

A photograph of an Arctic ringed seal resting on a piece of ice in the water. The seal is the central focus, lying on its side on a white, snow-covered ice floe. The water is a deep blue, and there are other smaller ice floes scattered in the background. The seal's fur is dark with lighter spots, and its head is turned towards the right. The overall scene is a natural, outdoor setting.

Assessing population structure in Arctic ringed seals

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Photo credit: NOAA Fisheries

- **Collaborators/Contributors**

- Peter Boveng and Heather Ziel, AFSC
- Lori Quakenbush and the Ice Seal Biomonitoring Program, ADFG
- Barb Taylor, Kelly Robertson, and Morgane Lauf, SWFSC
- Karyn Rode, USGS



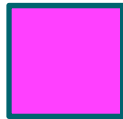
Taxonomy and status:



Arctic ringed seal (*P. h. hispida*)
IUCN: Least Concern
ESA: Threatened



Okhotsk ringed seal (*P. h. ochotensis*)
IUCN: Least Concern
ESA: Threatened



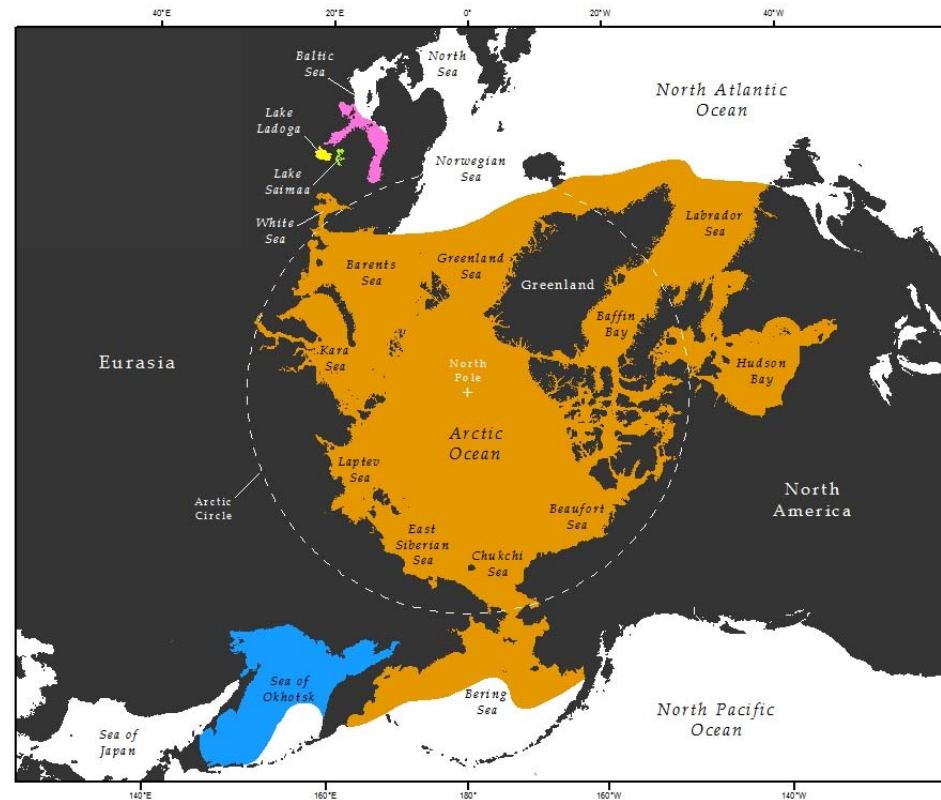
Baltic ringed seal (*P. h. botnica*)
IUCN: Least Concern
ESA: Threatened



