# Australian Marine Mammal Centre

# Final Report

**(subclause 9 and Schedule Item 5 of the Funding Agreement)**

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- **Project No**. – #09/9
- **Title** - Population genetic structure of Australian sperm whales
- **Chief Investigator** – Dr Luciana Möller
- **Organisation** – Flinders University

**Activity Period** – 9 March – 31 August 2010

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## 1. Activity Summary

A clear summary of approximately 500 words outlining the work undertaken and any significant findings (for publication on the Department's web site)

This study aimed to investigate the population genetic structure of Australian sperm whales using a combination of nuclear DNA markers (microsatellites and single nucleotide polymorphisms (SNPs)) and the maternally inherited mitochondrial DNA (mtDNA) control region. We analysed a total of 174 samples from six putative populations: New South Wales, Tasmania, Victoria, South Australia, Albany (WA), Carnarvon (WA). Contemporary samples were from NSW, Victoria and South Australia, while historical samples (50-60 years old) were collected from Victoria, South Australia, and Western Australia. We removed highly related individuals prior to analysis to control for the potential kin-sampling bias for population comparisons. To identify relatives, we calculated relatedness among each pair of individuals using the 13 microsatellite loci and removed one individual for any pair of individuals sampled in the same region with a relatedness value $\geq 0.5$. The restricted dataset included 146 individuals. NSW: 17 (16 males, 1 unknown), TAS: 48 (19 males, 29 females), SA/VIC combined: 17 (7 male, 4 female, 6 unknown), Albany: 56 (31 male, 23 female, 2 unknown) and Carnarvon: 8 (8 males).

Based on this restricted dataset, we found moderate levels of genetic variation (microsatellites: 7.1 alleles/locus and mean heterozygosity of 0.72), which is slightly lower than reported for sperm whales in the northern hemisphere (12.7 alleles/locus and mean heterozygosity = 0.79; Pinela et al. 2009). For the 13 SNP markers successfully genotyped, 11 were polymorphic and used for the analysis. Minor allele frequencies ranged from 0.04 to 0.45. For mtDNA data, we detected eleven distinct haplotypes with an average haplotypic diversity of 0.67 and nucleotide diversity of 0.0039 over all populations. Using several analytical approaches based on microsatellite and SNP data, we detected no significant genetic structure among the

six putative populations ($p > 0.05$ for all pairwise comparisons). Additional samples that were obtained from Norfolk Island (n=1) and Broome, WA (n=1) were also assigned with high confidence to this one population. Conversely, we detected complex patterns of population structure based on the mtDNA control region. For example, Albany was significantly differentiated from NSW, Victoria/South Australia and Carnarvon (Fst = 0.12, 0.19, 0.23, respectively; $p < 0.05$ for all pairwise comparisons), while genetic differentiation between Albany and Tasmania was significant only when females were included in the analysis (Fst = 0.39, $p < 0.05$). Samples from Tasmania were also significantly differentiated from Carnarvon and Victoria/South Australia (Fst = 0.10, 0.07, respectively; $p < 0.05$ for both pairwise comparisons), but not from NSW. Since few (or no) samples of females were available from NSW, South Australia/Victoria and Carnarvon, we were unable to test for genetic structure of females among these putative populations. Nevertheless, the significant differentiation among females from the Albany and Tasmania populations using the mtDNA control region and the lack of genetic differentiation with microsatellite markers is consistent with a matrilineal population structure, whereby females are philopatric to particular areas and males disperse between these female groups.

This pattern of male-biased dispersal is similar to previous studies on sperm whales in the northern hemisphere (Engelhaupt et al. 2009; Lyrholm et al. 1999). The results also suggest the possibility of strong matrilineal population structure among other regions in Australia. Finally, to sustain levels of genetic and demographic connectivity among female groups, a precautionary approach to conservation management is required, whereby each geographic region (NSW, Tasmania, Victoria/South Australia, Albany and Carnarvon) is considered as a separate management unit.

## 2. The Outcomes/Objectives

**The degree to which the Activity has achieved the objectives**

**Please refer to question 7 of the application.**

***Aim:*** **To investigate population genetic structure of Australian sperm whales and contemporary genetic diversity of Albany whales**

Using a combination of contemporary and historical samples, we have successfully assessed the genetic population structure of sperm whales in Australian waters. We have found evidence for matrilineal population structure in at least two regions in Australia (Albany and Tasmania), which suggests these populations should be considered as separate management units. Furthermore, we have discovered that genetic connectivity of sperm whales around Australia is facilitated primarily by the dispersal of males. Since our sample size of female sperm whales were inadequate for several regions (NSW, Victoria/South Australia and Carnarvon), the matrilineal structure of these putative populations remains to be tested.

Since we did not receive the funds to collect contemporary samples of sperm whales from the Albany region, we were not able to assess the contemporary levels of genetic variation of Albany whales (the second aim of this study). The collection of these samples in the future will help determine whether large-scale population declines as a

result of commercial whaling resulted in a significant decrease in genetic variation.

## 3. Appropriateness

**The appropriateness of the approaches used in the development and implementation of the Activity**

A considerable proportion of samples used in this study were obtained from teeth specimens that were collected 50-60 years ago. We were able to successfully extract DNA from these teeth and genotyped samples at 13 highly polymorphic microsatellite loci. The samples were also successfully sequenced at the mitochondrial control region and amplify well using the new SNP genotyping method. The level of genetic variation observed at these markers (nine mtDNA haplotypes and for microsatellites, a mean heterozygosity of 0.71) also provided us with sufficient power to conduct a detailed analysis of population genetic structure. We also successfully optimised 13 single nucleotide polymorphisms (SNPs) for the contemporary and historical DNA samples. Since two SNP loci were monomorphic for the Australian sperm whales, analysis was based on the remaining 11 SNPs. Supplementing the samples from stranded animals and teeth with samples from live biopsied whales would have increased the sample size for females but funds were not available to carry out this option.

## 4. Effectiveness

**The degree to which the Activity has effectively met its stated objectives**

The Activity has successfully achieved the objectives of this study. We obtained a set of highly polymorphic markers, we optimised these markers for degraded samples and obtained new tissue and teeth samples for analysis. The use of historical samples has provided us with a sufficient sample size to elucidate patterns of population structure and dispersal of Australian sperm whales. Due to the lack of contemporary samples from the Albany region (funding for fieldwork in Albany was requested to the AMMC but not granted), we were unable to meet our second objective of assessing contemporary levels of genetic variation in sperm whales.