

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

- **Project No.** – 2010/33
- **Title** - Population size, structure and habitat preferences of common dolphins in South Australia: enhancing the assessment, reduction and mitigation of fisheries operational interactions.
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- **Organisation** – Flinders University
- **Activity Period** – October 2010 – May 2012

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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 project investigated the population size, structure and habitat preferences of common dolphins in South Australia for enhancing the assessment, reduction and mitigation of fisheries operational interactions with the South Australian Sardine Fishery (SASF). For the population genetics component, we collected biopsy samples of short-beaked common dolphins in shelf, coastal and gulf waters of southern Australia, between Albany, Western Australia (WA), and eastern Victoria (VIC). Samples of 308 individuals from 11 sampling locations were genotyped for 14 microsatellite markers and sequenced for a fragment of the mitochondrial DNA control region. The genetic analysis unravelled fine-scale genetic structure for common dolphins in southern Australia. A total of six genetically differentiated populations were identified, five of which show moderate levels of gene flow among each other, and one that shows low gene flow with the others. The latter population is from south-eastern Australia, represented by animals sampled off south-eastern Tasmania and off southern NSW. We also genetically detected summer migratory movements of groups of animals from this population into central SA and western VIC. Altogether we identified at least six management units of common dolphins in southern Australia. At least two of these are likely subject to by-catch in the SA purse-seine and possibly gillnet fisheries: 1) a regionally distributed population with its western boundary approximately at Eyre Peninsula, SA, and its eastern boundary at western Wilsons Promontory, VIC; and 2) a population from south-eastern Australia that shows migratory movements into the identified core sardine fishing areas during the summer. Identification of the proportion of animals belonging to these two populations which are by-caught by the fishery requires future genetic analysis of by-

caught individuals. For obtaining abundance estimates of common dolphins in central South Australia (the core fishing area of the SASF), we conducted two blocks of aerial surveys in 2011, one in summer (March-June) and one in winter (August-September), using distance sampling techniques. The surveys were conducted as double observer experiments with two independent observation platforms, one at the front and one at the back of the survey plane. The sighting data were analysed using mark-recapture distance sampling techniques which can be used to estimate abundance without assuming that detection on the transect line is certain. The abundance of common dolphins in summer was 14,549 (CV=0.21; 95% CI =9,462-22,371) and in winter 20,749 (CV= 0.15; 95% CI = 15,206-28,313). At present, no corrections have been applied to these estimates for availability bias (i.e. dolphins that were submerged during the passage of the survey plane), thus both estimates are negatively biased. However, data on dive/surface cycles of common dolphins were collected using a helicopter and the data will be used in the future to correct for availability bias. These surveys provided the first estimates of common dolphin abundance from the SASF core. It is important to emphasise that these abundance estimates and subsequent PBR calculations are preliminary and not definitive, and thus should not be used for informing any management decisions. A more thorough and robust analysis of the data is currently under way. Based on the abundance estimates we calculated the Potential Biological Removal (PBR) for summer and winter of the central SA sub-population. PBR estimates given in this report are tentative only and are not to be used for management purposes. Although preliminary estimates indicate a high density of common dolphins in South Australia, the results from the genetic analysis reveal fine-scale genetic structure of common dolphins in coastal and shelf waters of southern Australia and the identification of six management units. At least two of these dolphin populations are at risk from fisheries by-catch, one distributed regionally in central/eastern southern Australia and one from south-eastern Australia that shows seasonal movements into the area. Management suggestions for mitigation of operational interactions with common dolphins in the SA purse-seine and the southern and eastern gillnet fisheries are given in section 2.4 of the report.

2. The Outcomes/Objectives

List of the Project Objectives

The project objectives were to

1. Investigate genetic connectivity of common dolphins in southern Australia;
2. Estimate the relative abundance of common dolphins in South Australia;
3. Determine habitat preferences of common dolphins within South Australian waters.
4. Determine biologically sustainable levels of common dolphin by-catch in South Australia and assess the power of line transect surveys to detect population trends

The degree to which the Activity has achieved each of the objectives

1. Investigating the genetic connectivity of common dolphins in southern Australia

Degree of Achievement: Successful

Sampling: The biopsy sampling scheme for project 2010/33 was highly successful. We were able to fill previously identified geographic gaps in sampling, and also increased the number of samples from coastal, gulf and shelf waters in southern Australia of which we already had samples (previous research by KB and LM). A good number of samples from regularly spaced sampling locations along the dolphin's distribution in southern Australia were therefore obtained and questions of genetic connectivity of common dolphins were answered.

