

# Report of the Intersessional Meeting on Southern Hemisphere Humpback Whale Assessment Methodology

The workshop was held at the National Marine Mammal Laboratory (NMML), Alaska Fisheries Science Center, Seattle, USA from 3<sup>rd</sup>-6<sup>th</sup> February 2009. The list of participants is given in Appendix A.

## 1. INTRODUCTORY ITEMS

### 1.1 Opening remarks

Zerbini welcomed the participants to the Workshop. He thanked the steering committee for their assistance in preparations for the meeting. He also thanked Jemma Miller from the IWC Secretariat and Jeff Breiwick and Amy Kennedy from NMML for logistical support.

Dr. John Bengtson, NMML director, welcomed the participants on behalf of the Laboratory and offered support and assistance to the meeting.

### 1.2. Terms of Reference

It has become evident that advances in the “isolated stock” methodology that has been used to assess breeding stocks A and G of the Southern Hemisphere humpback whales are necessary to handle the complexities of mixing and sub-stock structure associated with breeding stocks B and C, and D, E and F.

An intersessional workshop was proposed during the last year’s meeting in order to develop such methodology and to allow its ready application to data for these regions during the 2009 meeting of the Scientific Committee. Without this prior consolidation of methodology, it will not be possible within the time available at the annual meeting of the Scientific Committee to make the progress needed on agreeing both methodology and application to secure reasonable advance in the Comprehensive assessment of humpback whales in the Southern Hemisphere.

The terms of reference of the workshop were the following:

To progress and desirably agree the following aspects of the methodology needed for the assessment of the B and C, and the D, E and F breeding stocks in combination:

- (1) Mixing of these stocks/sub-stocks on the feeding grounds.
- (2) Allocation of past catches on the feeding grounds between stocks/sub-stocks, using genetic data to estimate the proportions of such stocks/sub-stocks in different longitudinal regions at high latitudes.
- (3) Disaggregation of population models by sex to take account of information indicating other than 50:50 sex ratios in data for catches or information relating to abundance.
- (4) Estimation of exchange rates between sub-stocks on or near breeding grounds using capture-recapture data.
- (5) Review results from initial simulation testing of models put forward to estimate exchange rates (see 4) above) and finalise further simulation tests to allow selection of appropriate models for this purpose on the basis of test results to be reported at the 2009 Scientific Committee meeting.
- (6) Clearly specify the various categories of input data needed to implement such models.

### 1.3 Election of Chair

Zerbini was elected Chair.

### 1.4 Appointment of Rapporteur

Jackson and Weinrich undertook the duties of rapporteur.

### 1.5 Adoption of the Agenda

The adopted agenda is given in Appendix B

## 1.6 Review of Documents

The list of documents is given in Appendix C

## 2. DATA CATEGORIES FOR ASSESSMENT MODELS

### 2.1 General

The Workshop focused initially on what information relevant for the assessment of Southern Hemisphere humpback whales was available for each breeding stock, in particular with reference to their use in population models. These included, but were not restricted to, catch data, estimates of abundance and trends, and information on catch per unit of effort (CPUE) and relative abundance indices. In addition, the Workshop gave preference to the consideration of information on Breeding Stocks B and C because the completion of their assessments is considered a priority by the IWC Scientific Committee (IWC, 2008; 2009).

#### 2.1.1. Allocation of feeding ground catches

The Workshop was informed that additional genetic data are now available (microsatellites, 10 loci) to update the analysis of humpback whale stock structure in the feeding grounds in the Antarctic presented at last year's Annual Meeting (Loo *et al.*, 2008). These new data will be analyzed prior to the next SC annual meeting (SC61) and will also be used to perform mixed stock assignment tests of the proportion of breeding ground stocks found in each of the feeding grounds, which can provide additional information to better allocate catches in the feeding grounds. In addition, the workshop was informed that biopsy samples from the 2006-2007 SOWER cruise (Area III, n=72) are in the process of being transferred to Rosenbaum, which will bring the total number of samples in Area III to n>200, permitting more fine scale analyses of Area III population structure.

In discussion of stock structure and catch allocation in the feeding grounds, two questions were raised: (1) Does current evidence suggest that the B/C boundary should be shifted? (2) Are the current samples informative as to the longitudinal sub-structuring on the feeding grounds associated with BSC? It was noted that shifting of the B/C boundary required a minor change to the assessment model (changing catch numbers) while information on longitudinal sub-structuring involved more substantial model revision. The low numbers and distribution of biopsy samples collected from the SOWER cruises might limit analysis of genetic differentiation on such a 'fine' geographical scale, pending the outcome of forthcoming analyses.

There are attempts underway to test various genetic assignment methods (e.g. Debevec *et al.*, 2000; Paetkau *et al.*, 1995) by comparing genotype frequencies from a sample set taken in the Antarctic with frequencies from breeding stocks in order to verify if individuals are strongly assigned to a particular sub-stock. However, using mtDNA haplotype frequencies from the small sample set currently available could result in very imprecise estimates, especially if data are to be used for assignment of historical catches. Given such small sample sizes, possible assignment signals within these data may not mean that breeding stocks are unique in terms of haplotype content, but instead that differences in frequency exist. On the further issue of the boundary of the feeding grounds between BSB and BSC, there were too few samples under current models to test these boundaries. Differences in timing between Soviet and pelagic catches suggest that some longitudinal segregation of the BSB and BSC samples may exist. One possible hypothesis to test is a latitudinal segregation of sampling north and south of 60°S between 0-10°E. Further, there were many catches between 30° and 40° E, where there is a paucity of biopsy samples. One solution is to assign some of the samples from the eastern part of the BSB feeding ground to the BSC feeding ground to increase the sample size for use in the assignment test. However, any estimate of mixing proportions from these data may be confounded by using a dataset that contains members of breeding stocks not used in the assignment testing. It was noted that there is one discovery mark from Madagascar recovered at approximately 10°E (Rayner, 1940), which is why that border between feeding grounds associated with BSB and BSC is set so far to the west. In conclusion, the Workshop **recommended** these stock assignment tests be carried out. However, it was observed that from a modeling perspective, it is unlikely that the results will affect the assessments appreciably (as has been shown by the similar assessment outcomes when using catch distributions corresponding to the Naïve/Core, Fringe and Overlap hypotheses defined by IWC (1998) (Johnston *et al.*, In press; Zerbini *et al.*, In press).

The Workshop **agreed** that Naïve models of catch allocation should be used as the baseline case for further assessments (they are more conservative with historic catches). It was noted that there is currently no fringe sector defined between the feeding grounds associated with BSB and BSC and the Workshop also **agreed** that establishing a new fringe area from 0-10° E (near the border of BSB and BSC in the feeding grounds) would be desirable as it allows for uncertainty in the feeding ground catch allocation between these two stocks to be accommodated. It was also **agreed** that the area between the borders of BSC and BSD (60-80°E) should be used

as a fringe area for the Fringe allocation hypothesis and that Fringe and Overlap hypotheses should be used as sensitivity analyses in the assessment models.

The group noted that the current delineations between breeding stocks in the feeding grounds are confusing. Therefore, an email group was appointed (Findlay (chair), Bannister, Best, Cerchio, Jackson, Loo, Rosenbaum, Weinrich, Zerbini) to review and clarify the various catch allocation hypothesis. This group should report to the subcommittee during SC 61.

## 2.2. Breeding Stock C (BSC)

Breeding Stock C correspond to whales wintering along the western coast of Africa. This stock is currently divided into three sub-stocks (IWC, In press) (Fig. 1): C1 (coast of mainland Africa, from South Africa north to Mozambique and possibly further north along the African continent), C2 (Archipelago of Mayotte and Comoros) and C3 (Madagascar).

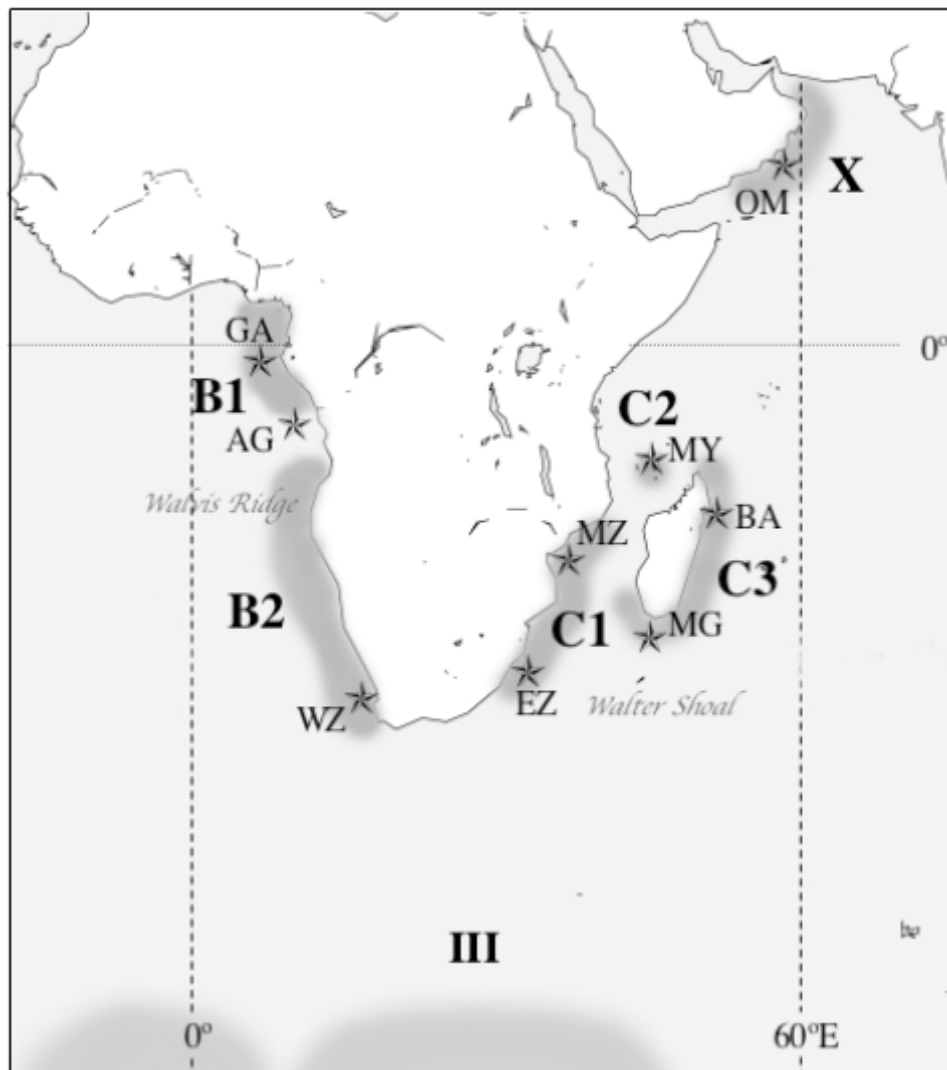


Fig. 1 – Map showing within stock sub-division for Breeding Stocks B and C (GA – Gabon, AG – Angola, WZ – Western South Africa, EZ – Eastern South Africa, MZ – Mozambique, MY – Mayotte and Comoros, BA – Antongil Bay, MG – Madagascar (from IWC, In press).

