Australian Marine Mammal Centre

Final Report

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

- **Project No**. – 0809/23
- **Title** - (Cetacean Aging) Identification of gene expression differences among cetacean age classes and their application to cetacean age estimation
- **Chief Investigator** – Dr Simon Jarman
- **Organisation** – Australian Antarctic Division

Activity Period – 21 January 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)
Samples for age estimation were collected from humpback whales at Evan's Head, northern NSW in May 2009. the levels of gene expression in juvenile, sub-Adult and Adult humpback whales were investigated through high throughput sequencing. Differences in gene expression level within age classes are clear from initial analyses. More analysis is needed to determine whether age-related gene expression is apparent.

2. The Outcomes/Objectives

The degree to which the Activity has achieved the objectives
The laboratory work so far has proved successful in that we have got a good quality assessment of total messenger RNA in three age classes of humpback whale. We examined several different RNA analysis methods on these samples and have found one to be significantly more useful than the others. RNA was purified from all samples collected. Pools were made of RNA from juvenile, sub-adult and adult whales. The total messenger RNA from each of these pools was sequenced using Illumina paired-end 65 bp read length sequencing. This resulted in approximately nineteen million reads (~ 1.2 gigabases) of sequence per age class. We have mapped the reads for highly conserved genes (~ 11% total) to the cow genome, which is the closest relative to whales that has a complete genome sequence. The reads for highly conserved genes are differentially expressed within age classes, but we have not yet analysed expression levels among age classes. We have also not yet aligned the other ~ 89% of the reads. Methods for *de novo* assembly of transcriptomes are in their

infancy and we will need to do more investigation of techniques. In short, the bioinformatics requirements for the project have turned out to be more significant than expected and more time will be needed before we can assess whether this approach is useful or not.

3. Appropriateness

The appropriateness of the approaches used in the development and implementation of the Activity
The experimental approach is clearly appropriate, but the data analysis is going to take more time than anticipated. The technologies used can clearly find differential gene expression and the coverage of mRNAs appears good, so if there are age-related gene expression patterns we should be able to detect them.

4. Effectiveness

The degree to which the Activity has effectively met its stated objectives
Not yet determined.