As part of this project boat surveys for biopsy sampling was conducted in the following locations: off Albany and Esperance, WA; shelf waters of the eastern Great Australian Bight, SA; shelf waters of central SA including Investigator Strait and southern parts of Spencer Gulf and Gulf St Vincent; in eastern South Australia; and in several locations along the coast of Victoria. A total of 375 samples were collected from common dolphins between November 2010 and January 2012. Samples of southern Australian common dolphins that were already held from research by KB and LM were also included in the analysis. For some regions, our sampling during this project was extremely successful (i.e. western and central Victoria), but due to limits in the budget only a sub-sample of 20 individuals per site were included for analysis. After removal of duplicate samples, the data set contained 308 individuals for the analysis of genetic connectivity in southern Australia. Western Australia: Albany (n=19), Esperance (n=33); South Australia: Great Australian Bight (n=32), South of Spencer Gulf (n=95), Investigator Strait/Gulf St Vincent (n=20), Robe (n=18); Victoria: Portland (n=17), Melbourne (n=18), East of Wilsons Promontory (n=18), NSW: Eden (n=20) and Tasmania: south-eastern TAS (n=15). The remaining additional samples (from SA and VIC) are still available for future genetic analysis if funding becomes available. The project aims of 2010/33 were successfully answered with the samples analysed here.

Data analysis: Each sampled individual was genetically sexed, genotyped for 14 microsatellite markers and sequenced for approximately 440bp fragment of the mtDNA control region. Duplicate samples were identified with CERVUS 3.0 (Marshall et al. 1998) and removed from the data set. For the microsatellite data set, we used MICROCHECKER (Oosterhout et al. 2004) to test for scoring errors and null alleles. One microsatellite marker showed a high null allele frequency and was therefore excluded from the analysis. The analysis was conducted with the remaining 13 microsatellites. We tested for Hardy-Weinberg Equilibrium and Linkage Disequilibrium using GENEPOP (Raymond and Rousset 1995). Genetic differentiation was assessed with the Bayesian clustering method implemented in STRUCTURE 2.3.3 (Pritchard et al 2000; Hubisz et al. 2009) applying the admixture model with correlated allele frequencies and performing runs with 100,000 burn-in and 1 million iterations. We conducted assignment test in GENECLASS 2.0 (Piry et al. 2004) using the Bayesian method of Rannala and Mountain (1997) with 10,000 iterations and setting the assignment threshold to 0.05. We used the populations identified with STRUCTURE and GENECLASS to group individuals for pairwise F_{ST} comparisons in ARLEQUIN 3.5 (Schneider, Roessli and Excoffier 2000). The

groupings of individuals were concordant with sampling locations with the exception of two cases where a sampling location was split into two genetic clusters due to the presence of groups of individuals that are likely to show migratory movements. These animals were found in the area of central SA and western VIC but showed high assignment to a population from south-eastern TAS and southern NSW by both STRUCTURE and GENECLASS results. Therefore these groups of individuals (all sampled from the same school in a given location) were considered as separate for F_{ST} pairwise comparisons. None of the sampling locations for pairwise comparisons contained less than 10 animals. We estimated contemporary migration rates between identified common dolphin populations in BAYESASS 1.3 (Wilson and Rannala 2003). We used the population groupings in concordance with the clusters obtained in STRUCTURE. Analysis in BAYESASS was performed with 3 million iterations and a sampling frequency of 2,000.

For mtDNA, sequences from 307 individuals were cleaned and aligned in SEQUENCHER4.0 (Gene Code Corp., Ann Arbor, MI, USA). Sequencing of one individual from Tasmania remained unsuccessful. All 307 samples were confirmed to be from short-beaked common dolphins by phylogenetic analysis in PAUP (Swofford 1998; neighbour joining method). MtDNA Φ_{ST} pairwise comparisons were performed in ARLEQUIN using the same groupings of individuals as for microsatellites. The mtDNA Φ_{ST} values were estimated using the Tamura-Nei model of sequence evolution as suggested by MODELTEST v. 3.06 (Posada & Crandall 1998), previously determined as the best model of sequence evolution for a subset of the data set (Bilgmann et al. 2008). Finally, a median joining network was constructed in NETWORK (Brandelt et al. 1999) using all 307 sequences from 11 sampling locations.

Results and Discussion: The analysis from microsatellites and mtDNA revealed fine-scale genetic structure of common dolphins in southern Australia. A total of six genetic populations were identified over a region spanning from Albany, WA in the West to Eden, NSW and south-eastern Tasmania in the East. One population from south-eastern Tasmania and southern NSW, showed much higher levels of genetic differentiation from the other five populations that are found in southern Australia.

For microsatellites, using the entire data set, STRUCTURE grouped individuals into two populations with high levels of genetic differentiation ($K=2$ determined with the ΔK 'Evanno method' in STRUCTURE HARVESTER (Earl et al. 2011); for Structure bar plot see Fig. 2). STRUCTURE further identified groups of individuals sampled in central SA and western VIC that show a high membership probability to the population identified for south-eastern Tasmania and southern NSW. These animals are hypothesised to show migratory movements from south-eastern Australia into SA and VIC (dolphins were biopsy sampled in SA and VIC whilst being genetically identified as being part of the south-eastern Tasmania/ southern NSW population).

The results from STRUCTURE were corroborated by assignment tests in GENECLASS. GENECLASS correctly assigned the individuals to their population of origin, including the migratory animals, revealing the same groupings as shown in the STRUCTURE graph (Fig 2). Simultaneously, 80% rejection of individuals took place for the opposite population, which is usually the case when allele frequencies of the populations are very different and a considerable level of genetic differentiation is

present. GENECLASS therefore also suggests that all identified migratory individuals found in SA and VIC stem from the south-eastern population represented in the data set by samples from south-eastern TAS and southern NSW. Since all Tasmanian animals in the data set (n=15) were from strandings along the coast of south-eastern Tasmania, obtained over a period of six years, including summer and winter (the only stranding samples of the data set), we suggest that animals of this population are likely to occur off south-eastern Tasmania year round.

