

Australian Marine Mammal Centre
Final Report
(subclause 9 and Schedule Item 5 of the Funding Agreement)

- **Project No.** – 0809/13
- **Title** - Unravelling the genetic structure and diversity of Balaenoptera musculus in Australia: the genetic identity of Geographe Bay blue whales
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Activity Period – 31 March 2009 – 30 April 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)

The Activity involved further elucidating the genetic structure and diversity of Australian blue whales by filling the gap in genetic assessment of Geographe Bay whales and performing a powerful investigation of Australian blue whale population genetics using 10 microsatellite loci and a 394 bp fragment of the mtDNA control region. The significant findings of the Activity are that Geographe Bay blue whales cannot be excluded from belonging to the Australian feeding aggregations genetic population and that the two known Australian feeding aggregations constitute one genetic population.

Genetic assessment of Geographe Bay blue whales

A large component of the Activity involved biopsy sampling Geographe Bay blue whales, which had never before been sampled. Seven individuals were successfully biopsied, 6 were laterally photo-ID on both right and left sides, and 6 on only one side. The paucity of individuals biopsied relative to the aim of 30 individuals is likely due to a less than usual level of blue whale numbers this season compared to previous seasons, and the peak of the season potentially occurring earlier than usual. Genetic analyses of Geographe Bay blue whales was conducted but must be considered in light of the paucity of samples.

The microsatellite data had no evidence for null alleles, stutter bands or short allele dominance, and there were no significant deviations from Hardy-Weinberg equilibrium or evidence of linkage disequilibrium. None of the individuals had been resampled at any of the Australian feeding aggregations (up to 2008/09 season). The microsatellite variation (average 4.20 alleles per locus (SD 1.14),

mean observed heterozygosity 0.602 (SD 0.040), mean expected heterozygosity 0.640 (SD 0.040), allelic richness 4.04) and mtDNA control region variation (haplotype diversity 0.714 (SD 0.181), nucleotide diversity 0.003 (SD 0.002)) is comparable to our findings for the Australian feeding aggregations (see manuscript attached to progress report).

Power analysis indicated that a microsatellite $F_{ST} \geq 0.040$ could be detected with $\geq 95\%$ confidence (96.2% Fisher's exact test, 99.0% chi-square). Fixation indices based on microsatellite loci ($F_{ST} = -0.013$, $P = 0.491$) and mitochondrial haplotypes ($F_{ST} = -0.057$, $P = 0.996$) show no significant evidence of genetic differentiation between Geographe Bay and the feeding aggregations. Also, the 4 sequenced mtDNA control region Geographe Bay haplotypes are all shared with the Australian feeding aggregations. Due to the paucity of samples, an assignment test was conducted which indicated that none of the Geographe Bay individuals could be excluded from the Australian feeding aggregations genetic population ($P > 0.05$). Additional analyses will be carried out when we receive the IWC Antarctic samples (we have been granted access by the IWC Scientific Committee). The samples collected from Geographe Bay as part of this Activity have greatly contributed towards determining the genetic identity of these blue whales, and AMMC 09/10 funding to Möller et al. (Population size of blue whales in Australian waters) will provide further samples that will allow more powerful analyses.

Powerful genetic analysis of Australian feeding aggregations

The Activity also involved biopsy sampling in one of the Australian feeding aggregations, the Bonney Upwelling (VIC/SA), due to the paucity of samples at this aggregation that has previously limited genetic analyses. Ten individuals were successfully biopsied during the main research period, plus an additional whale by Gill. These samples have substantially added to the resubmitted manuscript entitled "Genetic diversity and structure of blue whales (*Balaenoptera musculus*) in Australian feeding aggregations" (see manuscript attached to progress report). The increased number of good quality samples (from 14 to 25) and an increase in the number of microsatellite loci (from 6 to 10) has allowed more powerful genetic analyses which has confirmed that the two known Australian feeding aggregations of blue whales, the Bonney Upwelling and the Perth Canyon (WA), constitute one genetic population.

2. The Outcomes/Objectives

The degree to which the Activity has achieved the objectives

The objectives of the Activity were to (1) genetically resolve the subspecific identity of Geographe Bay blue whales, and (2) conduct a powerful investigation of the population structure and genetic diversity of Australian blue whales. Due to circumstances beyond our control, as described in the Activity Summary, we have only been able to conduct a preliminary genetic assessment of Geographe Bay blue whales. When the IWC Antarctic samples are received and the sample size is increased in Geographe Bay during the 2010/11 season we will have sufficient data for an in-depth subspecific assessment of Geographe Bay blue whales. The second objective was successfully and fully carried out as the

Activity has allowed us to increase the number of good quality samples available from the Bonney Upwelling (from 14 to 25), and number of microsatellite markers (from 6 to 10). We have resubmitted a manuscript to this effect.

3. Appropriateness

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

The research team comprised of experts in Australian blue whales and genetic analyses, and therefore their years of collective expertise and experience allowed the best possible development and implantation of the Activity. The approaches used were proven, standard techniques for carrying out genetic assessments and population genetic analyses on cetaceans. For example, field work was conducted during the expected peak of the season to maximise the number of biopsy samples, and photo-IDs were taken in conjunction with biopsy sampling to maximise the output of field work.

4. Effectiveness

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

The Activity was as effective as possible given the inherent risks and unpredictability associated with researching large cetaceans and the need to be cost effective. The Activity was able to provide the first blue whale samples ever collected from Geographe Bay. These samples allowed us to conduct a preliminary genetic assessment towards the objective of genetically resolving the subspecific identity of Geographe Bay blue whales. Due to circumstances beyond our control, and a potential risk in many cetacean studies, the less than expected number of whales and potentially earlier than usual peak in blue whale abundance prevented us from obtaining the desired number of samples necessary for powerful genetic analysis. The Activity effectively met the second objective of performing more powerful analyses of Australian blue whale population structure, as shown in our resubmitted manuscript detailing the population structure of the Australian blue whale feeding aggregations.