### 2.2.1 Existing data categories and progress in data evaluation

The group reviewed existing data for BSC that could be used in the assessment models. A table summarising these data and their associated strengths, likely limitations and biases is provided in Appendix D.

The workshop discussed the abundance estimates obtained from photo-identification data from western Madagascar (sub-stock C3, Cerchio *et al.*, 2008b). The group noted that the short residency times reported for Antongil Bay were likely due to movement of animals along the Madagascar coast during the breeding season, rather than aggregation in one location. There is a significant tendency for recaptures to occur at the same time every year. Recapture probability is low (2-4%), suggesting small sample sizes relative to the total population size. Not all whales moving through the coast of Madagascar may enter or may move throughout the Bay. The movement patterns of humpbacks in sub-stock C3 are poorly understood; thus it is difficult to interpret the recaptures and challenging to interpret the abundance estimates from data collected in this region. It was observed that if groups of animals move together, exhibiting patterns of temporary emigration/immigration to the sample area, it is hard to characterise the bias in a modelling framework. While these limitations are common to all mark-recapture based efforts, such movement patterns are still poorly understood in C3 and concomitant biases are thus also difficult to quantify. The implications of the relatively poorly understood movement patterns for abundance estimation are discussed further under Item 3.2.2.

The group noted that the genotypic dataset is slightly larger than the photo-identification dataset for sub-stock C3. Genotypic estimates of abundance are smaller than photo-identification estimates up to 2002 (Cerchio *et al.*, 2008b) but larger after 2004. There are proportionally fewer recaptures in later years (after 2004) than in early years (before 2002). The difference in estimated abundance between time periods, coupled with the contrast in estimates between methods, suggest that the genetic dataset warrants error checking (Tables 3 and 4 in Cerchio *et al.*, 2008b). Genotyping error rates will also be available by SC61 and an evaluation of their effect on estimated abundance could be conducted, at least for closed models. However, it was noted that changes to the recapture matrix arising from this evaluation are unlikely to be substantial.

The workshop noted that there is overlap in the genotypic and the photo-identification datasets, but the degree of overlap has not yet been determined. Thus, the two datasets represent non-independent sources of information on abundance, to an unknown degree. It was suggested that one option to investigate possible issues with lack of independence is to run a qualitative check by analysing the two datasets separately and assessing the difference between the estimates. An alternative is to use a model that incorporated estimates obtained from both datasets. It was **agreed** that the former would be a sensible strategy, given the practical difficulties of implementing the latter.

Estimating abundance from sub-samples of each dataset might provide a means of testing whether there is a difference between genotype and fluke estimates when the link between the samples is removed. Differences between estimates from photo-identification and genotype data may be driven by other capture heterogeneities between sampling approaches (i.e. sex-specific fluking rates, biopsy-shy individuals). The analysis of sex-specific genotypes can provide a test of the extent of this bias.

It was suggested that sex-specific estimates for males only could resolve some of the problems of heterogeneity in capture probability highlighted in Cerchio *et al.* (2008b) and previously discussed by the IWC SC (IWC, in press). However, it was noted that within each sex bias may be introduced by differences on age and fitness. In this respect, it was noted that male-specific abundance estimates were also considered by the “Years of the North Atlantic Humpback Whale” (YONAH) project (Mattila *et al.*, 1998). A possible issue with estimates of sex-specific abundance for photo-identification data is that the sex of some individuals may not be known. It was suggested that separate estimates could be obtained for males, females and a third group (the “unknown” whales). However, the group was informed that, in general, sex-disaggregated mark-recapture estimates will be biased if animals of unknown sex are either excluded from the analysis or included as a third group. A simple way to eliminate the bias is to include only the sighting (capture) for which an animal was sexed, plus all subsequent re-sightings (recaptures) of that animal (i.e. no retrospective sex assignment). A disadvantage of this approach is that not all the data are used in the analysis. An alternative method is the one used for western gray whales (Cooke *et al.*, 2008; Reeves *et al.*, 2005). In these studies, each unsexed animal has a probability of being female, which is updated with each capture or non-capture in each year based on the year and sex-specific capture probabilities. Each unsexed animal will therefore acquire an individual female probability that depends on its capture history. This approach has the advantage of using all the data, but the disadvantage of not yet being implemented in standard computer software such as Program Mark (which was used to obtain estimates of sub-stock C3 by Cerchio *et al.* (2008b). The possible implications of producing sex-specific estimates of abundance are further discussed in Item 3.4.

#### 2.2.2 Additional data

SC/F09/SH2 describes two episodes of whaling carried out by the *Uniwaleco* (1937-39) and the *Anglo Norse* (1949-50) expeditions, which took a total of 6,083 humpback whales from the coastal waters of Madagascar. This paper attempts to provide indices of relative abundance from both episodes for use in the comprehensive assessment of southwest Indian Ocean humpback whales. Both episodes were characterized by substantial and

statistically significant declines in catch per unit effort (CPUE), and the second episode by marked changes in the size and gender composition of the catch. In the 1937 season the Uniwaleco expedition also operated on the east coast of southern Africa, where the CPUE proved to be about 21% of that off Madagascar and the proportion of mature animals was much lower, suggesting that the migratory streams on the east African and Madagascar coasts had been subject to different catch histories. In discussion, the authors noted substantial declines over each whaling period (SC/F09/SH2, Figure 5). Catches off Durban and north C1 show similar age and sex structure while catches off Madagascar show a different pattern. This suggests that two different populations were being exploited over this period. Notably, the same whaling operation was used in both regions during the same period, and found different patterns.

It was proposed that these differences suggest heavier exploitation on the C1 stock than the C3 stock, and that the differences in age and sex between regions suggest some isolation of the two stocks (i.e. low interchange). However the group considered that there were alternative explanations for the data:

- (1) Stocks are at different levels of depletion (implying no/low interchange). A test of this hypothesis was proposed, where a simple age-based model with knife-edge selectivity is used to test the implications of catch selectivity on animal lengths. It was noted that in simulation studies of this problem (Cooke, 1984) only under specific conditions, requiring high catch selectivity followed by indiscriminate catching, would such changes in length be observed. However this is a specific case and the interpretation of results from simulating such a specific scenario could be limited. An alternative approach to simulating such a model would be to search for a set of catch conditions that produce the observed length difference without assuming a specific scenario, then evaluating their plausibility.
- (2) Animals migrate to different regions based on age (does not imply low interchange) so that stocks tend to be geographically segregated and relative proportions may be different just based on biology rather than exploitation. However, it was observed that vessel catches occurred along the coast and remain consistent in terms of age and sex, suggesting that the African mainland catches are representative of the C1 population. It was noted that these catches in C3 occurred mainly near the southern tip of Madagascar and that age segregation may exist.
- (3) Body sizes of the two stocks are slightly different, due to either strong differences in natural selection between habitats (which does not imply low interchange) or from selection and/or genetic drift (which does imply low interchange). This has been shown in other populations (e.g., humpback whales in the Arabian Sea were estimated to be larger than Antarctic humpback whales Mikhalev, 1997). Under this hypothesis, the difference in body size would not necessarily imply different depletion levels in the two populations.
- (4) Whaling selectivity is occurring differently between regions, although catches in both regions were made by the same vessel. In this respect, it was noted that catches in C3 occurred primarily only at the southern tip of Madagascar, so that the possibility of size-segregation on the breeding ground exists.

It was observed that the large catches of immature animals in C1 were made on a breeding ground, which was surprising because from mark recapture studies on other breeding grounds, juveniles had a lower probability of capture. In addition, catches of larger mature animals would be expected on breeding grounds. In order to address some of the hypotheses raised above, it was proposed that a spatio-temporal analysis of catches be performed for each region (catch data compared spatially by year), as this may shed some light on how geographic sampling might have influenced these age category results, although for Madagascar this may be less informative (catches are tightly clustered, see Figure 1 in SC/F09/SH2). A large number of catches were taken over three years in Madagascar so are likely to cover most age categories of the population.

In response to a question about information on Discovery marks from BSC, the group was informed that only two marks known indicate a connection of sub-stock C3 with Management Area III (Paton and Clapham, 2006) (Fig. 2). Five additional Discovery marks deployed in Area III south of 40°S were also recovered within Area III. No other information from Discovery marks is available.

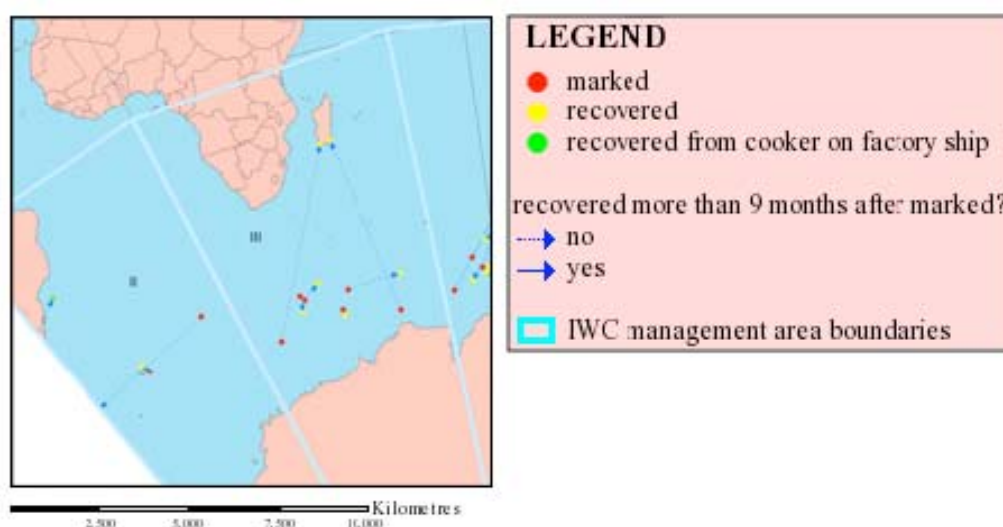


Fig. 2 - Locations of marked and recovered Discovery marks from humpback whales in IWC Management Areas II and III under the International Marking Scheme. Magnified section of Figure 12 in (Paton and Clapham, 2006)

### 2.3. Breeding Stock B (BSB)

Breeding Stock B corresponds to whales distributed off the western coast of Africa. Population structure within this stock is not completely understood. It is currently divided into two sub-stocks, B1 and B2 (IWC, 2006). B1 is a breeding ground which may contain one or more breeding populations. B2 is a feeding ground and a migratory corridor within productive waters of the Benguela upwelling system. The border between these two sub-stocks occurs in the vicinity of 18°S (near Walvis Ridge) (Fig. 1).