Altogether, results from STRUCTURE and GENECLASS are possibly best explained by migratory movements of dolphins from this south-eastern population into central South Australia and western Victoria (animals of this south-eastern population are displayed in green in the structure graph). These movements are likely to be seasonal, during summer, and are potentially driven by local oceanographic currents and upwelling events (Bonney upwelling and upwelling West of Kangaroo Island) that allow for seasonal high densities of small pelagic fish, particularly sardines. None of the individuals that were sampled in winter in SA and VIC were found to be assigned to this south-eastern population, hence suggesting seasonality of movements. Since sampling effort was greater during the summer months in both SA and VIC than during winter, future research is needed to confirm that the migratory influx of dolphins from south-eastern Australia only occurs during the summer months.

The results also correspond with microsatellite F_{ST} pairwise comparisons that show highly significant values between the sampling sites from shelf/gulf habitats in southern Australia and the sites off Tasmania/southern NSW, as well as for the groups of potential migratory animals. In contrast, all sampling site comparisons of the distinct south-eastern population (displayed in green in the structure graph) showed non-significant F_{ST} values close to zero. Interestingly, the remaining nine southern Australian sampling sites along the southern Australian coast (displayed in red in the structure graph) showed significant to highly significant F_{ST} values for most pairwise sampling site comparisons. For data sets that show significant F_{ST} values, while conventional models in STRUCTRE do not have sufficient statistical power to detect structure, it is recommended to use more powerful models implemented in the latest version of STRUCTURE as developed by Hubisz et al. (2009).

We therefore further analysed the data set by excluding all individuals of population 2 (displayed in green in Fig 2) and used the models in STRUCTURE that incorporate geographic sampling location information (Hubisz et al. 2009) for data sets with low statistical power to discern genetic structure. The results from three independent runs revealed the presence of fine-scale genetic structure of common dolphins in southern Australia, with the detection of five genetically differentiated populations ($\Delta K=5$, Evanno et al. 2005, see Fig 3).

The five identified populations of common dolphins were from 1) the embayment of King George Sound, Albany, WA; 2) Recherche Archipelago, Esperance; WA; 3) the Great Australian Bight between Head of the Bight and the region south of Coffin Bay; 4) waters off Eyre Peninsula to the eastern Melbourne regions; and 5) waters east of Wilsons Promontory, VIC. In contrast to the marked genetic differentiation detected for the population from south-eastern Tasmania/ southern NSW (Fig. 2), these five populations in southern Australia show slightly lower levels of genetic differentiation (Fig. 3). This explains why STRUCTURE failed to detect all populations while the

highly genetically differentiated population of south-eastern Tasmania/southern NSW was included in the data set (with and without the STRUCTURE models that incorporate population location). It is important to mention that STRUCTURE, when using these newer models, does not tend to detect genetic structure when none is present (Pritchard et al 2010). The results agree with those obtained from microsatellite pairwise F_{ST} comparisons as described above.

Overall the microsatellite analysis revealed six populations of common dolphins in southern and south-eastern Australia. These six populations were used to estimate migration rates between populations in BAYESASS (Table 1). Migration rates between the population from the East (south-eastern TAS and southern NSW) and any of the five southern Australian populations were extremely low. This is in accordance with the high level of genetic differentiation found for this population using a range of different analyses. Migration rates among the other less differentiated populations ranged between 0.00 and 0.30 (0% and 30% genetic migration). Again the results reflect the slightly lower genetic differentiation found among these populations compared to the highly genetically differentiated population from the East.

The results from the mtDNA analysis (n=307) shows a pattern for Φ_{ST} pairwise comparisons similar to those obtained for microsatellite F_{ST} . The majority of sampling site comparisons in southern Australia show significant to highly significant values, while comparisons among the south-eastern Tasmanian/southern NSW groups are largely non-significant. A total of 83 haplotypes were found in the data set, of which only 8 haplotypes were shared between the south-eastern Tasmania/southern NSW population and any other population from southern Australia. Twenty-seven haplotypes were specific to dolphins from south-eastern Tasmania and southern NSW and not found in any of the other populations, which again corroborates the marked genetic differentiation detected by the microsatellite analysis.