Ladoga ringed seal (*P. h. lagodensis*)
IUCN: Vulnerable
ESA: Endangered

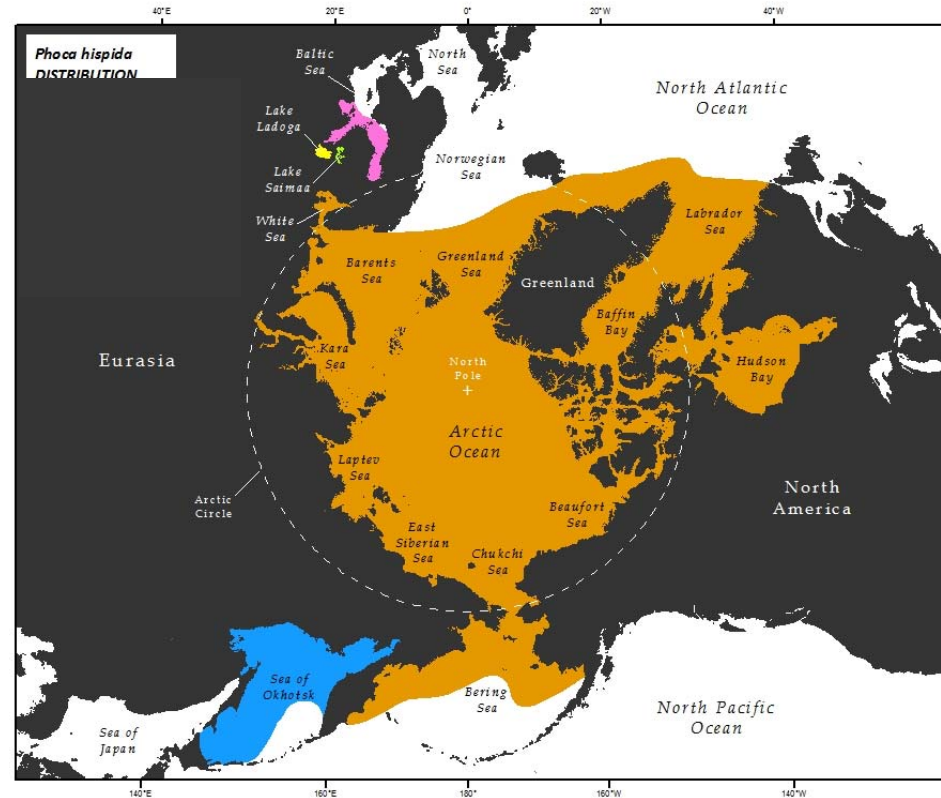


Saimaa ringed seal (*P. h. saimensis*)
IUCN: Endangered
ESA: Endangered



Within the Arctic:

- Widely distributed and abundant
 - ~3 million across range (Laidre et al. 2015)
 - ~300,000 in the Alaskan Chukchi and Beaufort (Kelly et al. 2010)
- Within U.S. waters, only a single Alaskan stock is recognized
 - Co-managed by NMFS and the Ice Seal Committee



Conservation and management concerns:

- Ringed seals depend on sea ice and snow cover for survival and reproduction
- Sea ice extent, thickness and seasonal duration is declining
- Declines in body condition, reproductive rates, pup survival, and foraging behavior have been reported in some areas¹

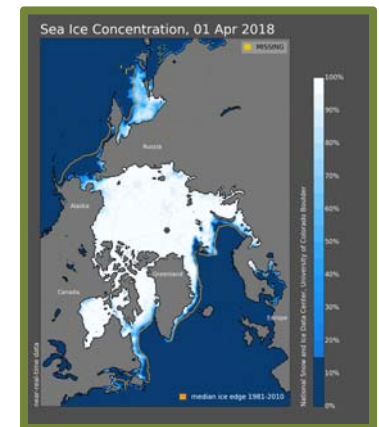
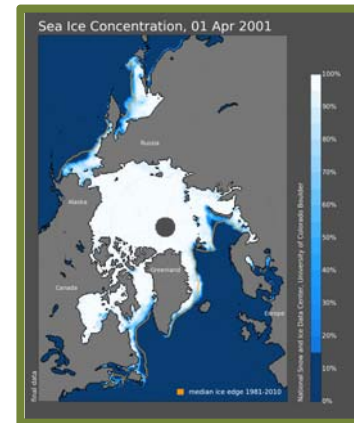


Photo credit: Shawn Dahle, NOAA
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¹ Ferguson *et al.* 2005, 2012, 2017; Stirling 2005, Harwood *et al.* 2012b, Hamilton *et al.* 2016, Yurkowski 2016)

Why do we need to understand population structure?

- Some regions of the Arctic are impacted by climate warming more severely than others
 - If no population structure exists, then seals that have previously used impacted areas will move to other areas where suitable habitat remains
 - If seals return to breed in the same area where they were born (i.e., natal philopatry), localized depletion may occur



Images:nsidc.org

Population structure: What do we know so far?

