

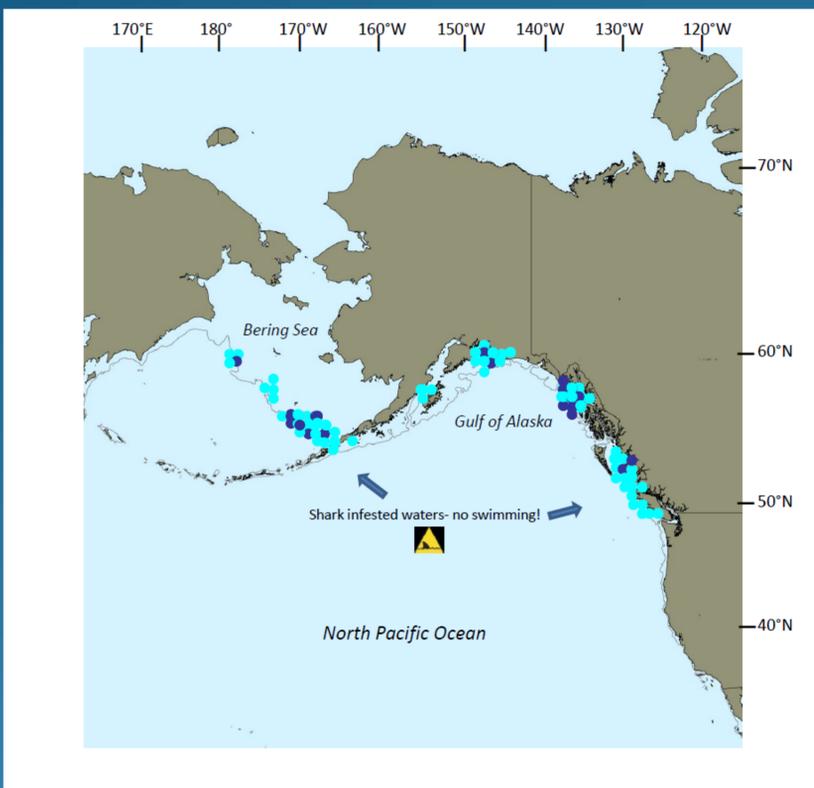


Two Genetically Distinct Populations of Sleeper Sharks in Alaska and British Columbia

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The purpose of this investigation was to examine the population structure of sleeper sharks (*Somniosus pacificus*) in Alaskan waters.



Tissue samples, collected 1998-2013, were kindly provided by the University of Washington Fish Collection, Fisheries and Oceans Canada, International Pacific Halibut Commission, and the University of Windsor, Canada.

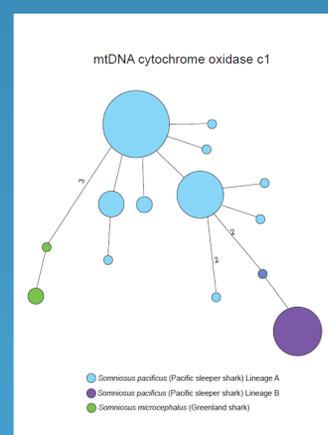


Primers were developed for three regions of the mtDNA genome. DNA was amplified and sequenced. Resulting haplotypes were aligned with CodonCode, analyzed with Arlequin software, and visualized by creating haplotype networks in Sneto.

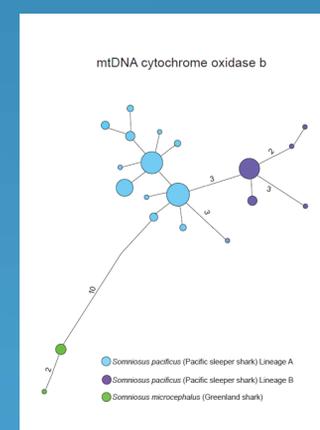
Haplotype networks (below) depict sequence divergence among Pacific sleeper sharks. Circle size represents the number of individuals with that haplotype, and the lines represent a one base pair difference, unless otherwise noted. Blue and purple circles represent two *Somniosus pacificus* lineages. Green represents Greenland Shark (*Somniosus microcephalus*).

Map of collections of *Somniosus pacificus* samples. The two colors (blue and purple) depict the two distinct lineages, which were likely separated by a physical barrier in the past (ice?). The geographic distribution reveals both types are found throughout Alaskan waters.

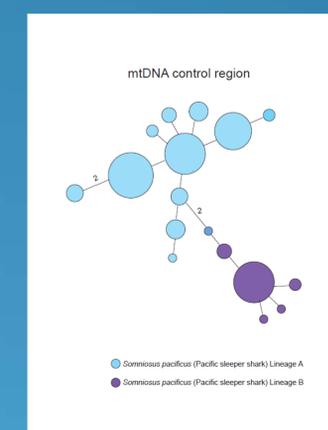
Greenland sharks were collected in Baffin Bay near Greenland (not pictured), and were examined to test the hypothesis that one of the Alaskan sharks may be Greenland shark. Our study indicates that neither of the *S. pacificus* lineages are Greenland shark.



CO1, the barcode gene, typically used to examine speciation, separates the three *Somniosus* by 3 base pairs each.



Cyt-b is the best marker to detect speciation of *S. pacificus* and *S. microcephalus* with a 10 base pair divergence.



Control region (D-loop), further confirms the discrete segregation of each lineage. No data was available for *S. microcephalus*.

Conclusion: Two distinct lineages of sleeper sharks in Alaskan waters were identified from three regions of the mtDNA genome. These two historical lineages are now found sympatrically throughout the range sampled. Neither of the lineages is Greenland shark. Nuclear markers are needed to ascertain the current level of introgression.