Conclusions and Management Implications: Altogether, we identified five genetically differentiated populations of common dolphins in southern Australia between Albany, WA and Eastern Wilsons Promontory, VIC, that show low to moderate levels of gene flow; and a sixth population of common dolphins that shows marked genetic differentiation (previously identified in studies on common dolphin population genetic structure in waters of south-eastern Australia by Bilgmann et al. 2008 and eastern Australia by Möller et al. 2011). This considerably higher level of differentiation and the very low estimated migration rates of the population from south-eastern Australia suggests little to no genetic exchange with the other populations in southern Australia. Potential migratory movements of groups of individuals from this genetically highly differentiated population from south-eastern waters were detected. Animals moved from the East into central SA and eastern VIC. The very low estimated genetic migration rates show that interbreeding may rarely occur between individuals of the population from south-eastern TAS and southern NSW and any of the other five populations of southern Australia, even when they are found in the same geographic area. Our results show that these movements are likely to be seasonal, occurring during the summer months. Migratory movements are hypothesised to be associated with upwelling events in central SA and western VIC, and resulting local high densities of prey. The genetic analysis of common dolphins that stranded in south-eastern Tasmania over a period of six years, and over summer and winter, suggests a year-round presence of this population in waters south-east of

Tasmania. Considering the results from the genetic analysis, all six populations detected in southern Australia should be considered as separate management units: (1) King George Sound, Albany, WA; (2) waters of the Recherche Archipelago, Esperance, WA; (3) Great Australian Bight, SA (coastal and shelf waters between Head of Bight and Eyre Peninsula); (4) coastal and shelf waters between Eyre Peninsula, SA and western Wilsons Promontory, VIC, including Spencer Gulf, Gulf St Vincent and Investigator Strait; (5) coastal and shelf waters East of Wilsons Promontory ; and (6) the wider region of south-eastern Tasmania and southern NSW.

Populations subject to operational interactions with the SA purse-seine and southern and eastern gillnet fisheries: Common dolphins that are found in waters over the southern Australian continental shelf year round and that are subject to by-catch in the purse-seine fishery in central SA and likely the gillnet fishery in several locations of SA (mainly eastern SA) have a genetic population boundaries approximately to the West at Eyre Peninsula, and to the East in the wider Melbourne region, likely the western side of Wilsons Promontory, VIC. This management unit includes individuals from Spencer Gulf, Investigator Strait and Gulf St Vincent. Dolphins west and east of the above described geographic boundaries belong to separate management units. Evidence from aerial surveys conducted in summer and winter, and from SAIMOS boat surveys for biopsy sampling of common dolphins (surveys were conducted to the edge of the SA continental shelf) suggested that dolphins remain in waters less than 100m deep and are only occasionally found beyond the 100m depth contour (KB, GP and LM personal observations). Therefore boundary of the population to the South is likely to be over the continental shelf around the 100m depth contour.

Since animals from two management units utilise waters of the core purse-seine fishing area in SA and also those of the gillnet fishery, there is the potential risk that both management units are subject to operational interactions and by-catch in these fisheries. To elucidate this, tissue samples from by-caught dolphins are needed to assign the individuals to their respective management units. The large genetic data set that we collated as part of this project is ideal for assignment of individuals from unknown population origin since we now hold genetic information (microsatellite allele frequencies) of the six reference populations. In summary, the SASF and possibly the southern and eastern gillnet fishery may therefore impact on two management units of common dolphins: one locally distributed with boundaries as described above, and one from waters off south-eastern Tasmania and southern NSW, when animals of this population move into the fishing area.

Further research needs to confirm whether dolphins from both management units are by-caught, and if so to what proportion. It also needs to be confirmed whether described potential migratory movements of south-eastern Australian common dolphins into SA and VIC only occur in summer (e.g. during the upwelling season) For the summer season of 2011 we have shown that these migratory individuals were found in the core fishing area of the SASF, as evidenced by biopsy sampling of dolphins from this region during this season and the genetic analysis of the biopsy samples. For January 2012 we also have shown that dolphins from the population of south-eastern TAS and southern NSW were present in waters utilised by the gillnet fishery (waters south of Robe).

2. Estimating the relative abundance of common dolphins in South Australia

Analyses and subsequent interpretations of common dolphin abundance estimates and Potential Biological Removal calculations presented in the report are preliminary and highly simplified for expediency. The estimates provided are not definitive and should not be used for informing any management decisions at this stage. A more thorough and robust analysis of the data is currently under way. Results of additional analyses will be provided to AMMC as soon as available.

Degree of Achievement: Successful (preliminary analysis only)

Survey design and protocol: As proposed for project 2010/33, we conducted two blocks of aerial surveys over the core fishing area in central South Australia, one in summer and one in winter, respectively. The summer aerial surveys took place between March and June 2011 and the winter surveys between August and September 2011.

The survey design consisted of transects aligned east–west or north–south, systematically spaced 7–8 km apart within 4 different strata (Figure 1). Transects in stratum 1 and 4 extended up to the 100m depth isobath. Surveys were conducted from a Partenavia; twin-engine, six-seat, high-wing aircraft commonly used in aerial surveys of cetaceans. All survey lines were flown at a speed of 100 knots (185.2 km/h), at an altitude of 500 feet (152.4 m) and in good sighting conditions (i.e. winds less than 15 knots and Beaufort Sea state ≤ 3). Surveys were conducted in “passing mode (i.e. survey effort was not to be suspended to circle back when a sighting was made) except when species identification or school size were uncertain. In these cases, survey effort was suspended to circle the animals and survey effort resumed at the point line transect effort was suspended.