- Satellite tagging:
 - Seals range widely during the foraging season
 - Movements more restricted during the winter-spring months
 - Tagged seals have been shown to return to the same wintering areas in subsequent years
- Genetics:
 - Genetic analyses have failed to detect population structure throughout most of the range of the Arctic subspecies (Davis et al. 2008, Martinez-Bakker et al. 2013)
 - These studies have relied on mtDNA sequence data and a small number of nuclear markers (9-11 microsatellites)



Photo credit: Michael Cameron, NOAA
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Population structure: What do we know so far?

- Genetics:
 - But
 - Genetic differences accumulate slowly in large populations
 - Traditional markers may have little power to detect low, but potentially biologically significant, levels of differentiation
 - Recent technological advances (“Next Generation Sequencing”) allow large numbers of SNPs to be genotyped
 - Cost-effective
 - Genome sequence data not required
 - Such extensive datasets have been shown to substantially increase the power of genetic analyses even with limited sample sizes

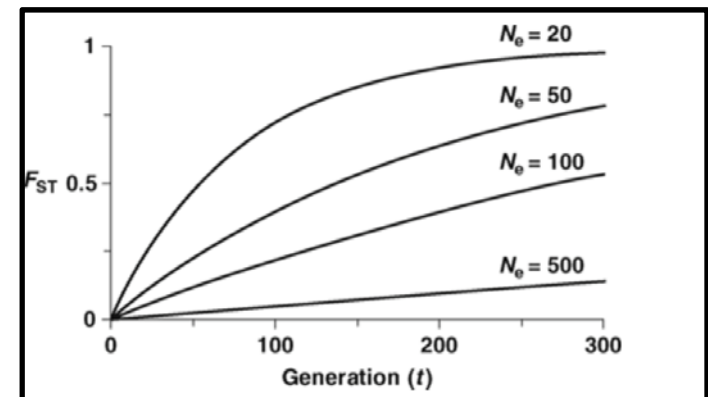


Fig 14.8. Relationship between F_{ST} , effective population size (N_e), and time (in generations). From Allendorf et al. 2010

Objective: Evaluate whether population structure can be detected in Arctic ringed seals using a large genome-wide dataset of SNP markers

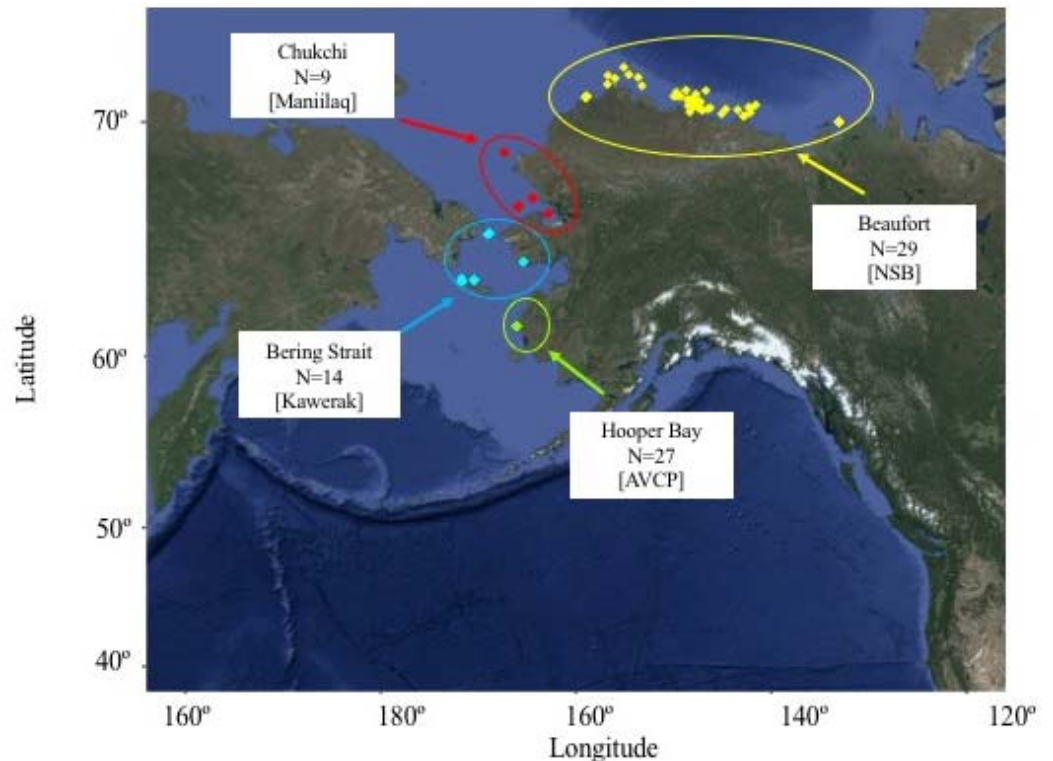
- SNP discovery and genotyping approach: DArTseq
 - Diversity Arrays Technology Pty Ltd
 - ddRADseq-like approach



Get a bigger hammer!