#### 2.3.1 Existing data categories and progress in data evaluation

The group reviewed existing data for sub-stock B1 that could be used in the assessment models. A table summarising these data and their associated strengths, limitations and likely biases is provided in Appendix D.

#### 2.3.2. Additional data

The only new data from BSB corresponds to the addition of 225 new genotypes to the sub-stock B2 dataset.

### 2.4 Information on exchange between BSB and BSC

High migration rates between breeding sub-stocks indicate that gene flow occurs between stocks B and C (Rosenbaum *et al.*, 2006). While significant pair-wise genetic differences exist between B1 and C, there are no significant differences between B2, C1, and C3 for males. The Workshop was informed that a lack of significant differentiation between these breeding sub-stocks may lend support to the hypothesis of gene flow between regions. However, it was noted that in general, interpretation of a lack of significant differentiation is problematic without an appropriate assessment of the power of the approach to detect various levels of difference. Genotypic data also indicate movements of two individuals between B1 and, one published in (Pomilla and Rosenbaum, 2005) and one recently confirmed from an analysis of 11 nuclear markers. In one case, the whale was first sampled as a putative yearling with its mother in Madagascar in 2000, and recaptured in Gabon in 2002. The other animal was sampled in 2000 in Madagascar and off of Gabon in 2006 – both times sampled in large groups acting competitively. Discussion on this topic was taken under Item 3.2.4 below.

### 2.5 Breeding stocks D, E and F

There was insufficient time to discuss this topic. This will be covered in future meetings.

#### 2.5.1 Information on interchange data among BSD, BSE and BSF

There was insufficient time to discuss this topic. This will be covered in future meetings.

## 2.6 Data available for sex-disaggregation of population models

One of the possible approaches to improve assessment models of Southern Hemisphere humpback whales is the use of population models disaggregated by sex, which could take into account information on other than 50:50 sex ratios in catches data or sex-specific abundance estimates.

Data were presented describing the current IWC catch records for which individual sex information is available. Substantial data exists in the catch records from breeding stocks B and C, although there are still a large number of animals of unknown sex in both sets of records for the current allocation of catches by breeding stock (45.3% and 56.4% of catches are of known sex for stocks B and C, respectively). In order to generate sex-specific models, some assumptions about sex ratios need to be made for both breeding and feeding stocks and catches of unknown sex need to be appropriately accounted for in a sex-specific catch history. A simple linear regression indicated a negative trend in the proportion of females over time in the wintering ground catches for the whole Southern Hemisphere ( $r^2 = 0.1835$ ,  $p < 0.01$ , Appendix E).

In discussion of this information, the workshop suggested that an analysis of sex ratios in the catches should be performed in a multiple regression framework, with appropriate co-variables explored and model selection used to determine the co-variables explaining the majority of the variability. The catch data should be partitioned across pelagic areas (by latitude and sector), with more northerly areas divided into practical sizes. In this framework, once the driving co-variables have been found, data can then be extrapolated across all regions in order to provide sex ratios for data-absent regions for time periods. The resulting variance may be sufficiently low that data can be treated as fixed in the subsequent assessment (although it is non primary data and this would need to be archived appropriately). It was also suggested that models have a quasi binomial error structure (because of presence of over-dispersion), which could allow for testing of driving co-variables such as area. It was further noted that a temporal effect may emerge from examination of the residuals in the regression, and that one way of accounting for this is to fit splines into the regression. If the co-variables are not able to explain the sex ratio, then other temporal effects should be explored (e.g. whaling changes in sex-preference in catches). It was noted that selective whaling methods (such as seen in east Australia and New Zealand) could influence the observed sex ratio. For example, on the northward migration females were taken, but on the southward migration females with calves were spared as the taking of these was prohibited.

The Workshop **agreed** that an analysis of the sex ratios in catch data should be carried out, but concluded there was insufficient time for that to be completed the purposes of the assessment of BSB and BSC. The group **agreed** that for the present time, a sensitivity test should be performed where average sex ratios of catches from each region are calculated and used to approximate regional catch sex ratios for those years in which these data are unknown.

## 3. ASSESSMENT METHODOLOGY

Punt presented an overview of the use of population modelling within the context of the resource management. Modelling is generally used to assess the status of a population relative to some reference point. However, models can also be used to examine if a set of hypotheses is consistent with the available data, assess what are the prospects of a stock under various scenarios, and to check for self-consistency of the data.

### 3.1 Models for stock/sub-stock mixing in the feeding grounds

The models required for Southern Hemisphere humpback populations need to address certain difficulties. The first is that although breeding stocks are demarcated reasonably well, and catches made in low latitudes can be readily allocated amongst such stocks, these stocks mix on their high latitude feeding areas. There is limited data to disaggregate stocks in these areas, so that assumptions have to be made about how to allocate feeding ground catches amongst breeding stocks. Another difficulty is sub-stock structure on certain of the breeding grounds (notably B, C and E), which requires not only assumptions to split past low-latitude catches amongst these stocks, but also allowance for the possibility of interchange amongst these sub-stocks. Further, given the possibility of such interchange, it becomes unclear as to which combination of sub-stocks a population estimate from mark-recapture data from a limited area might apply. The sections following address resolution of these issues.

Assessment models implemented by Johnston and Butterworth (2005) and in SC/F09/SH8 allocated feeding ground catches in a density dependent fashion. This is a reasonable assumption, though it is also a simplification as the level of population sub-structuring on feeding grounds is currently unknown.

The cultural origins of breeding ground fidelity were discussed. In general, it has been thought breeding stocks not to be resource limited, unlike feeding areas. In terms of animal flexibility regarding breeding grounds, the

group noted cases where humpback breeding grounds have apparently shifted since the onset of whaling (Hawaii, east Australia). However fidelity to particular regions depends on age, sex and condition to an extent that is currently unknown. It has been recognized that breeding ground environment preferences by whales (e.g. shallow coastal waters and bays) may mean that density dependence acts on the breeding grounds before the feeding grounds and may explain the rapid spatial expansion of recovering populations at their breeding ground locations. It was also observed that since feeding areas are clearly resource limited in terms of prey, they may influence density dependence to a greater extent than breeding grounds, and thus carrying capacity ( $K$ ) would depend more on feeding ground than breeding ground density. In this case a model combining multiple breeding stocks utilising a shared feeding ground may more adequately capture the true  $K$ . It was noted that fidelity to feeding grounds (and associated genetic differentiation) exists in the north Pacific, in contrast to the apparent lack of genetic differentiation reported between some Southern hemisphere feeding areas (such as between Areas associated with breeding stocks B and C, (Loo *et al.*, 2008)). However southern regions such as the Antarctic Peninsula and Magellan's Strait also show strong differentiation, suggesting that feeding ground fidelity could exist in the Southern Hemisphere. The Workshop **recommended** that a test for model sensitivity to density dependence on feeding grounds be performed, as described in Item 3.5.

### 3.2 Estimation of exchange rates between sub-stocks of near breeding grounds using capture-recapture methods

#### 3.2.1 General considerations

One of the purposes of the Workshop was to discuss the utilization of mark-recapture data and methods to estimate exchange rates between sub-stocks on or near breeding grounds. As a background for discussion, the workshop **agreed** that since there are not catch records or abundance information for C2 and that this sub-stock is not significantly different from C3 based on genetic (mtDNA) analysis and photographic mark-recapture exchanges (Rosenbaum *et al.*, 2006), the former would be grouped with C3 for assessment purposes.

#### 3.2.2 Within BSC

The Workshop was informed that an International Stock Assessment Workshop was held in December 2008 in Cape Town, South Africa, with the objective of reviewing and discussing further lines of research for assessment analyses of five Southern African marine populations. One of these was the Southern Hemisphere humpback whale BSC, with a focus on modelling of possible interchange between breeding stocks C1 and C3. The specific intent was to identify work to be usefully carried out prior to the present Workshop (SC/F09/SH1).

The Cape Town meeting identified four initial alternative conceptual interchange models for humpback whales in the C1 and C3 breeding stocks:

- (1) The *Resident Model* assumes no interchange between stocks on the breeding grounds.
- (2) The *Sabbatical Model* assumes there is a probability in any year that a C1 sub-stock whale will move to the C3 breeding area off Madagascar. Similarly, a C3 whale may instead move to the C1 breeding ground. This does not affect the situation in the following year, where the whale remains more likely to move from the Antarctic to its home breeding ground. Under this model a whale will visit only one of the two breeding grounds in any one year.
- (3) The *Migrant Model* is similar to the Sabbatical model, except that if a C1 whale travels to C3 breeding area in one year, it then joins the C3 sub-stock and behaves thereafter as a C3 whale (with the same probability of subsequent migration back to C1).
- (4) The *Tourist Model* is similar to the Resident model, except that in any one year in addition to returning to the C1 breeding area, there is a probability that a C1 sub-stock whale may also visit the C3 breeding area (and similarly for a C3 breeding stock whale).

In discussion, the Workshop noted that these concepts represent extreme examples of movement behaviour, with true movement likely to fall somewhere in between. Some Workshop participants felt that a combination of the tourist and sabbatical models may be the most realistic. In this intermediate scenario, the same whales initially go to either C3 or C1 in a given year, then move between them, with the result that some whales return to the new area the next year but can also return to the initial region in subsequent years.

An alternative model, referred to as the *Cape Vidal Treatment* model, is a potential variant of any of the migrant, sabbatical or tourist models where all whales migrate past Cape Vidal and then some continue to travel to Mozambique (C1) and others to Madagascar (C3). This case would be similar to that seen in Mexico with



coastal Mexico and the Revillagigedo Islands sharing one migratory stream off of Coastal Baja (Urbán *et al.*, 1999; Urbán R and Aguayo L, 1987).

When considering the interchange of individuals among areas within a region, it was suggested that the degree of interchange could be viewed as a function of distance (*e.g.* a clinal population). Such a structure has already been suggested for humpback whales on their feeding grounds in the North Atlantic (Stevick *et al.*, 2006), and there are indications of it in the North Pacific breeding and feeding grounds during in results from the “Structure of Populations, Levels of Abundance, and Status of Humpback Whales” (SPLASH) program (*i.e.* the majority of inter-area photo-identification matches came from those areas closest in spatial proximity). This may represent a fundamentally different structure than the idea of a series of adjoining but separate binned populations. Whether the difference between these two structures would affect the model outputs in the current situation is unknown, and it was suggested that this would be a good avenue to explore in a simulation trial.