The survey team consisted of six people: the pilot, a front-right survey leader, and two teams of tandem observers (front and rear), one on either side of the aircraft. Front and rear observers were visually (with a curtain) and acoustically (wearing headphones) isolated from each other while on effort. The observers and the survey leader communicated via aviation headsets connected to two intercoms, so that the rear observers could be isolated acoustically from the front observers while on effort. Each intercom was connected to a separate track of a two-track digital voice recorder. This arrangement allowed the sightings of the two observers on each side of the aircraft to be recorded independently. The front observers had bubble windows that allowed them to view the track line directly below the aircraft, while rear observers had flat windows that allowed them to view down to a 65 degree declination angle. The observers recorded declination angles to sightings when abeam using inclinometers and collected data on species, group sizes and sighting conditions (sea state, visibility, turbidity, cloud cover and glare). The survey leader entered survey effort data, sighting conditions, and all sighting data called by the front observers, together with time stamp signals of position from a GPS system, into a handheld computer using a Cybertracker software sequence developed specifically for dolphin aerial surveys. Both front and back seat observer data was recorded on the two-track digital voice recorder.

Data analysis: Preliminary estimates of the relative abundance of common dolphins for each survey block were derived for each survey stratum using the double-platform observation data from aerial surveys. We use mark-recapture distance sampling (MRDS) methods to estimate abundance without assuming that detection on the transect line is certain (Laake and Borchers 2004). This analysis was carried out using Distance 6 (release 2) (Thomas et al. 2009) with the MRDS engine. In this analysis, the 2 observers in the front of the plane were considered to be one platform (observer 1), and the two observers in the rear were considered to be a second platform (observer 2). Sightings detected by both observers (duplicates) were assigned based on coincidence in timing, species, and similarity in distance from track line and group size. When perpendicular distances and group sizes differed between duplicates, the average distance and group size of the duplicate pair was used for analysis.

We used a point independence MRDS model to estimate detection probability because detection probabilities of observers can be correlated due to factors such as group size (e.g. although both observers are acting independently, they are both more likely to see only large groups at long distances) (Laake and Borchers 2004). MRDS models were fitted using various permutations of both the half-normal and hazard-rate functional forms, and covariates (i.e. distance, group size, Beaufort, turbidity, cloud cover, glare and side of the plane) thought to affect the scale of the detection function of the distance sampling and mark-recapture model components. The data for both aerial survey blocks were right truncated at a perpendicular distance of 865m (i.e. very few observations were made past this distance). The 65 degree inclination angle limit in the field of view of back observers, equates to a distance of 71m from the transect line, thus this distance was set as our left truncation. Analysis was carried out on exact perpendicular distances and no attempt to group distances into intervals for analysis has yet been conducted. Akaike Information Criterion (AIC) values of these models were compared to select the best model (i.e. model with lowest AIC). A density estimate was derived for each stratum, incorporating the probability of detection and total transect length. The variance of the density estimate was calculated based on Innes et al. (2002).

Results: A total of 5,234 km of transect line was flown during the summer block and 5,284 km during winter covering an area of 42,437.8 km². A summary of survey effort and the number of common dolphin sightings made by each observer platform in each stratum is shown in Table 2. A total of 147 and 401 schools of common dolphins were sighted during summer and winter, respectively (Figure 5).

Comparisons of the AIC from all permutations of the detection functions and potential scaling variables, the hazard-rate key function had a lower AIC than the half-normal key function; therefore this was selected for subsequent models. The most promising MRDS model for the summer aerial survey block involved a distance sample model scaled with all covariates (perpendicular distance + school size + Beaufort sea state + glare + cloud cover + turbidity + side of the plane) and a mark-recapture model specified with perpendicular distance. The fitted detection function for this model is given in Figure 6. The mean detection probability at the transect line for the primary observer during the summer survey block was 0.89 (CV=0.03) and the pooled probability of detection was 0.98 (CV=0.009). The same procedures for the winter aerial survey block indicated that the best model involved a distance sample model

scaled with perpendicular distance + school size + Beaufort sea state and a mark-recapture model specified with the same covariates. The respective fitted detection function for this model is given in Figure 7. The mean detection probability at the transect line for the primary observer during the winter survey block was 0.74 (CV=0.04) and the pooled probability of detection was 0.92 (CV=0.02). Based on the selected models the abundance of common dolphins in summer was 14,549 (CV=0.21; 95% CI=9,462- 22,371) and in winter 20,749 (CV=0.15; 95% C =15,206-28,313). Estimates per stratum are presented in Table 3. No corrections have been applied to these estimates for availability bias (i.e. dolphins that were submerged during the passage of the survey plane), thus both estimates are negatively biased. However, data on dive/surface cycles of common dolphins were recently collected during 10min focal follows of different sized dolphin schools (n=19) using a helicopter and we will be using these data in the future to correct for availability bias.

Discussion and conclusions: These surveys provide the first estimates of common dolphin abundance from the core fishing area of the SASF. The estimates are preliminary and not definitive or final and should not be used for informing any management decisions at this stage. A more thorough and robust analysis of the data is currently under way which may provide more refined estimates. Nevertheless, the estimates for both survey blocks indicate a high relative density of common dolphins within central South Australia. This high density of common dolphins in the region could potentially be driven by local oceanographic currents and upwelling events (Bonney upwelling and upwelling West of Kangaroo Island) that allow for seasonal high densities of small pelagic fish such as sardines.

