

**Genetic analysis of eastern Pacific seals (*Phoca vitulina richardsi*) from British Columbia and parts of Alaska using mitochondrial DNA and microsatellites.**

In British Columbia the population of harbour seals, *Phoca vitulina richardsi*, has increased from 9,000 to 135,000 since their protection 25 years ago. Difference in pelage patterns and pupping times suggest that more than one population of harbour seals may be present in the eastern Pacific.

Molecular analyses were used to investigate the genetic diversity and population structure of harbour seals along the B.C. coast and in parts of Alaska. The allele frequency at seven microsatellite loci and the haplotypic diversity of the mitochondrial control region (D-loop) were examined.

A 475 base pair fragment containing the tRNA proline and part of the mitochondrial control region was amplified and sequenced from 128 animals. Sixty variable sites defined 72 mtDNA haplotypes with pairwise nucleotide differences as high as 5%. Only 14 haplotypes were shared between two or more seals. Some of the more frequent haplotypes were unique to specific areas, while others were distributed over a broad geographic range. Three groups representing the southern Strait of Georgia, southern B.C. and northern B.C./southeast Alaska were observed using parsimony and distance based phylogenetic reconstruction. Additional analyses using sequences from Washington and California revealed the presence of another population comprising the outer coast of Washington, Oregon and California.

The order of the clades suggests that the Pacific Ocean was colonized twice. The first invasion occurred approximately 0.67 MYA and represents only a small portion of today's harbour seals in southern Vancouver Island. Seals from the second invasion, about 0.38 MYA, are distributed throughout the Pacific.

Analyses of five polymorphic microsatellite loci show that the allele frequency distribution is significantly different in southern British Columbia and northern British Columbia/Alaska. Average heterozygosity was similar for northern and southern populations, however the allelic diversity was higher in the southern population. The migration rate for males based on microsatellite data (3-7 seals/generation) was higher than that obtained for females from the mtDNA (0.3 females/generation). This suggests that although migration rates are low they are sufficient to allow gene flow between the two populations.