SC/F09/SH3 and its addendum reported on Bayesian stock assessments of sub-stocks C1 and C3 using an age-aggregated population model integrated with an open population mark-recapture model with constant natural mortality and year and area specific capture probabilities. The model allows for interchange on the breeding grounds as well as mixing on the feeding grounds. The four different conceptual models specified above were implemented. All models were fitted to the same data, which included a recent absolute abundance estimate for C1 (Findlay *et al.*, In press), aircraft SPUE data for C1 (Best, 2003), trend estimated from relative abundance data from the migratory stream for C1 (Cape Vidal, Findlay and Best, 2006), and the capture-recapture photo-ID data for C1 and C3. The median interchange probability estimates (where estimated) are small. Allowance for interchange results in a small reduction in the median abundance of the C3 population, but the results for C1 hardly differ in median terms.

In discussion, it was noted that upper confidence intervals for proportions exchanged each year were maximally 0.17 for the population model estimators of SC/F09/SH3, but were appreciably higher at 0.38 for the MARK analyses for equal interchange probabilities in both directions (Cerchio, 2009), in circumstances where the underlying estimators used the same data and were of similar form. However it was observed that the population model in SC/F09/SH3 had additional data available in the form of a line transect estimate of abundance for C1 with a relatively low CV=0.17, which would substantially improve a C1 abundance estimate otherwise based only upon 7 photo-ID recaptures, and with it the precision of estimates of interchange proportions.

In response to a question about how the first captures were included in the mark-recapture model within the assessment framework, it was noted that total captures were included in the representation between abundance and assumed time dependant capture probability in the assessment model. It was also suggested that more detail regarding the fit of the assessment model to the mark-recapture data (posterior predictive distributions, which should be available from the model outputs) and the mathematics of the mark-recapture model would help to illuminate the differences in outputs between this model and that presented in Cerchio *et al.* (2008b). It would be useful to display the fit of the model predictions of numbers of recaptures to the observed recaptures.

Concerns were raised regarding the practice of fixing survival parameter in the population assessment model. It was noted that in the context of this model, this additional fix is reasonable because constraints are placed on these data by the rest of the population model structure. It was also noted that growth rate estimates in this case are different from those provided in the mark-recapture models.

The Workshop further discussed the population estimates from sub-stock C3 (Cerchio *et al.*, 2008) with respect to the results of the assessment models. It was noted that the model-predicted abundance estimate for 2006 was greater than that obtained by Cerchio *et al.* (2008b) for all modelling scenarios, although the wide probability intervals of the model predicted abundance encompass this abundance estimate. In this respect, it was pointed out that calves and yearlings (the latter defined by body and fluke coloration) are an appreciable fraction of the animals in the population, which were excluded from the analysis of Cerchio *et al.* (2008b). This is a normal procedure to control for the violation of closure assumptions. Removal of calves and yearlings might therefore result in negatively biased estimates of abundance. A simple analysis was conducted by Wade using a Leslie matrix to calculate what proportion of a population with humpback whale life history would be expected to be in the first two age classes (calves and yearlings) under the assumption of a stable age distribution (Table 1). Several different scenarios were run to examine the effect of different calf and yearling survival rates, while maintaining the rate of population growth ( $\lambda$ ) at 7.5%/year. For the values specified, the proportion of the population composed of calves and yearlings ranged from 18-23%, suggesting calves and yearlings do represent an appreciable proportion of the population for which adjustments should be made if they are excluded from the mark-recapture abundance estimation. This difference should be taken into account when considering assessment model predictions. The workshop noted that these simulation scenarios were designed so that each combination of life history parameters generated a population lambda ( $\lambda$ ) value of 7.5%. However, Cerchio (2003) estimated the proportion of immature males in the Revillagigedo Archipelago population (Mexico) for a

molecular assessment of paternity, and estimated that 18% of the population was between the ages of 1 and 4. The Workshop did not have time to discuss this issue in any detail but noted the absence of calves and yearlings in mark-recapture abundance estimates is a generic issue and agreed to refer it to the Scientific Committee. Following this discussion, it was also pointed out that in the North Atlantic Ocean, not all young juveniles return to the breeding grounds (Barco *et al.*, 2002), which might also lead to a negative bias in breeding ground abundance estimates.

Table 1 – Proportion of calves and yearlings in a putative humpback whale population under various combinations of life-history parameters and the assumption of a stable age distribution

Scenario	1	2	3
Survival Age 0	0.95	0.85	0.88
Survival Age 1	0.96	0.92	0.95
Survival Age 2	0.96	0.97	0.95
Survival Age 3	0.97	0.99	0.95
Survival Age 4	0.97	0.99	0.95
Survival Age 5+	0.98	0.99	0.95
Age Sexual Maturity (+1 for Age First Parturition)	5	5	5
Fecundity	0.167	0.167	0.250
Calving interval (years)	3.0	3.0	2.0
Maximum age	60	60	60
Lambda ( $\lambda$ )	1.075	1.075	1.075
Stable Age Distribution % calves	9.6	9.9	12.4
Stable Age Distribution % yearlings	8.5	7.8	10.2
Stable Age Distribution % both calves and yearlings	18.1	17.7	22.6

Analysis of sub-stock C3 photo-identification data (Cerchio *et al.*, 2008b) were conducted in Program MARK using the Pradel model (Pradel, 1996) and revealed an unrealistically low survival probability ( $\phi = 0.75$ ). This relatively low survival occurs because in the Pradel model it includes both survival and immigration during the period of the study ( $\phi$  = apparent survival). Therefore, the estimate of abundance obtained with the Pradel model represents a conservative estimate.

The biological interpretation of the growth rate parameter ( $\lambda$ ) value obtained with the Pradel model was discussed. The CV of  $\lambda$  was more precise than that obtained in a previous assessment of BSC (Johnston and Butterworth, 2008a) also an open population model analysis. Open model estimates of growth rates may represent sampling across different habitats, sampling of animals with different arrival/departure times and of animals that do not visit the area every year. This has been shown to occur in southern right whales, where cyclic appearances of females every three years and the sporadic migratory behaviour of juveniles led to biases in biological parameters using mark recapture methods (e.g. low-biased survival and high-biased growth rates). However, humpbacks typically calve on a shorter (1-3 year) cycle and some individuals may not migrate to the breeding grounds every year. It was noted that the capture-recapture framework of the assessment model (Johnston and Butterworth, 2008b) accounts for mortality and capture heterogeneity between years, but that age-specific factors and some heterogeneities (such as the possible cyclical appearances) are not.

Simulations conducted by fixing survival ( $\phi$ ) and the rate of increase ( $\lambda$ ) in the Pradel model resulted in point estimates greater than the ones observed in the closed population models (Table 2a and 2b) and closer to the trajectory predicted by the assessment models. In this respect, it was noted that  $\lambda$  corresponds to the current rate of increase, which assessment suggests should be close to zero in 2006 (Johnston and Butterworth, 2008b); SC/F09/SH3 and addendum.

Table 2a. Estimated abundances (2001) under the Pradel model for fixed growth rates ( $\lambda$ ) = 1.01-1.12 and survival probabilities ( $\phi$ ) = 0.9-0.99

$\lambda$	$\Phi$								
	0.9	0.91	0.92	0.93	0.94	0.95	0.96	0.97	0.98
1.01	6709	6903	7102	7308	7519	7735	7958	8188	8424
1.02	6470	6657	6848	7046	7249	7457	7672	7892	8119
1.03	6243	6423	6607	6797	6992	7193	7399	7611	7829
1.04	6027	6200	6378	6561	6749	6942	7140	7345	7554
1.05	5822	5989	6160	6336	6517	6703	6894	7091	7293
1.06	5627	5787	5953	6122	6297	6476	6660	6850	7044
1.07	5441	5596	5755	5919	6087	6260	6437	6620	6807
1.08	5264	5414	5567	5725	5887	6054	6225	6401	6582
1.09	5096	5240	5388	5540	5697	5858	6023	6193	6367
1.1	4935	5074	5217	5364	5515	5671	5830	5994	6163
1.11	4781	4916	5054	5196	5342	5492	5646	5805	5967

Table 2b. Estimated abundances (2006) under the Pradel model for fixed  $\lambda$  = 1.01-1.12 and survival rates ( $\phi$ ) = 0.9-0.99

$\lambda$	$\Phi$								
	0.9	0.91	0.92	0.93	0.94	0.95	0.96	0.97	0.98
1.01	7051	7255	7465	7680	7902	8130	8364	8605	8853
1.02	7144	7350	7561	7779	8003	8233	8470	8714	8964
1.03	7237	7446	7660	7880	8106	8339	8578	8824	9077
1.04	7333	7543	7760	7982	8211	8446	8688	8936	9191
1.05	7431	7643	7862	8087	8318	8555	8799	9050	9308
1.06	7530	7745	7966	8193	8426	8666	8913	9166	9427
1.07	7631	7849	8072	8301	8537	8780	9029	9285	9548
1.08	7735	7954	8180	8412	8650	8895	9147	9406	9671
1.09	7840	8062	8290	8524	8765	9013	9267	9529	9797
1.1	7947	8171	8402	8639	8882	9133	9390	9654	9925
1.11	8056	8283	8516	8756	9002	9255	9514	9781	10055

The group **agreed** that the modelling framework described in SC/F09/SH3 and its addendum was adequate for assessment with respect to including mark-recapture. The group also **agreed** that parallel analysis of the mark-recapture data with more standard methods (e.g. those implemented in MARK) should be carried out to present a comparison with the outputs from the assessment model. It was generally **agreed** that the Pradel model was the most similar to the mark-recapture framework of the assessment model and therefore the most appropriate candidate for such a comparison. However, some members considered that if mixing of individuals is random throughout sub-stock C3, so that all individuals have equal probabilities of being captured in the sampling region (irrespective of whether they actually visit the sampling region in any year), then the closed model abundance estimates reported in (Cerchio *et al.*, 2008b) would be relatively unbiased. This is assuming that the estimates are made from a short span of years (2004-2006) to minimize closure violations, as presented. If heterogeneity exists, and there is non-random visitation of the sampling areas such that mixing is not equal throughout sub-stock C3, then the closed model estimates will be biased low. Thus, in addition to Pradel, other

models should be explored and, without information on mixing throughout C3, closed models should not be excluded.

In discussion of the mark-recapture effort in Antongil Bay (C3), it was noted that the field efforts in this limited area may result in heterogeneity of capture for the stock, or that there may be some likelihood of capture for the whole population (if full mixing occurs within the stock). The resolution of this may suggest whether open or closed population models are more appropriate to use in population estimates. In contrast, surveys of C1 animals represent area-bound density estimates, so are likely to under-estimate the size of the stock. Biases to the C1 estimate are dependent on area coverage relative to the extent of the habitat that the whales use, while biases to C3 depend on what proportion of individuals use the bay under survey. The Workshop noted that differences in data collection between the two regions may cause further bias to estimates. For example, the C3 genetic and photo-identification data are collected more consistently than in C1. In addition, all of C3 genetic samples are from the breeding ground, while the majority of C1 photo-ID data are from the migratory corridor.