3. Determining habitat preferences of common dolphins within South Australian waters

Degree of Achievement: Currently in progress

The analysis of habitat preferences of common dolphins using the summer and winter aerial surveys is currently in progress. Both aerial survey periods extended over considerable amounts of time due to windy weather conditions unsuitable for flying (March - May and August- September for summer and winter surveys, respectively) which ultimately left less time for the data analysis. We will proceed with the analysis of habitat preferences with the aim of publishing the results in an international peer-reviewed journal upon its completion. We prioritised estimates of abundance over the habitat preference analysis to be able to calculate PBR of the common dolphin population.

4. a) Determining biologically sustainable levels of common dolphin by-catch in South Australia, and b) assess the power of line transect surveys to detect population trends

Analyses and subsequent interpretations of common dolphin abundance estimates and Potential Biological Removal calculations presented in the report are preliminary and highly simplified for expediency. The estimates provided are not definitive and should not be used for informing any management decisions at this stage. A more thorough and robust analysis of the data is currently under

way.

a) ***Degree of Achievement:*** Successful (tentative results due to preliminary abundance estimates)

Method: Potential Biological Removal (PBR; Wade 1998) was calculated from abundance estimates of common dolphins in the core purse-seine fishing area in South Australia.

PBRs (Wade 1998) are calculated as a product of the minimum population size (N_{\min}), one-half of the maximum productivity rate (R_{\max}), and a 'recovery' factor (Wade and Angliss 1997).

$$\text{PBR} = N_{\min} \times 0.5 R_{\max} \times \text{RF} \quad (\text{Wade 1998})$$

The minimum population estimate, N_{\min} , is the lower limit of the two-tailed 60% confidence interval of the log-normally distributed best abundance estimate. This is equivalent to the 20th percentile of the log-normal distribution, which is specified by Wade and Angliss (1997). The maximum productivity rate (R_{\max}) is usually set to a default value of 0.04 for cetaceans. This value of 0.04 is based on theoretical modelling showing that in general, cetacean populations may not grow at rates much greater than 4% given constraints of their reproductive life history (Barlow et al. 1995). The 'recovery' factor is set to a default of 0.5, which is the standard value used for populations of unknown status relative to optimum sustainable population (OSP).

Application for common dolphins in SA: PBR of the sub-population of common dolphins in central SA was calculated using the preliminary summer and winter common dolphin abundance estimates. Due to the preliminary nature of abundance estimates and the size of the area surveyed (only part of the area was covered that the regional common dolphin population utilises), and also because the maximum reproductive rate (R_{\max}) of this population is unknown, the PBR presented in this report is associated with a high level of uncertainty. PBR results are therefore highly simplified for expediency.

We show the general application of PBR for southern Australian common dolphins by using the preliminary abundance estimates as an example and by additionally providing a PBR table to present how the PBR differs when different values of N_{\min} are combined with differing maximum reproductive rates (Table 4). We used two different values for R_{\max} , the default value of 0.04 often used for cetaceans and a more conservative value of 0.02. These values represent a maximum growth rate of 4% and 2% respectively. In the Eastern Tropical Pacific (ETP), two Delphinids that are closely related to short-beaked common dolphins, i.e. spotted dolphins *Stenella attenuata* and spinner dolphins *S. longirostris*, have been largely impacted by operational interactions with the tuna purse-seine fishery between 1960 and 1972. Since the 70s, both populations have shown no signs of increase in numbers indicating no population recovery although both populations are well below carrying capacity (Wade et al. 2007). Twelve abundance estimates conducted in the ETP between the years of 1979 and 2000 revealed that neither of the stocks are recovering (Gerrodette and Forcada 2005) and maximum population growth rates were <3%, with estimated median recovery rates of 1.7% and 1.4% for the two dolphin stocks

(Wade et al. 2007). We therefore decide to include the value of $R_{\max} = 0.02$ (2%) as a second, more conservative rate for estimating the PBR.

PBR for common dolphins in the core fishing area: PBR was calculated from N_{\min} of the summer abundance estimates ($N_{\min} = 12,214$) and winter abundance estimates ($N_{\min} = 18,300$), and first setting R_{\max} to 0.04 and the recovery factor to 0.5 (default values). Resulting PBR for the summer estimates is 122, and for the winter estimates 183. Secondly, we calculated a more conservative approach using the same N_{\min} , but setting R_{\max} to 0.02 and keeping the default recovery factor at 0.5, leading to a PBR of 61 per annum for summer abundance estimates and 92 for the winter estimates for maintenance of OSP.

In addition to the PBR calculations from the winter abundance estimates, we produced a table with hypothetical PBR values for varying minimum population estimates (N_{\min}) and maximum productivity rates (R_{\max}) (Table 5), given that the population is found in a larger geographic area than the one covered by the aerial surveys. We used N_{\min} for a range of values between 10,000 and 40,000 individuals, and two different values for R_{\max} , 0.04 and 0.02.

