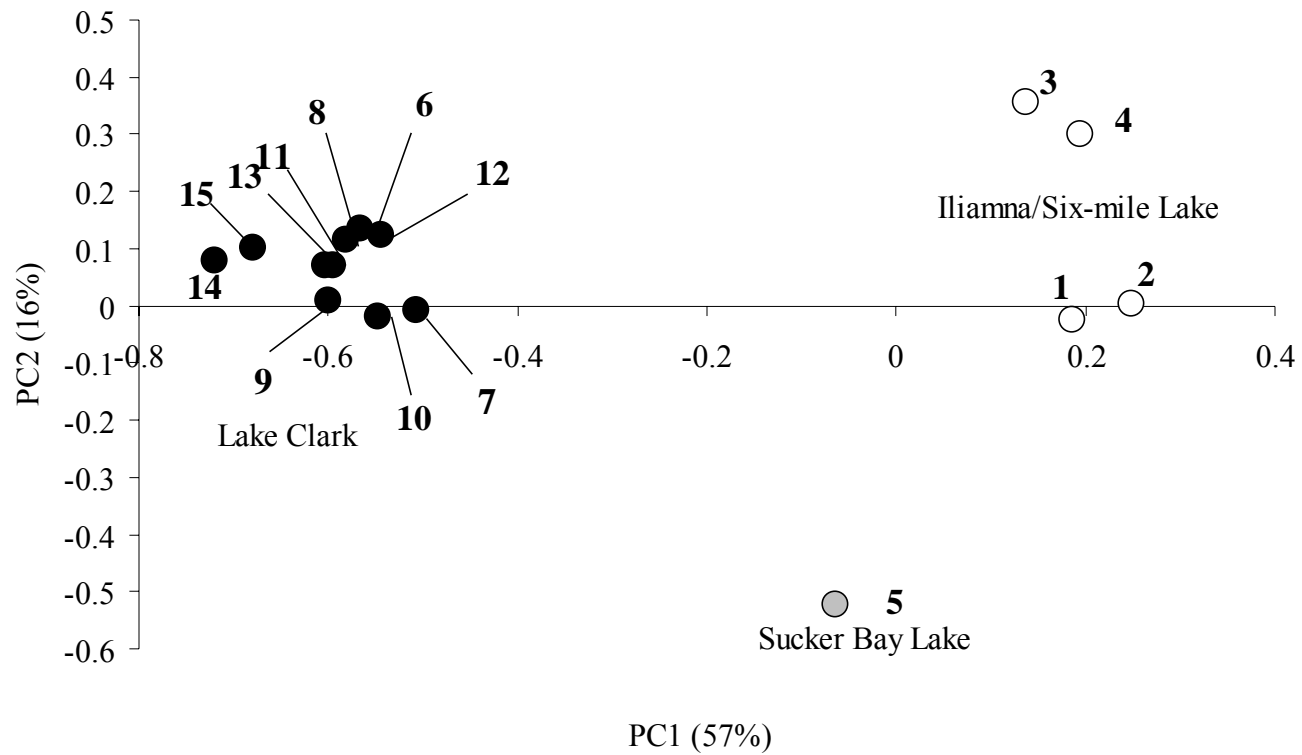


Figure 2. Principal component analysis of allele frequencies at 11 microsatellite loci. Percentages in parentheses indicate amount of variation explained by each principal component. Three major population groups are detected: Iliamna/Six-mile Lake = outlined, Lake Clark = black, and Sucker Bay Lake = shaded points. Refer to Table 1 for population numbers.