The group noted that the degree of movement of animals around the breeding ground within BSC is unknown and that this may influence estimates of population growth rates. In this respect, it was suggested that a single-sex mark-recapture analysis (item 2.2.1) may illuminate some aspects of this movement. It was observed that estimates of abundance become lower with greater exchange, which is consistent with the results for the resident and mixture models in sub-stock C3. The resident model provides a higher combined  $K$  than the mixture models. The low number of re-sights between the regions ( $n=1$ ) is in contrast to a proportionally larger number of re-sights in C3, which strongly influences the low mixing estimate. It was noted that in simulation, the resident model should be positively biased when the true model is mixed.

It was noted that exchange parameters for the movement models are all derived from the recapture data, which is sparse, with some years poorly sampled. It was suggested that the only years from C1 which are acceptable for inclusion in the model are 2003, 2005 and 2006, a sub-set of those used in the current assessment. While it was noted that excluding additional years will likely increase interchange probability, change estimated abundance and widen confidence intervals, these are the years for which temporal and spatial sampling has been most consistent. The group **agreed** that a subset of the mark-recapture data should be used in the population model as a sensitivity test.

It was noted that near the start of the 20<sup>th</sup> century estimates of abundance for C3 remain high for longer periods than for C1, (Figures 2b and 4b in SC/F09/SH3), and  $N_{min}$  for C3 was not as low as that for C1. The high growth rate estimates imposed by the trend data for C1 in fact drive the population trajectory for C3, which is influenced by catches but for which there is no informative growth rate data available. It was noted that the posterior distribution of  $r$  for C3 was slightly narrower than that of the prior (which was the BSA posterior). This minor effect reflects influence of the C3 mark-recapture information on  $r$ . The group noted that sensitivity and simulation testing of the interchange model could confirm whether they provided relatively robust results, however the model choice depends on an agreed movement hypothesis and these must be qualitatively evaluated before the model selection can proceed.

After discussion of documents SC/F09/SH3 and its addendum, the workshop **agreed** to specify a number of categories of input data for the interchange models for analysis to be presented at SC61. These specifications are discussed under Item 3.5 below

### 3.2.3. *Within BSB*

In view of the absence of data from the B2 breeding ground, the group noted that there is currently insufficient information to estimate exchange rates within BSB and encouraged the comparison of photo-identification data to assess the degree of interchange between B1 breeding grounds and the area of B2 sampled off west south Africa.

### 3.2.4 *Between BSB and BSC or their substocks*

The mechanisms of exchange between B and C are poorly known. Some ideas were postulated in (Pomilla and Rosenbaum, 2005); some inter-stock movement likely occurs due to overlap on the feeding grounds. In the known cases, a juvenile male moved one time (potentially a case of temporary emigration), and in the latter an adult moved (suggesting potential for gene flow). In both case, the whales were initially sighted in Antongil Bay (C3), then off of Gabon (B1).

Without taking into account the original sample sizes, the degree of interchange appears to be of the same magnitude between oceanic basins as within them. The movements were detected from samples of 1,648 animals and 1,363 genotypes off of Gabon (collected between 2000-2006), and 1,126 animals and 922

genotypes off of Madagascar (collected during the same period). The index of interchange originally computed is less than one migrant per generation (Pomilla and Rosenbaum, 2005).

However a simple calculation using photo-identification data in Collins et al. (2008) and Cerchio et al. (2008) allows a crude estimation of exchange. These data provide cumulative recapture rates of  $39/922 = 0.042$  for C3 compared with  $95/1363 = 0.070$  for B1. The greater probability of recaptures in B1 suggests that the three C3 whales from C3 recaptured in B1 (Pomilla and Rosenbaum 2005, Loo and Pomilla pers comm.) corresponds roughly to  $3 \times (0.042/0.070) = 1.8$  whales if recaptured in C3. Then the proportion of C3 whales moving to B1 compared to those remaining in C3 is  $1.8/39 = 0.047$ . This suggests a net movement of about 5% of C3 whales to B1. This will underestimate the total movement as the capture-recapture database increased in size over the seven year period considered, so that annual movement rates are probably non-negligible and worth noting. The Workshop found this work interesting, and suggested that a similar issue might exist between East and West Australia, where Discovery tag data may shed some light on interchange.

The implications of B/C interchange to the assessments was discussed, in particular whether the movement observed represents enough exchange to have any affect on assessment estimates. In principle interchange can be crudely estimated between B1 and C3 as population estimates and proportions of captures are available from both regions. However, it was cautioned that the interchange took place in the two most distant places, C3 to B1, which are the only places where data are available for comparisons. Comparisons between B1, B2 and C3 are ongoing, and the spatial proximity of C1 to B2 makes interchange more likely there, but no data are yet available to provide an estimate of interchange.

The group discussed the consequences of the interchanges for the structure of populations and whether possible divisions between stocks are artificial. It was noted that song in Madagascar was also very similar to song off of Gabon in the two years analyzed so far. In other areas, similarity and/or differences in song and other call types have been used to distinguish different populations. However, the utility of song in assessing population differentiation has been regarded as limited in humpback whales (IWC, 2006). While similarities in song do not confirm panmixia, they suggest at least distributional overlap. In combination with other evidence this may help shed light on gene flow (since song is a breeding display). In other well documented taxa, sharing of culturally transmitted breeding displays is strong evidence for gene flow (e.g. Payne and Westneat, 1988). In Northern Hemisphere feeding grounds (Alaska, Straley, 1990) and the Gulf of Maine (Clark and Clapham, 2004; Mattila *et al.*, 1987), song has been recorded on the feeding grounds, also suggesting that the cultural transmission may take place without individuals moving between areas. It is also unclear how many, or the proportion of animals required to move to influence song in a new area. Despite the uncertainties, the workshop **agreed** that there is some interchange between stocks B and C. It was noted that population structure and the exchange of individuals were not necessarily mutually exclusive. For example, in North Pacific humpback whales there are strong genetic differences between breeding areas (Baker *et al.*, 1998) but there are also several photo-identification matches between these areas (Calambokidis *et al.*, 2008), suggesting either that the individuals that move do not stay or do not successfully mate, or that the exchange is not great enough to eliminate genetic differences between the areas.

In consideration of these issues, the group recognized that interchanges may occur, and that they may affect the dynamics of the population, but for now the group **agreed** to consider stocks B and C separate for purposes of the assessment. However, given the possible interchange between these stocks the group also **agreed** to perform a sabbatical model assessment of C3 and B1, using genetic data, to estimate the rate of exchange (with a caveat that it will be difficult to allocate historical catches for this model). It was felt that this is important, since from a gene flow perspective alone, an exchange rate of 4% would potentially eliminate genetic evidence for stock structure in a short period if accompanied by inter-breeding. It would also be helpful to investigate if there were any predictions that arose from using the migrant model in addition to the sabbatical model. In the sabbatical model (which is the base case agreed upon), animals will later return to their original populations. The crude level of interchange estimated may not influence separate assessments. However, greater interchange rates between B2 and C1 might invalidate this conclusion.

The group also discussed why consideration of C1-C3 interchange is important, if the rate of interchange between B1 and C3 is considered insufficient evidence for panmixia. The group concluded that since the sample sizes of recaptures in C1 are greater (only 7 recaptures within C1, and 1 exchange with C3), there is greater uncertainty in the range of interchange which is possible. The higher research effort in B1 and C3 (where there are many more re-sights within each area) makes it possible to more precisely estimate the rate of interchange.

### 3.2.5. Among BSD, BSE and BSF

There was insufficient time to discuss estimation of exchange rates among BSD, BSE and BSF.

### 3.3. Simulation testing

#### 3.3.1 Review of results from initial tests of models to estimate exchange rates

SC/FO9/SH5 developed operating models of the C1 and C3 sub-stocks, which allowed for interchange between the two on the basis of the Sabbatical model for this mixing process. These operating models are used to compare the performance of the Sabbatical and Resident estimators, in what is intended as a preliminary exercise whose primary aim is to illustrate this simulation testing approach in the context of the sub-stocks of breeding stock C of Southern Hemisphere humpback whales.

The group welcomed this useful start. It was noted that the resident model did not provide a higher estimate of abundance when exchange was occurring, in contrast to the real dataset (see SC/FO9/SH3). A metric displaying the percentage of time that this was the case would be illustrative. Another useful metric to display is the posterior percentile in which the true value falls. This can be informative as to whether the posterior probabilities are too narrow. It was suggested that this metric be added to the outputs of future model simulations.

It was suggested that these data are also analysed in Program MARK in order to afford a comparison between the two population models. In order to achieve this, a recapture history equivalent to the poisson-distributed recaptures used in the assessment model must be generated, as MARK is based on individual recapture histories. Two of the operating models considered in SC/FO9/SH5 (simulation models based on the Sabbatical estimator which exhibit low and high exchange probabilities (0.1,0.3) and photo-identification captures (numbers photographed in reality, five times the numbers photographed in reality) could be used in a comparison with MARK. For the operating models with low photo-identification captures, no animals are recaptured more than once so building a dataset of individual captures is feasible in this circumstance. However operating models with high photo-identification captures have more associated recaptures, which would provide a greater challenge in constructing an equivalent capture history in MARK.

#### 3.3.2 Finalisation of further simulation tests

The group **agreed** that simulation testing be restricted to the Sabbatical model as the assessment (estimation) model, because this had been chosen as the baseline estimator. The operating model for each simulation test would be conditioned on existing data to the extent pertinent. Given that Bayesian estimation under sampling-importance-resampling (SIR) was generally conducted by first generating 500,000 realizations of the joint prior distribution, and then computing the likelihood for each sample from the prior, generation of data from an operating model would be based on the parameter vector with the highest likelihood, as a good approximation to the maximal likelihood estimate.

Full simulation testing would be carried out on the following models.

- (1) Basic alternative interchange models: Migrant, Sabbatical and Tourist.
- (2) Sex-disaggregated model, for which mark recapture data would be generated accounting for the sex-structure of the population, but these data would be pooled over both sexes to use as input to the (sex-aggregated) estimation model.
- (3) Density-dependence: for the two alternative models introduced above (see Item 3.5).
- (4) A three sub-stock model, incorporating an additional sub-stock between the C1 and C3 sub-stocks. This is to reflect an initial approximation of a clinal structure. Conditioning would be on all the standard data except for capture-recapture interchanges. Interchanges would take place on a Sabbatical model basis between the C1 and C3 substocks, and similarly between each of these substocks and an additional sub-stock X. These additional annual interchange proportions would all be set at 0.05 (the average of the two direct C1-C3 interchange proportions). The  $r$  value for the X stock would also be set equal to the average for C1 and C3. There are no direct observational data for the X sub-stock, which was not directly affected by past catches, except those on the feeding grounds. Results would be examined for two input choices for the size of the X stock.

