Preliminary parentage analysis of 2014 SEAK chum alevin

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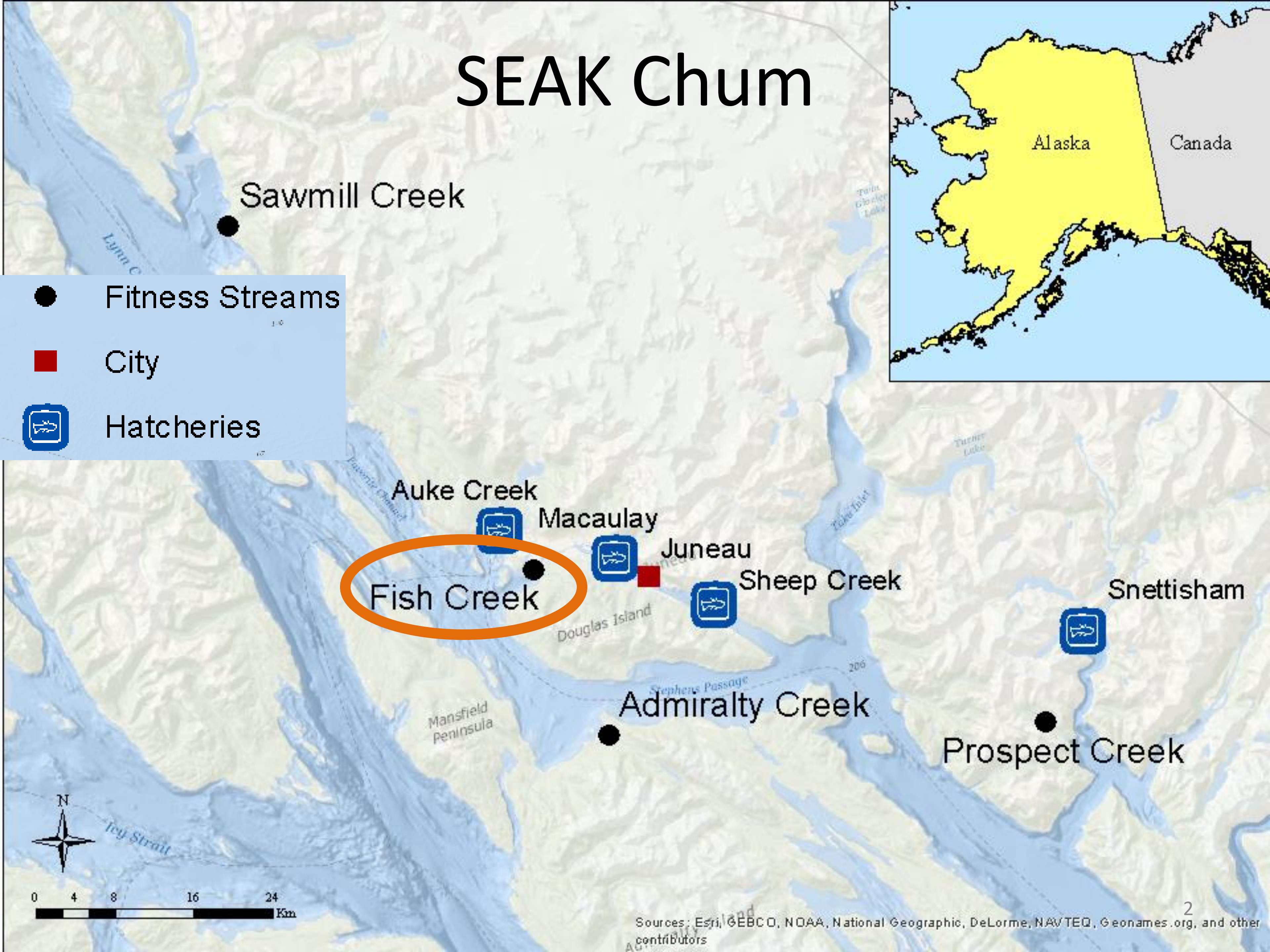
SEAK Chum



Sources: Esri, GEBCO, NOAA, National Geographic, DeLorme, NAVTEQ, Geonames.org, and other contributors

Sample size

ADULTS

	Floy Tagged	Carcass	Total
Field	241	767*	1008

*** Includes 24 floy tagged fish re-sampled**

OFFSPRING

	Alevin
Field	567

QC Process

- Individuals
  - ✓ 80% loci genotyped
  - ✓ No duplicated individuals
- Loci
  - ✓ 80% individuals/collection

Sample size

ADULTS

	Floy Tagged	Carcass	Total
Field	241	767*	1008
Genetics	239	720	959

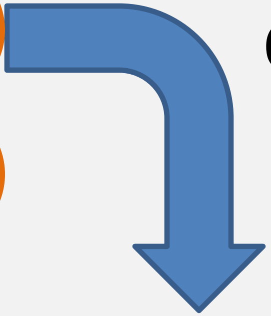
* Includes 24 floy tagged fish re-sampled

OFFSPRING

	Alevin
Field	567
Genetics	553

Sample size

	Genotyped	Used
Adults	976	959
Alevin	567	553



Otoliths

	Female	Male	Unknown
Hatchery	230	235	1
Natural	116	153	0
Unknown	98	126	0

Preliminary parentage analysis

\# Parents = 959

\# Offspring = 553

\# SNP Loci = 176

- FRANz
  - ➢ Parentage analysis
    - More offspring to 1 parent than 2
  - ➢ Sibling analysis
    - Non-random among pump sites

QCed data available
Tuesday

Genetic Parentage Assignment Works!

Future work (Winter 2015)

- Compare with other methods
- Tech Doc on parentage assignment methods
- Determine RRS
  - ➢Parentage + otolith data → RRS
  - ➢n = # of families / origin group
- More detail on sibling relationships
- Marker selection
  - ➢Repeat with fewer SNPs

Timeline

	Done	2015				2016			
		Winter	Spring	Summer	Fall	Winter	Spring	Summer	Fall
Extract 2013 chum	■								
Genotype Fish Creek adults & alevin	■								
Parentage methods Tech Doc		■							
2014 chum alevin results		■							
Chum SNP selection		■							
Extract 2014 chum			■	■					
Extract 2013 & 2014 pink			■	■					
Genotype 2013 & 2014 chum				■	■				
Pink SNPs available					■				
Genotype Stockdale adults & alevin						■	■		
Pink SNP selection							■	■	