Samples:

- Samples from 90 individuals
- All collected between March – May (breeding season)
- Majority from harvested seals; remainder from seals killed by polar bears

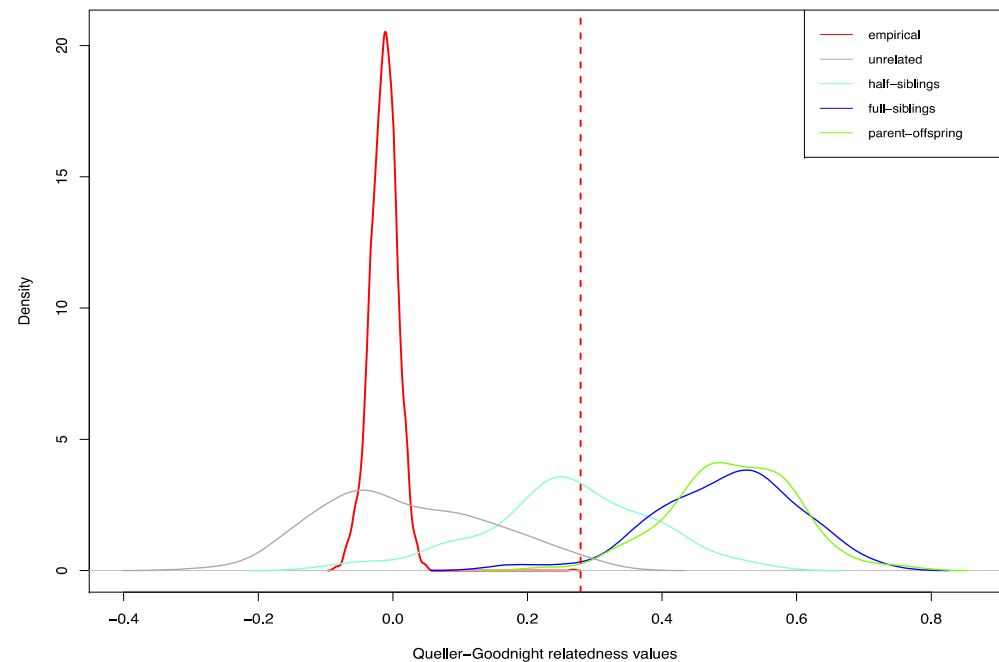


Results: Quality control

Filtering Criterion	# of individuals	# of loci removed	# of loci remaining
Unfiltered dataset	90	100,281	100,281
Multiply aligned	90	660	99,621
Avg read count < 15	90	34769	64,852
Avg read count > 100	90	2697	62155
Monomorphic*	85	12760	49395
Call rate \leq 0.8	85	11402	37993
Reproducibility < 0.95	85	253	37740
Secondary loci	85	12927	24813
Individual coverage < 0.8	83	132	24681
Minor allele frequency < 0.05	83	16632	8049

Results: Relatedness

- Two samples collected in Hooper Bay in the spring of 2008 appear to be paternal half-siblings
- Based on the harvest data, one individual was ~8 mos old and the other ~12 mos old
- Provides evidence of a single male mating with multiple females within a given season
- Highlights need to understand more about movements of seals during their first year



Results: Genetic Differentiation

Little to no genetic differentiation between a priori defined geographic strata was detected, although the comparison of samples collected in Hooper Bay and those from the Beaufort Sea were close to significance.

Strata compared:	F_{ST} (p-value)	X^2 p-value
Hooper Bay (n=27) v. Bering Strait (n=14)	-0.001 (p=0.755)	0.638
Hooper Bay (n=27) v. Chukchi (n=9)	0.001 (p=0.199)	0.056
Hooper Bay (n=27) v. Beaufort (n=29)	<i>0.001 (p=0.081)</i>	0.035
Bering Strait (n=14) v. Chukchi (9)	0.000 (p=0.423)	0.468
Bering Strait (n=14) v. Beaufort (n=29)	0.000 (p=0.445)	0.341
Chukchi (n=9) v. Beaufort (n=29)	0.000 (p=0.638)	0.638

What's next?