Outputs to be reported would include, at least, the medians with 5<sup>th</sup> and 95<sup>th</sup> percentiles of the distribution of estimates from simulated data.

The following would be conducted as sensitivity tests (see Item 3.5), but in such a way that they could readily be extended to full simulation testing if this were to be requested:

- (1) Age structured model: a simple conversion of the existing age-aggregated operating model, with knife-edge maturity and selectivity, fitted using the same data and using the same estimation framework that

would form the basis for the operating model. One reason for considering such an operating model is to examine the possibility (see Item 2.2.2) that length structure differences between catches off Mozambique and Madagascar in the late 1930s could be explained as consequences of differential harvesting histories.

- (2) Additional analyses could consider age-specific exchange rates.
- (3) Negative bias in absolute abundance estimates (e.g. arising from fixing  $g(0) = 1$ ). The estimate from the 2003 line transect survey of the C1 area (Findlay *et al.*, In press) would be increased by 20% prior to use when conditioning the operating model. The estimate available to the estimation model would, however, be negatively biased.
- (4) Sabbatical with pre-specified interchange rates: for two versions of this model, the exchange rates in each direction would be set first at 0.1 and then at 0.3. Conditioning would not incorporate capture-recapture data on inter-sub-stock interchange. If an effect is observed, a number of exchange rates should then be explored.

Heterogeneity in data used for capture-recapture was considered, but seen more as an (important) generic issue, and therefore better addressed in a more generic study (e.g. by developing an individual-based operating model in which there is heterogeneity in capture probability and applying MARK to datasets generated from the operating model).

### 3.4 Disaggregation of population models by sex

SC/F09/SH6 described the standard IWC modelling approach for age-aggregated population models disaggregated by sex, and suggested some ways in which extra data could be incorporated into such models.

It was noted that capture uncertainty in photo-identification and genotype data (described in Item 3.2) is focussed almost entirely on females, which have more variable probability of capture and possibly shorter residency times on the breeding grounds than males. However, analysis from YONAH has shown that some females are not non-migratory (Stevick *et al.*, 2006), and this brings into question probability of capture as well as the difference between availability on migratory routes and proper breeding grounds. If sex structure is incorporated, therefore, excluding females would allow use of a male-only model as a sensitivity analysis against a non-structured model.

The Workshop **agreed** that it would be useful to explore sex structuring within the context of the operating model for BSC, and observed that creating a sex-specific estimation model would be of great interest, but is very difficult to achieve.

### 3.5 Specification of categories of input data for interchange models for final analyses

Considering the discussions on the available data, the stock structure and the modelling approaches, the group **agreed** the following input data and sensitivity analysis for the assessment models to be presented at SC 61.

Sensitivities to be explored in the assessment model:

- (1) Inclusion of SOWER data for trend (as likelihood input)
- (2) Exclusion of aerial sighting index (as likelihood input)
- (3) Consistency checks (e.g. CPUE, trends)
- (4) "Alternative Cape Vidal" treatment, described in Item 3.1.
- (5) Two different forms of density dependence are to be investigated:
  - (a) Density dependence operates on the sum of the abundances of the two stocks, rather than independently for each stock. This might be appropriate for food-related limitations, as the two populations mix on the feeding grounds. This does mean that on complete recovery from exploitation, the relative abundances of the two populations may equilibrate at levels differing from those pre-exploitation.
  - (b) Density dependence on the number of animals present on the breeding grounds (including, for example, animals visiting from the other substock under the Sabbatical model) rather than only on the number of whales in the corresponding breeding substock itself.
- (6) Priors for  $r$ :

The baseline model incorporates a uniform prior  $U[0;0.106]$  for  $C1$ , and an informative prior for  $C3$  provided by the posterior for this parameter from a Bayesian assessment for breeding stock A. Alternatives for sensitivity tests are:

- (a) Uniform prior where  $r$  for  $C1$  and  $C3$  is the same. The population history of stock  $C3$  will thus be informed by trend information for stock  $C1$ .
- (b) Uniform prior with  $r$  estimated separately for  $C1$  and  $C3$ .

Questions were raised concerning estimation of the trend in population abundance for breeding stock A (Ward *et al.*, In press). These concerns related to possible pseudo-replication and hence under-estimation of the confidence interval for the trend. These matters will be resolved at SC61, but in the meantime the existing prior for stock A would continue to be used.

- (7) Years of photo-ID capture-recapture data to exclude (photo-ID)
  - (a) Analyse 2003, 2005 and 2006 only for  $C1$ .
  - (b) Omit all  $C1$  data
- (8) Input of capture-recapture population estimates.
- (9) Use of the Pradel capture-recapture model to obtain a  $C3$  abundance estimate for comparison with model output, which should include results for abundance in 2006 and trend over 2000 to 2006. Other capture-recapture models can also be used in this comparison, noting that the Pradel model is most similar to the recapture model implemented in the assessment model.
- (10) Refinement of Vidal relative abundance estimates. Use a GLM approach to extract a year factor from the full dataset for each Vidal series, assuming a common density pattern with data during each year. This approach would be valuable, but technically challenging and unlikely to be complete before SC61.
- (11) It was suggested that Borel's paradox applies to the use of genetic constraints ( $N_{min}$  estimates) to provide a minimum bound on population abundance. The effect that such a bound has is to modify the prior selected for  $r$ . Although other approaches might be argued (and this matter will be discussed at the next SC meeting) the approach currently being pursued was considered satisfactory. A few concerns about the means of obtaining  $N_{min}$  were noted, particularly the assumptions underlying the 4x correction used in the assessment model. However the Workshop **agreed** that this value represents a conservative boundary as it has not been corrected for population sampling, sequence length, and population frequency distribution.
- (12) Explore model sensitivity to exponent  $z$ , and integrate model across a range of  $z$  (1-11.2), corresponding to a maximum sustainable yield range of 0.5-0.8.

Other options were discussed but not included as sensitivity tests at this time as they were considered of secondary importance relative to those presented above. These were the use of a sex disaggregated model, genetic capture-recapture data and exploration of models intermediate between the sabbatical and tourist scenarios (discussed in more detail in Items 3.1 and Items 3.3.2).

Output statistics reported should include posterior medians and 90% probability intervals for  $r$ ,  $K$ ,  $N_{min}$ ,  $N_{2006}$ ,  $N_{2006}/K$ , and the average annual rate of increase over 2000 to 2006 for each sub-stock. In addition, plots for the baseline run and those of sensitivities with greater influence should compare estimated trajectories with abundance inputs and show comparisons of cumulative model predicted recaptures over time.

#### 4. OTHER

There was nothing to discuss under this agenda item.

#### 5. WORK PLAN AND RECOMMENDATIONS

The Group **agrees** that it should be possible to complete the assessments for Breeding Stock C and B1 based on the discussions held at the Workshop. In addition, the Group agrees that high priority should be given to the following tasks, which must be conducted by the deadlines specified below:



**Data**

Task	Deadline	Responsible	Submit to:
<i>Abundance and interchange estimates</i>			
Genotype error checking	By 31 Mar 2009	Loo / Rosenbaum	Cerchio
Sex-aggregated and male-specific abundance estimates using genotype data (closed model, error rates included)	SC/61	Cerchio	Meeting document
Additional M-R estimates for C3 (e.g. Pradel Model, other M-R models) with photo-id data	31 Mar 2009	Cerchio	Meeting document
Individual capture histories from photo-identification data for M-R abundance estimates for C3	31 Mar 2009	Cerchio	Johnston/Butterworth
Provide sex-specific capture-recapture data from regions B1 and C3	31 Mar 2009	Rosenbaum	Johnston/Butterworth
C1: Reconcile 2007 photo catalogue	31 Mar 2009	Findlay	Johnston/Butterworth
Comparison of genotypes samples from B1, B2 (225 genotypes), C1 (50-60 genotypes) and C3 to look for genotypic matches	SC/61 tentative	Loo, Carvalho, Rosenbaum	Cerchio
B2 abundance estimate	SC/61	Barendse/ Best	Meeting document
B1/B2 photographic interchange estimate	SC/61 low priority	Barendse/ Collins	Meeting document
Revised B1 abundance estimate	SC/61	Collins	Meeting document
<i>Trends/CPUE</i>			
Improvement of Aerial SPUE data (Durban)	SC/61	Best/ Butterworth	Meeting document
<i>Genetic analysis/Stock structure</i>			
Testing of new stock structure hypothesis in the feeding grounds (mixture modeling- mitochondria and microsatellites) with ten additional microsatellite loci (update of Loo <i>et al.</i> , 2008)	SC61	Loo/Rosenbaum	Meeting document
Analysis of 2006-2007 IDCR/SOWER samples	Depends on sample availability from Southwest Fisheries	Rosenbaum / Loo	Meeting document, if possible
Look at haplotype richness estimates from B/C for use in <i>Nmin</i> constraint	31 Mar 2009	Loo, Carvalho, Rosenbaum	Johnston/ Butterworth
<i>Catches</i>			
Summarize and clarify the various catch	SC/61	Findlay (chair),	Meeting document or

allocation hypotheses used in the Assessment of SH HW in the past 10 years.		Bannister, Best, Cerchio, Jackson, Loo, Rosenbaum, Weinrich, Zerbini	summary
Spatio-temporal analysis of catches in C region	SC/61	Best	

### Modelling

Task	Deadline	Responsible	Submit to:
<i>Assessment Models</i>			
Development of sex-specific models	31 Mar 2009	Findlay- catch	Johnston/Butterworth
		Johnston/ Butterworth-model	Meeting document
Incorporation of genotype error	SC/61	Johnston/Butterworth	Meeting document
Sensitivity tests (see Item 3.5)	SC/61	Johnston/Butterworth	Meeting document
Develop sabbatical model concerning C3/B1 using genetic data.	SC/61	Johnston/Butterworth	Meeting document
<i>Simulations</i>			
Further simulation testing (see Item 3.3.2)	SC/61	Johnston/Butterworth	Meeting document
Simulation of catch selectivity scenarios to explore potential effect of whaling on body length.	SC/61	Best/ Butterworth	Meeting document
<i>Longer term priorities</i>			
General linear modelling of the spatial distribution of sex ratios in C region	Not specified	Butterworth/Findlay	Not specified
Improvement of Cape Vidal trend data	Not specified	Findlay	Not specified

## 6. ADOPTION OF THE REPORT

The report was adopted on the 2<sup>nd</sup> June, 2009.