An R_{\max} of 0.4 is conventionally used as a default for cetacean populations (Wade 1998). We also used $R_{\max} = 0.2$ as a conservative approach to account for potential reduced maximum productivity rates in the dolphin population caused by factors during and post dolphin encirclement. These factors include encirclement caused mother-calf separation (Archer et al 2001), declines in numbers of calves (see Wade et al 2007) and high foetal mortality (Perrin 1968), all population-level effects. In addition there may be encirclement related stress causing change in tissue chemistry of dolphins (reviewed in Wade et al 2007). Although this has not been proven to have population level effects, it potentially does when it affects the ability for females to conceive or leads to increased foetal mortality. The ‘cryptic’ (unseen) deaths from purse-seine fishing encirclements of dolphins in the ETP, in particular of calves during the first 6 months of life, is likely to be much larger than previously expected (Wade et al. 2007). It is therefore possible that these factors also play a role in the impact of purse-seine fishing on common dolphins in SA, even in cases when the animals are released successfully by opening the front of the purse-seine nets as part of the Code of Practice (CoP) in mitigating interactions in SA (Hamer et al. 2007), the post-encirclement population level effects remain unknown with the potential for cryptic deaths. The above listed factors are likely to play an important role in population recovery as indicated by the lack of recovery of two closely related Delphinid populations with similar ecology in the ETP (Wade et al. 2007).

Conclusions and management recommendations: For an appropriate management of operational interactions of common dolphins with the SA fishing industries accurate estimates of rates of interactions and death associated with the interactions are needed. In detail, we recommend to:

(1) estimate the proportion of common dolphins by-caught in the SASF and gillnet fisheries by genetic assignment of carcasses to the southern Australia and south-eastern Australia genetically identified management units;

(2) implement mandatory collection and delivery of genetic samples and/or whole bodies of by-caught dolphins from the SASF and the Gillnet, Hook and Trap (GHAT) Sector of the Southern and Eastern Scalefish and Shark Fishery to the South Australian Museum (and give access to Flinders University which holds the genetic data set);

(3) obtain more accurate estimates of by-catch in the SASF and gillnet fisheries by implementation of mandatory 100% observer coverage in all months the fishery operates (either by on board mounted cameras or attendance of independent observers);

(4) obtain additional abundance estimates of the regional SA population that include geographic areas that have not yet been surveyed (i.e. eastern SA to Wilsons Promontory, VIC);

(5) if common dolphins of the management unit of south-eastern TAS/southern NSW are found to be subject to by-catch in the SASF and gillnet fisheries (verified via genetic assignment), to obtain abundance estimates for this management unit;

(6) undertake modern ecological modelling approaches (i.e. Population Viability Analyses) to assess population level effects of by-catch on the regional common dolphin management unit (Eyre Peninsular to western Wilsons Promontory), and if animals are also found to be by-caught from the population of south-eastern TAS and southern NSW, then also for this management unit.

We recognise that the AFMA has already implemented a 100% observer program for the 'Dolphin Observation Zone' in the GHAT Sector of the Southern and Eastern Scalefish and Shark Fishery. We commend this approach and emphasize the importance of similar regulations for the SASF. However, confirmation of species caught and permission of access to samples for genetic analysis has not yet occurred. We urge managers to collaborate with the relevant scientists for identifying what species and population(s) of dolphins are being affected.

The management of common dolphin-fishery interactions has become a more pressing issue given our recent research findings of fine-scale genetic structure in this species in southern Australia and the subsequent identification of a minimum of six management units.

For future population-level assessments, we recommend using advanced ecological modelling approaches such as Population Viability Analyses rather than PBR because they can incorporate detailed population parameters that have the potential to better account for the ecology and life history of a species. These sophisticated modelling approaches can be used to better estimate levels to which operational fishery interactions need to be reduced in order to allow for sustainable common dolphin populations, while allowing fishing activities to continue.

b) Assessment of the power of line transect surveys to detect population trends

Degree of Achievement: Currently in progress

The assessment of the power of line transect surveys to detect population trends is currently in progress. The data collected on abundance estimates during summer and winter provides an excellent platform to estimate the sample size (survey effort /number of years) required to detect a given trend in population size using statistical power analysis. This will be critical for the development of future monitoring programs and the use of surveys to test the efficacy of mitigation strategies.

**Figures and tables are available upon request to Luciana Moller,
Luciana.moller@flinders.edu.au**

3. Appropriateness

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

The approaches were appropriate for carrying out the objectives of the project. Due to the fact that the project had a proposed running time of two years but was only funded for one year, some of the analyses are still under way.

The biopsy sampling of common dolphins in southern Australia was extremely successful, and molecular analysis of samples in the laboratory was efficient due to a well equipped molecular ecology laboratory at Flinders University and our well established methods developed specifically for cetacean molecular ecology in the lab over many years. A comprehensive genetic analysis was undertaken using a large

genetic data set.