- Clustering analyses (e.g., STRUCTURE, DAPC)
 - A priori stratification of samples not required
- Detecting loci under selection
 - May allow for detection of adaptive variation



Photo credit: Michael Cameron, AFSC
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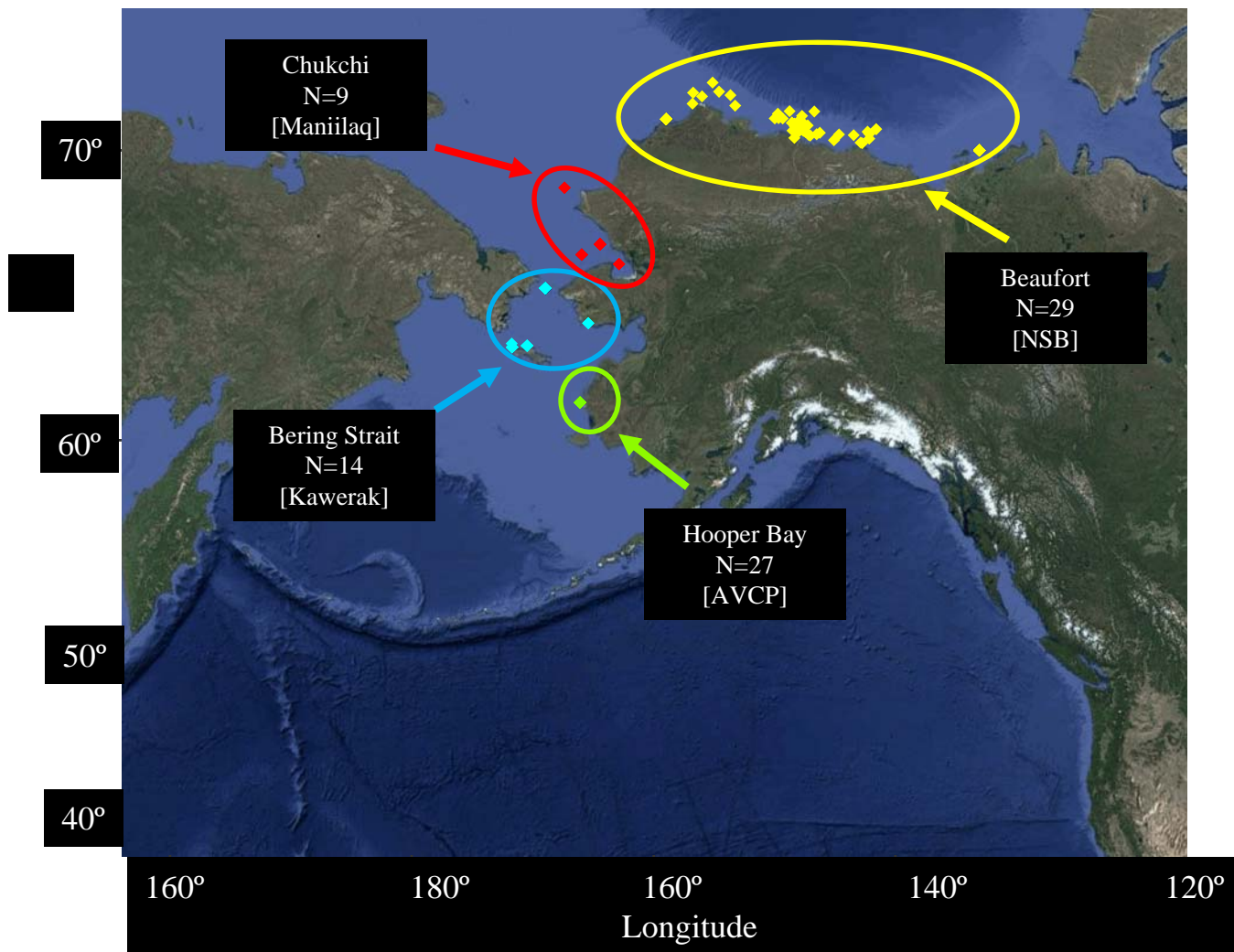
Implications (so far):

- Despite greatly increasing the power of the analyses, the results are generally consistent with previous studies suggesting little to no population structure is present within the Arctic
 - Suggests that the loss of sea ice habitat may not result in the loss of genetic diversity
- However, small, but statistically significant, differences were seen between the most geographically distant strata
 - Genotyping additional samples could be valuable
 - Increase power by increasing sample sizes
 - Fill in sampling gaps

Thank you to the Marine Mammal Commission for funding this work!