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Appendix A

Butterworth

Cerchio

Cooke

Donovan

Findlay

Friday

Jackson

Johnston

Kaufman

Laake

Punt

Rosenbaum

Wade

Weinrich

Zerbini

## Appendix B

**AGENDA****Intersessional Meeting on Southern Hemisphere Humpback Whale Assessment Methodology, Seattle 3-6 Feb 2009**

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1. Introductory Items
  - 1.1. Opening Remarks
  - 1.2. Terms of Reference
  - 1.3. Election of Chair
  - 1.4. Appointment of rapporteur
  - 1.5. Adoption of the agenda
  - 1.6. Review of documents
  
2. Data Categories for Assessment Models
  - 2.1. General
    - 2.1.1. Allocation of feeding ground catches
    - 2.1.2. Breeding Stock C (BSC)
    - 2.1.3. Existing data categories and progress in data evaluation
    - 2.1.4. Additional data
  - 2.2. Breeding Stock B (BSB)
    - 2.2.1. Existing data categories and progress in data evaluation
    - 2.2.2. Additional data
  - 2.3. Information on exchange between BSB and BSC
  - 2.4. Breeding Stocks D, E and F (BSD, BSE, BSF)
    - 2.4.1. Information on interchange data among BSD, BSE and BSF
  - 2.5. Data available for sex disaggregation of assessment models
  
3. Assessment Methodology
  - 3.1. Models for stock/sub-stock mixing in the feeding grounds
  - 3.2. Estimation of exchange rates between sub-stocks of near breeding grounds using capture-recapture methods
    - 3.2.1. General considerations
    - 3.2.2. Within BSC
    - 3.2.3. Within BSB
    - 3.2.4. Between BSB and BSC or their sub-stocks
    - 3.2.5. Among BSD, BSE and BSF

- 3.3. Simulation testing (Papers: SC/F09/SH5)
  - 3.3.1. Review of results from initial tests of models to estimate exchange rates
  - 3.3.2. Finalization of further simulation tests
- 3.4. Disaggregation of population models by sex
- 3.5. Specification of categories of input data for interchange models for final analyses
- 4. Other
- 5. Work Plan and Recommendations
- 6. Adoption of the Report

## Appendix C – List of Documents

SC/F09/SH

- 1 BUTTERWORTH, D.S. and JOHNSTON, S.J. Report on discussions on modelling studies of possible interchange between the C1 and C3 breeding substocks of Southern Hemisphere humpback whales, Cape Town, December 2008.
- 2 BEST, P.B. and BRANDÃO, A. Humpback whaling at Madagascar, 1910-1950.
- 3 JOHNSTON, S.J. and BUTTERWORTH, D.S. Bayesian assessments of Southern Hemisphere humpback whale breeding substocks C1 and C3, including allowance for interchange on the breeding grounds.
- 3-Addendum JOHNSTON, S.J. and BUTTERWORTH, D.S. Addendum to: Bayesian assessments of Southern Hemisphere humpback whale breeding substocks C1 and C3, including allowance for interchange on the breeding grounds.
- 4 FINDLAY, K. Further information on humpback whales from the southwestern Indian Ocean (breeding stock C).
- 5 JOHNSTON, S.J., BUTTERWORTH, D.S. and MULLER, A. Simulation testing of two estimators for the assessment of Southern Hemisphere humpback whale breeding stock C and its component sub-stocks.
- 6 BUTTERWORTH, D.S. A note on disaggregating population models by sex.
- 7 JACKSON, J. Southern Hemisphere humpback whale Comprehensive Assessment workshop, Seattle, February 2009: Summary table for BS Ei, Eii, Eiii, American and Independent Samoa, Fi and Fii (revised table from SC/58/Rep5).
- 8 JACKSON, J.A., ZERBINI, A., CLAPHAM, P., CONSTANTINE, R., GARRIGUE, C., HAUSER, N., POOLE, M.M. and BAKER, C.S. Progress on a two-stock catch allocation model for reconstructing population histories of east Australia and Oceania.



## Appendix D

Summary Table of data available for Breeding Stocks B1, C1 and C3 (update to Johnston, 2008a; Johnston, 2008b)

<b>Data</b>	<b>Will be used in assessment model (M), or as 'consistency check' (C), or not used (N)</b>	<b>When available (A = available, N = not available)</b>	<b>Strengths</b>	<b>Possible Limitations and Biases</b>	<b>Observations</b>
<b>Breeding sub-stock C1</b>					
<i>Commercial catches</i>					
Southern Cape, Durban, Mozambique (Findlay, 2001), Area III, IWC catch database	M	A			
<i>Population abundance</i>					
<i>Yacht-based line transect</i> (Mozambique) N=1954 (CV=0.38) (Year, 1991) (Findlay <i>et al.</i> , 1994)	N	A		Negatively biased: less spatial coverage than new estimate by Findlay et al. (in press) and assumption that $g(0)=1$	
<i>Ship-based (Mozambique) N=5965</i> (CV=0.17) (Year, 2003) (Findlay <i>et al.</i> , In press)	M	A	Best abundance estimate available	negatively biased – no full spatial coverage of breeding grounds and assumption that $g(0)=1$	
<i>Shore-based counts of migration (Cape Vidal)</i>  1990 Northward: 1711, Southward: 1647  1991 Northward: 1777 (Findlay and Best, 1996)	C	A			
<i>Population trend</i>					

<b>Data</b>	<b>Will be used in assessment model (M), or as ‘consistency check’ (C), or not used (N)</b>	<b>When available (A = available, N = not available)</b>	<b>Strengths</b>	<b>Possible Limitations and Biases</b>	<b>Observations</b>
<i>C1 Migratory corridor (northward)</i> Cape Vidal (Findlay and Best, 2006) 1988-1991, 2002 (6-22 July series)	M	A	Only direct measure of trend for C1		GLM approach proposed to extract year factors (assuming a common density pattern with date each year)
<i>C1 Migratory corridor (northward)</i> Cape Vidal (Findlay and Best, 2006) 1990-91, 2002 (6-30 July series)	N	A		Shorter period relative to the previous series	
<b><i>Relative abundance:</i></b>					
1910-1912 Olsen (1914), Durban (1 CPUE series)	C	A		Different views in regards to use of CPUE series as “consistency check”.	See discussion of the use of CPUE indices for assessment in IWC (1997, CPUE Workshop)
CPUE, Durban (Best, 2003), Three series (1920-1928, 1954-1963, 1969-1975)	C	A		1920-1928 shows evidence of shift in whaler species preference during this period	
Aircraft SPUE, Durban (Best, 2003), 1954-1975 (1 CPUE series)	M	A		Only information available from that period of time - surveys in the migratory route may be “representative sampling” but are non scientific surveys.	Improvements proposed in the workplan
<i>Feeding ground</i> IDCR/SOWER (Branch, 2006) CPI (1979) 1043 (CV = 0.62)	M	A		Poor coverage of the range of the stock in the feeding grounds. A portion of the population remains N of 60°S.	Used in population models only as a sensitivity analysis. Future value of SOWER data for trend should be examined in the

<b>Data</b>	<b>Will be used in assessment model (M), or as 'consistency check' (C), or not used (N)</b>	<b>When available (A = available, N = not available)</b>	<b>Strengths</b>	<b>Possible Limitations and Biases</b>	<b>Observations</b>
CPII (1987) 926 (CV = 0.57) CPIII (1993) 2391 (CV = 0.41)					light of (1) shifts in patterns of humpback presences around the ice shelf (2) potential influence of immigration confounding trends.
(9) Mark-recapture Photo-ID 2000-2006, mostly migration corridor. Fluke catalogue size = 451 (after filtering for quality), (Cerchio <i>et al.</i> , 2008a)	M	A	Three years show most consistent sampling effort and are recommended as the best years to use in the model for computing abundance estimate.	Some years (2000, 2004) were excluded due to concerns with temporal sampling effort	
Photo 2007, mostly migration corridor. Fluke catalogue size (n= 167)	M	Available by 31 March 2009		Photos are available to use but there is not a concurrent 2007 sample for the remaining C3. No time to match until Madeira. Same weaknesses as previous year catalogues (temporal and spatial inconsistency)	Use to estimate abundance within C1.
<b>Breeding Sub-Stock C3</b>					
<b>Commercial catches</b>					
IWC Database					
<b>Population abundance</b>					
<i>Line-transect survey</i> Southern Madagascar (1994), 2532 CV = 0.27 (Best <i>et al.</i> , 1996)	C	A		Negatively biased because of insufficient geographical coverage. Does not account for perception bias.	

<b>Data</b>	<b>Will be used in assessment model (M), or as 'consistency check' (C), or not used (N)</b>	<b>When available (A = available, N = not available)</b>	<b>Strengths</b>	<b>Possible Limitations and Biases</b>	<b>Observations</b>
<i>Mark-recapture (photo-ID) Chapman's modified Petersen</i>  Antongil Bay (2000), suggested 'lower/upper-bound estimates' 5197 (CV=0.35) (2002), 7458 (CV=0.29), (Cerchio <i>et al.</i> , 2006)	N	A			New abundances will be computed possibly accounting for error checking and using alternative models
Antongil Bay (2005), suggested 'lower/upper-bound estimates' 6737 (CV=0.31), 7715 (CV=0.24), (Cerchio <i>et al.</i> , 2008a)	N	A			New abundances will be computed possibly accounting for error checking and using alternative models
<i>Mark-recapture (genotype), Chapman's Modified Petersen</i>  Antongil Bay (2005), suggested 'lower/upper-bound estimates' 8348 (CV=0.32), 10123 (CV=0.24), (Cerchio <i>et al.</i> , 2008a)	N	A			New abundances will be computed possibly accounting for error checking and using alternative models
<b>Population trend</b>					
<i>Feeding ground</i>  IDCR/SOWER (Branch, 2006)  CPI (1979) 1043 (CV = 0.62) CPII (1987) 926 (CV = 0.57) CPIII (1993) 2391 (CV = 0.41)	M	A		May be confounded as a measure of a B1 and C because of mixing in the feeding grounds.  Poor coverage of the range of the stock in the feeding grounds. A portion of the population remains N of 60°S.	Used in population models only as a sensitivity analysis.  Future value of SOWER data for trend should be examined in the light of (1) shifts in patterns of humpback presences around the ice shelf (2) potential influence of immigration confounding

<b>Data</b>	<b>Will be used in assessment model (M), or as 'consistency check' (C), or not used (N)</b>	<b>When available (A = available, N = not available)</b>	<b>Strengths</b>	<b>Possible Limitations and Biases</b>	<b>Observations</b>
					trends.
<b>Mark recapture data</b>					
(9) Mark-recapture data Antongil Bay, (Cerchio <i>et al.</i> , 2008a) photo-ID (2000-2006), fluke catalogue size= 843	M	A		Most complete dataset for the stock	
Genotypes (2000-2006), sample size = 1126	M	A		Sex information will be made available by end of March. Error checking of genotypes required	Sex information will be made available by end of March. Error checking of genotypes required
<b>Sub-stock B1</b>					
<b>Commercial catches</b>					
Breeding and Feeding ground catch data, available from (IWC, 2006)	M	A			
<b>Population abundance</b>					
(7) Population abundance <i>Aerial survey</i> (Strindberg <i>et al.</i> , In press), n=1259, CV = 0.32, for 2002.	N	A	Minimal mixture of B2 animals.	Incomplete coverage of the breeding grounds. No estimation of perception bias	
<i>Mark-recapture</i> (Collins <i>et al.</i> , 2006), for 2002 Chapman's: 5641, CV=0.24 Schnabel: 5317, CV=0.21	N	A	Most complete dataset for the stock		New abundances will be computed using alternative models