Aerial surveys conducted over a large area of central SA were successfully conducted for two seasons. The lack of 'good weather' days during the survey periods has majorly restricted our ability to fly as frequently as we originally planned. We applied a considerable amount of effort to complete the surveys over the entire survey area in both seasons, resulting in two data sets of high quality. Weather conditions made it mandatory to run the surveys over a much larger time period than previously planned, which delayed the start of the data analysis for both abundance estimates (summer and winter). We want to emphasise that we understand the importance of collecting high quality data and did not want to compromise the quality of the data collection by flying under non-optimal conditions that would give us more time for analysis at the end. We therefore chose to produce high quality data sets and are currently still proceeding with the data analysis (only preliminary results for abundance estimates are presented in this report).

We further want to emphasise that because the project was only funded for one year (including only a one year salary for one of the Chief Investigators, KB, who was appointed as a Research Fellow) but the proposed project was planned for a running time of two years, time was short. After one year running time of project 2010/33 KB had to take on additional responsibilities to earn a salary. Nevertheless, KB has shown much dedication and worked very hard to continue the work for project 2010/33 without a salary. The amount of work performed since the start of the project 2010/33 is considerable, and we are dedicated to continue the analysis of the data after submission of this report with the aim of publishing the findings in peer-reviewed international journals of high impact. We understand that a large amount of funding has been provided for this project, and we are keen to bring it to completion with a robust data analysis. We are avoiding rushing the results and risking misinterpretation of the data. Therefore the results for abundance estimates and the PBR are only preliminary and should, as they stand in this report, not be used to inform any management decisions.

A comprehensive genetic analysis has been conducted with robust results as they stand in this report. This analysis together with further analysis currently under way will have strong implications for conservation of common dolphins in SA and should support management actions and decisions.

4. Effectiveness

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

All research activities have either already effectively met the stated objectives at the time of writing this report, or have the potential to do so once the data analyses of all project components are complete. The methods applied for data collection have all been successful resulting in a comprehensive genetic data set of 308 analysed samples as well as two sets of aerial survey data of high quality. The funding of only one year for the project, without the additional funding of another year as originally requested in the project proposal, made it unfeasible to fulfil all project objectives in full within the running time of the project. Considering the originally planned time requested to complete the project, we believe we are ahead of time. Below are the degree to which the stated objectives were effectively met at the time of submission of this report.

Objective 1, aerial survey abundance estimates: preliminary results delivered, a more comprehensive analysis that will deliver more accurate estimates is currently under way;

Objective 2, defining dolphin population boundaries: this objective has been met in full and results from a comprehensive data analysis have been presented. We recommend using the results from the genetic analysis for management decision making.

Objective 3, habitat preferences of common dolphins: We prioritised the analysis of aerial surveys data to deliver abundance estimates. Analysis to determine habitat preferences is currently under way.

Objective 4, PBR and management suggestions: Only tentative PBR calculations are included that are not final and should not be used for informing any management decisions. More accurate PBR estimates can only be delivered upon completion of final data analysis of abundance estimates from aerial surveys, although recognising that the aerial surveys did not cover the full geographic range of the population. We have demonstrated the application of calculating PBR in this project and included, besides a tentative calculation for SA common dolphins, a hypothetical PBR table with a range of varying estimates under two different maximum reproductive rates. Management suggestions are given relative to the information available from the data analysis at time of report writing.

We are committed to continuing the analysis of the data as fast as possible with the aim of publishing the findings in international peer-reviewed journals. We are planning to submit at least two of the publications (genetic results and abundance estimates from aerial surveys) between mid and end of this year.

5. Communication

How results will be communicated to management

Upon completion of the analyses, final results and suggestions for best practice management will be given to state and federal governments, and will be available for relevant management bodies such as the AFMA, and the purse-seine and gillnet fishery associations. Where appropriate, the media and public will be informed.


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6. Financial Account of the Activity

Signature of Chief Investigators	
Name Luciana Möller/ Guido J. Parra/ Kerstin Bilgmann	
Date 30/04/2012	
Signature of Organisation Representative	
Name	
Date	

Please forward 4 hard copies, and one electronic Word document of this report to:

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AUSTRALIAN MARINE MAMMAL CENTRE

STATEMENT OF INCOME & EXPENDITURE

2009/10

Name of Grantee:			
Organisation:			
Project No.:			
Project Title:			
FUNDING AGREEMENT BUDGET			
Amount of Grant	Exclusive of GST	GST	Total including GST
Commonwealth Government Contributions			
Organisation Contributions			
Other Contributions			

EXPENDITURE TO DATE - Commonwealth Government Contributions			
A. Item	B. Expenditure (\$ GST incl)	C. Committed (\$ GST incl)	D. Unspent (\$GST incl)
Total expenditure			

- (b) salaries and allowances paid to persons involved in the Activity are in accordance with any applicable award or agreement in force under any relevant law on industrial or workplace relations;
- (c) unless the Activity Period has expired or the Agreement has been terminated, the unspent portion of the Funds (if any) is available for use within the next Reporting period;
- (d) the financial information is presented in accordance with any other financial Reporting requirements the Department may notify to the Organisation;
- (e) where an Asset has been acquired with the Funds, paragraphs 7.5(d) and (g) (where applicable) have been complied with in respect to the Asset.

Signature of Responsible Person (as defined by subclause 9.6 of the Funding agreement)	
Name	
Position	
Date	