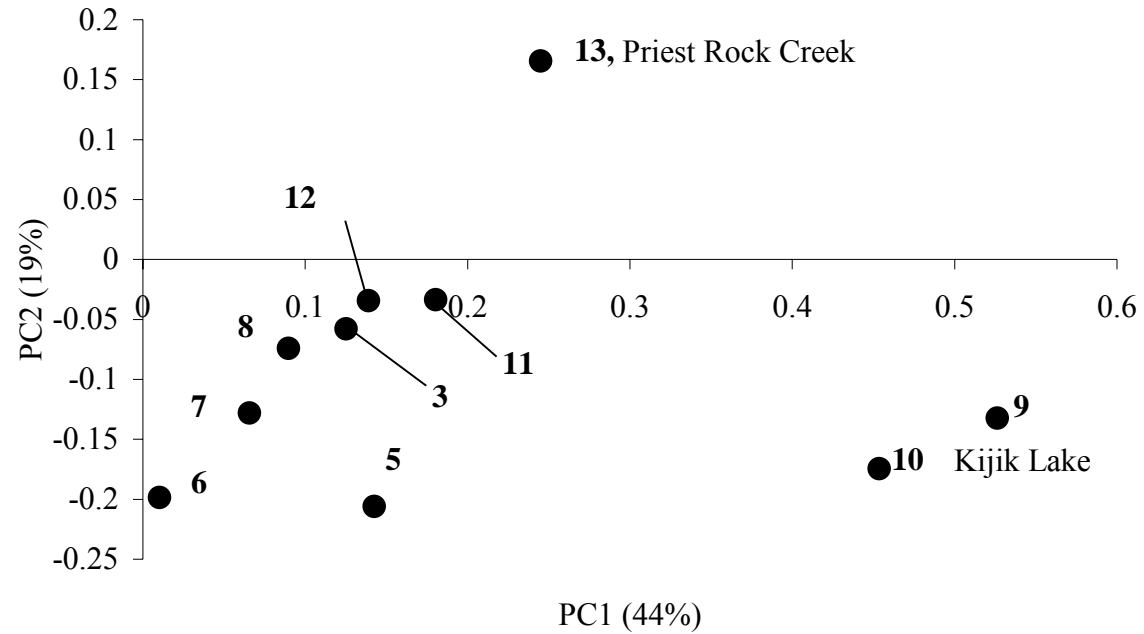


Figure 3. Principal component analysis of Lake Clark population allele frequencies at 11 microsatellite loci. Highly divergent populations of Kijik Lake and Priest Rock Creek are identified. Percentages in parentheses indicate amount of variation explained by each principal component. Refer to Table 1 for population numbers.

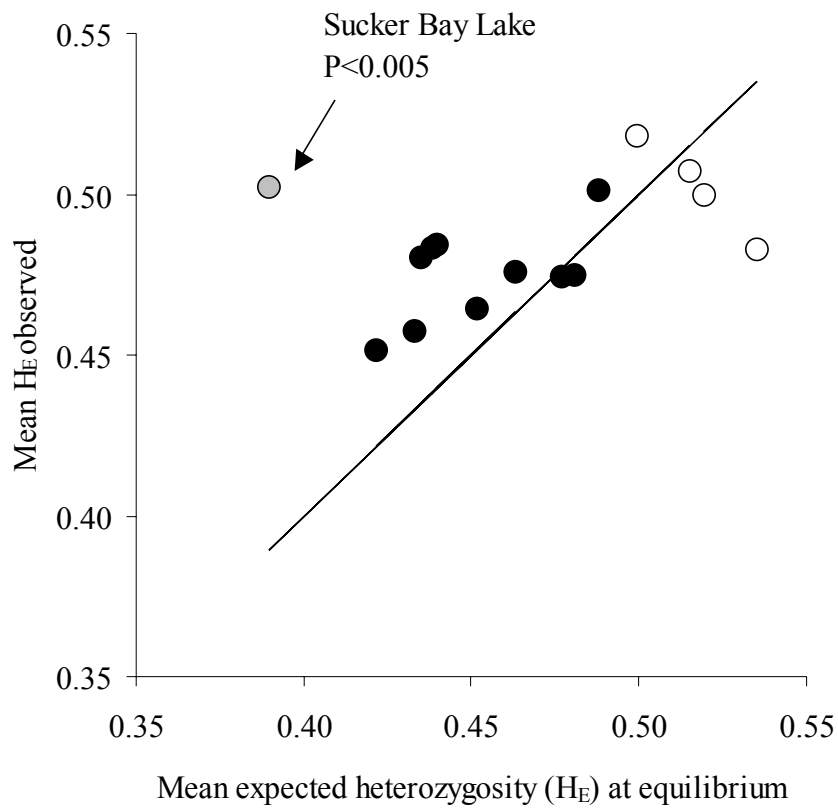


Figure 4. Relationship between mean expected heterozygosity (H_E) observed and expected under the Infinite Alleles Model of mutation (IAM). Recently bottlenecked populations will have greater heterozygosity (H_E) than expected at migration-drift equilibrium with the same number of alleles due to the loss of rare alleles. Non-bottleneck populations will have an H_E that is equal to or less than that expected under IAM (on or below equality line). Three major population groups are coded as follows: Iliamna/Six-mile Lake = outlined, Lake Clark = black, and Sucker Bay Lake = shaded circles.