<b>Data</b>	<b>Will be used in assessment model (M), or as 'consistency check' (C), or not used (N)</b>	<b>When available (A = available, N = not available)</b>	<b>Strengths</b>	<b>Possible Limitations and Biases</b>	<b>Observations</b>
Chao's: 5766, CV=0.20					
(Collins <i>et al.</i> , 2008), for 2003 Photo-ID (MARK)- Iguela only: 6432, CV=0.18 Genetic (MARK)- Iguela only: 7196, CV=0.15	N	A	Most complete dataset for the stock		New abundances will be computed possibly accounting for error checking and using alternative models
(8) Population trend <i>Feeding ground</i> IDCR/SOWER (Branch, 2006) CPI (1980) 692 (CV=0.84) CPII (1986) 70 (CV=0.63) CPIII (1995) 595 (CV = 0.51)	M	A		May be confounded as a measure of a B1 and C because of mixing in the feeding grounds	Used in the model as a sensitivity test.  Future value of SOWER data for trend should be examined in the light of (1) shifts in patterns of humpback presences around the ice shelf (2) potential influence of immigration confounding trends.

## Appendix E

### PRELIMINARY EVALUATION OF SEX RATIO INFORMATION IN SOUTHERN HEMISPHERE HUMPBACK WHALE CATCHES

Alexandre N. Zerbini and Ken Findlay

The Scientific Committee (SC) of the International Whaling Commission (IWC) indicated that a possible improvement in the assessment of Southern Hemisphere (SH) humpback whales include the development of sex-specific population models (IWC, in press). Such models would require dividing the catch data by sex. Recent assessments of humpback whale breeding stocks (BS) A and G using sex-aggregated models have shown that variations or errors in the catch series have important implications to the estimation of pre-exploitation population size (IWC, 2007). For this reason, it is important to investigate and understand the possible limitations of the catch series for the development of sex-specific assessment models.

In the present document we reviewed information on sex ratio of humpback whale catches in the IWC database as an attempt to address the following questions:

- (1) What proportion of the catches has information on sex ratios for each one of the breeding stocks currently recognized by the IWC and what levels of uncertainty for each BS would have to be considered if catches were to be split by sex for assessment purposes?
- (2) Is there any evidence of trends in sex ratios over time in feeding and breeding grounds?

Two sources of information were examined: (1) The IWC *summary database*, which contains information on catches by expeditions and regions, and (2) the IWC *database of individual catches*, which contains biological data (including sex) on an individual basis in addition to information on expedition and region. Catches in the individual database are included in the summary database, but the opposite may not necessarily be true (e.g. because no biological information is available for certain areas or years). Catches in the summary database have been used for the ongoing assessment of humpback whale (IWC, 2007).

In this study catches were summarized for each BS (A-G) and were split into breeding ground catches (whales taken to the north of 40°S) and by feeding ground (catches to the south of 40°S) associated with each breeding stock (as defined by IWC, 1998; 2007; In press). Feeding ground catches followed the Naïve catch allocation hypothesis as proposed by IWC (1998) for all but BSA and BSG. For these two stocks “Core” areas were recently established and used in the recent assessments (IWC, 2006). A “Core” area was also proposed for BSD, but for consistency with adjacent stocks<sup>1</sup> this was not considered here. Longitudinal divisions for catch allocations of are summarized in Table 1. For the purpose of this study, the 313 whales taken in this region were grouped with whales taken in the Antarctic Peninsula (BSG).

Table 1 – Longitudinal sectors for division of Southern Hemisphere humpback whale catches.

Breeding Stock	Breeding Grounds (north of 40°S)	Feeding Grounds (south of 40°S)
A	Western South Atlantic Ocean west of 20°W (Eastern coast of South America)	20°W-50°W
B	Eastern South Atlantic Ocean east of 20°W (Western coast of Africa)	10°E-20°W
C	Western Indian Ocean west of 60°E (Eastern coast of Africa)	10°E-60°E
D	Eastern Indian Ocean east of 60°E (Western coast of Australia)	60°E-120°E
E	Western South Pacific Ocean west of 170°W (Eastern coast of Australia and New Caledonia)	120°E-170°W
F	South Pacific Islands east of 170°W and west of 100°W (Fiji, Tonga, Cook Islands, Samoas, French Polynesia)	100°W-170°W
G	Eastern South Pacific Ocean east of 100°W (Western coast of South America)	50°W-100°W

<sup>1</sup> BSD was assessed as a single stock during IWC 58, but this requires revision once BSE is assessed because of mixing of whales from these two stocks in the feeding grounds (IWC, 2007). In addition, while a Core catch allocation area has been proposed for BSD with consequential shifts in longitudinal boundaries, the IWC SC has not agreed on Core areas for the adjacent BSC and BSE. Therefore, it seems more appropriate to allocate catches here following the Naïve rather than the Core model for BSD.

Information on sex in the individual catch database were be coded according to four categories: “Female”, “Male”, “Unknown” or “Hermaphrodite”. For the purpose of this document, individuals classified as the latter (only a single whale) were grouped in the “unknown” category.

### Summary of catches with information on sex and proportions per breeding stock

The summary catch database indicates that a total of 219,972 humpback whales were taken in the Southern Hemisphere (Table 2). A total of 97,615 and 122,357 whales were taken in the breeding and feeding grounds, respectively. Biological information is available for only 107,732 individuals (49% of the total catches), but 2,508 have no capture location and may not be allocated to any stock. Of the remainder 105,524 records, 51,838 and 53,386 were observed in breeding and feeding grounds, respectively. However, sex information from 8,094 individuals was classified as “Unknown”, leaving 99,644 catches that can be split between males and females.

Table 2 – Total catches in the Summary and Individual catch databases. Numbers in parenthesis correspond to catches with data on sex of individual catches.

Breeding Stock	Summary Database			Individual Catch Database		
	Breeding Grounds	Feeding Grounds	Total	Breeding Grounds	Feeding Grounds	Total
A	1,836	29,334	31,170	378 (363)	4,845 (4371)	5,223 (4734)
B	29,833	5,056	34,889	10,192 (10180)	3,209 (3138)	13,401 (13318)
C	20,807	8,128	28,935	9,297 (9178)	7,188 (7126)	16,485 (16304)
D	28,281	20,352	48,633	23,130 (23049)	14,942 (14149)	38,072 (37198)
E	14,513	35,971	50,484	8,627 (8626)	14,480 (9373)	23,107 (17999)
F	0	8,147	8,147	0	5,388 (4382)	5,388 (4382)
G	2,345	15,369	17,714	214 (109)	3,334 (3103)	3,548 (3212)
Total	97,615	122,357	219,972	51,838 (51,505)	53,386 (45,642)	105,524 (97,152)

The use of sex disaggregated models would require assumptions about sex ratios for each breeding stock, because the proportion of females to males is not known for the whole catch series in any BS (Table 3). More information about the sex of individuals taken is available for for BSD (with 76.5% of the catches containing sex information) and less data exist for BSA and BSG (with less than 20% of the catches containing such information).

Table 3 – Proportion of catches with information on sex ratios in breeding and feeding grounds for each BS

Breeding Stock	% of catches with known sex		
	Breeding Grounds	Feeding Grounds	Total
A	19.7%	14.9%	15.2%
B	34.1%	62.0%	38.2%
C	44.1%	87.7%	56.4%
D	81.5%	69.5%	76.5%
E	59.4%	26.1%	35.6%
F	-	53.8%	53.8%
G	4.6%	20.2%	18.1%
Total	52.7%	37.3%	44.2%

### Trends in sex ratio over time

Trends in sex ratios over time were examined for breeding and feeding grounds for all BS combined. A simple linear regression was applied to the proportion of females in the catches in an attempt to investigate whether a temporal (year) effect could be found. For this analysis, years in which the number of catches with sex information was less than 10 were removed for the analysis. The simple regression indicated that the proportion



of females in the breeding ground catches declined over time (Year effect = -0.00195, SE = 0.0006,  $R^2 = 0.1835$ ,  $p = 0.00465$ ) (Fig. 1). Such pattern was not observed in the feeding grounds.

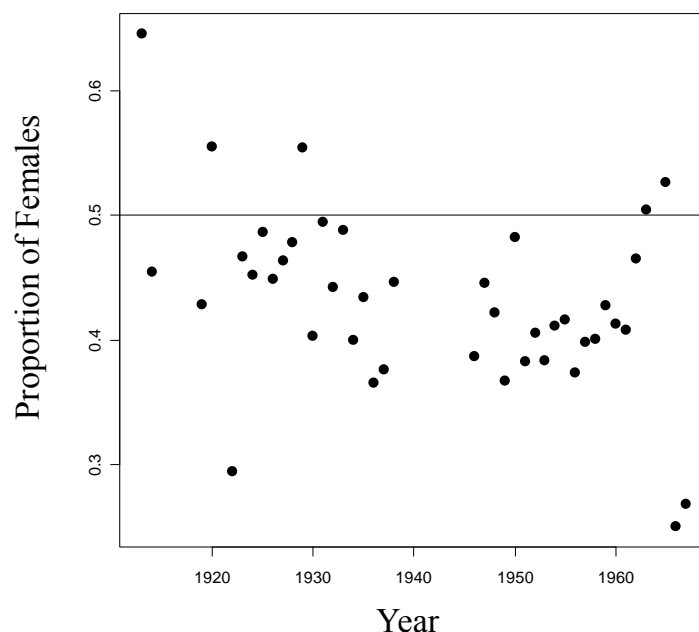


Fig. 1 - Proportion of females per year in humpback whale catches in the Southern Hemisphere wintering grounds (all stocks combined). Horizontal line corresponds to an even proportion.

### Conclusions

The purpose of this document was to summarize existing data on sex ratios of humpback whales in the Southern Hemisphere. It is clear that sex information is missing for all humpback whale breeding stocks at different degrees. For some stocks (e.g. BSA, BSB, BSE and BSG), sex ratios can be computed to less than 50% of the catches and the effect of certain assumptions about the ratios in the catch series should be carefully evaluated.

The analysis presented above is simple and is not meant to be conclusive, but to generate discussion among members of the workshop on how to address lack of information on sex ratio if sex-disaggregated models are to be implemented for the assessment of Southern Hemisphere humpback whales.

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