

## Genetic Studies of the Pacific Walrus

Chadwick Jay, Sandy Talbot, Anthony Fischbach, Kevin Sage, James Jackson

U.S. Geological Survey, Alaska Science Center  
 1011 E Tudor Road  
 Anchorage, Alaska 99503 USA  
[Chad\\_Jay@usgs.gov](mailto:Chad_Jay@usgs.gov)

Presented at the Marine Mammals of the Holarctic III, October 11, 2004

The USGS Alaska Science Center has initiated research to investigate the genetic structure of the Pacific walrus (*Odobenus rosmarus divergens*). The study will analyze genetic data from walrus inhabiting regions in Alaska and Russia to evaluate hypotheses regarding the genetic structuring of breeding aggregations and non-breeding regions. As a precursor to this study we developed and tested markers suitable for detecting population structure in walrus: probes for 15 nuclear DNA micro-satellite loci and probes for sequencing the control region of the mitochondrial DNA. These markers have been found suitable for distinguishing among individuals, including family members, thus allowing investigation of family relationships. The probability of two walrus sharing the same genotype for the nuclear microsatellite markers is less than 1 in 6 billion, allowing unambiguous identification of individual walrus. A high haploid diversity index of 0.62 ( $n = 35$  walrus) will allow us to investigate hypotheses of the distribution of maternal lineages.

To allow us to investigate hypotheses of sex-specific structuring of the Pacific walrus population, we optimized and tested a genetic sex determining technique. We evaluated its reliability by examining the sex of 249 Pacific walrus tissue and blood samples from animals field identified to sex. The molecular technique concurred with the field reported sex for 99.2% (95% confidence limits: 99.8%–96.5%) of the observations. High concordance between the molecular and field

verified sex indicates that this technique is suitable for sex determination of walrus tissues for harvest monitoring, behavioral, and population genetics studies when a verified field sex is not available.

Although we have optimized the genetic tools required to assess population structuring in Pacific walrus, we need additional samples to conduct the full analysis (Figure 1). For the breeding period, we have sufficient samples from the Nuivak Island polynya, but we require additional samples from the St. Lawrence Island polynya and the Gulf of Anadyr. For the non-breeding period, we have sufficient samples from males of the southeastern Bering Sea, the southern Chukotkan coast, and the region south of the Andayr Gulf, but we require additional samples from the northwestern Bering Sea and the western Chukchi Sea. The available samples have been collected through collaborations with Russian researchers from the Pacific Institute of Fisheries and Oceanography (TINRO), the former All-Union Institute of Fisheries and Oceanography (VINRO), and the Soviet Ministry of Fisheries; through harvest monitoring efforts in Russia conducted by Chuktoka-TINRO and the Association of Traditional Marine Mammal Hunters of Chukotka; and through harvest monitoring efforts in the U.S. conducted by the U.S. Fish and Wildlife Service and the Eskimo Walrus Commission. We hope that collection of additional samples will be possible through continuing internationally coordinated research cruises and harvest monitoring efforts.

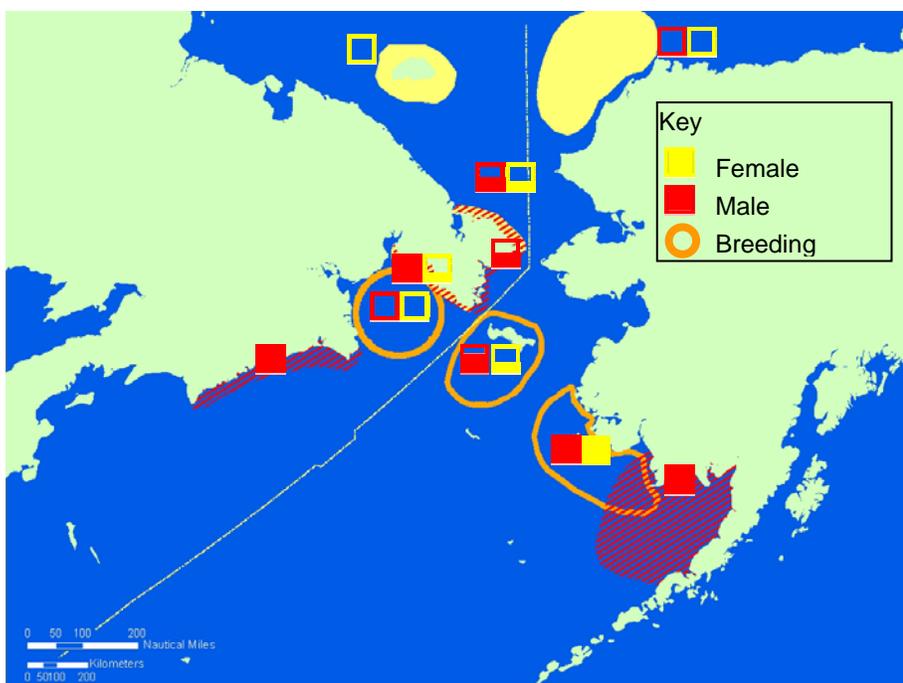


Figure 1: Distribution of samples collected for the genetic analysis of Pacific walrus population structure.

Orange polygons represent winter breeding grounds.

Yellow and dashed red polygons represent female and male summering grounds respectively.

Squares represent the status of sample collection in each region. Full squares represent 30 or more samples, which is required for population genetics analysis.