Photo credit: Shawn Dahle, AFSC
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Management:

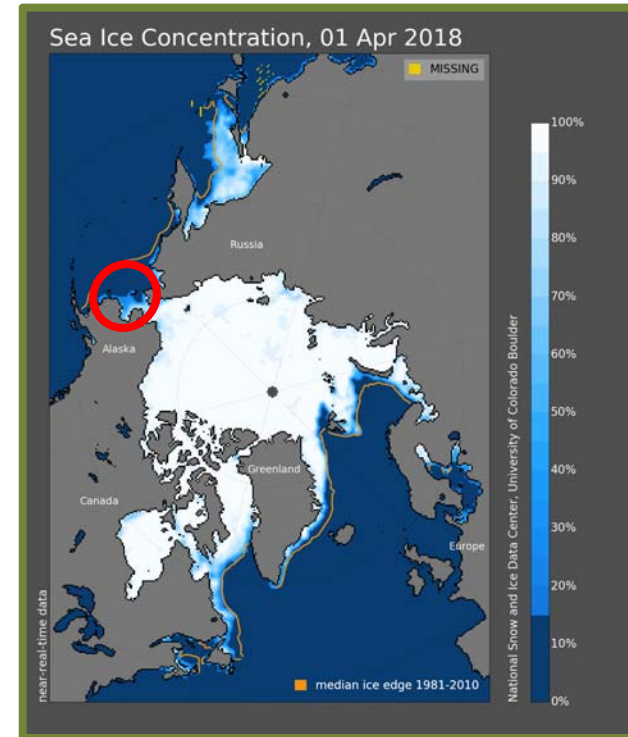
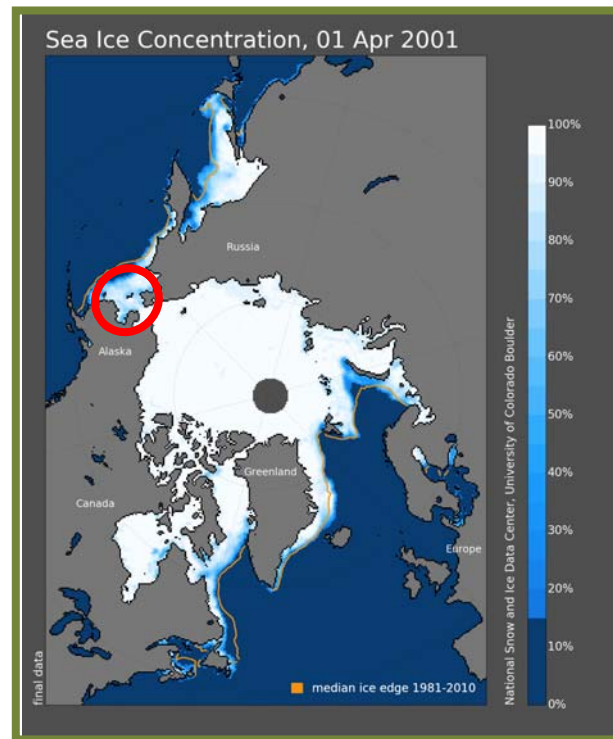
- Objectives of the ISC:
 - Maintain healthy ice seal populations in AK waters
 - Provide for adequate subsistence harvest of ice seals
 - Protect hunting privileges for AK Native subsistence hunters

Results: mtDNA

Little to no genetic differentiation between geographic strata was detected, although the comparison of samples collected in the Bering Strait region and those from the Beaufort Sea were statistically significant.

Strata compared:	Φ_{ST} (p-value)
Hooper Bay (n=39) v. Chukchi (n=34)	0.003 (p=0.363)
Hooper Bay (n=39) v. Bering Strait (n=105)	-0.003 (p=0.604)
Hooper Bay (n=39) v. Chukchi (n=34)	0.003 (p=0.311)
Hooper Bay (n=39) v. Beaufort (n=116)	0.007 (p=0.130)
Bering Strait (n=105) v. Chukchi (n=34)	0.010 (p=0.118)
Bering Strait (n=105) v. Beaufort (n=116)	0.009 (p=0.024)
Chukchi (n=34) v. Beaufort (n=116)	0.007 (p=0.148)

Unstable habitat?



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