Report of the First RMP Intersessional Workshop for western North Pacific common minke whales

Contents

1.   INTRODUCTORY ITEMS

The primary objective of the Workshop was to develop the *Implementation Simulation Trials* structure and to specify the appropriate conditioning such that it can be carried out before the 2011 Annual Meeting. The relevant section of the 'Requirements and Guidelines' is included as Annex D. Following a recommendation from the Scientific Committee, a preparatory meeting for the Workshop was held in Tokyo, Japan, from 25-27 September 2010. The preparatory meeting represented an additional step to the usual *Implementation* process {, 2005 #32809}, primarily due *inter alia* to the complex nature of the stock structure hypotheses proposed and the fact that the direct (and incidental) catches occurred on migration rather than on the feeding grounds (the RMP had originally been developed for catches on the feeding grounds). The purpose of the preparatory meeting had been to undertake technical discussions and ensure that: (a) the stock structure hypotheses were sufficiently well specified to allow coding to begin; and (b) that the data necessary for 'First Intersessional Workshop' (hereafter the 'Workshop') were available in time and in a suitable format for the *Implementation* process to continue on schedule.

The relevant discussions of the preparatory meeting were reviewed at the Workshop and integrated into this final report. The Workshop was held at the Paradise Hotel, Pusan, Republic of Korea, from 14-17 December 2010. The President of NFRDI, Mr. Young Man Kim, welcomed participants to Busan. A list of participants for both meetings is given as Annex A.

1.1 Convenor's opening remarks
Butterworth referred to IWC {, 2005 #32809} and noted that the primary objective of the Workshop was to develop an appropriate *Implementation Simulation Trials* structure and to specify the associated conditioning so that it can be carried out before the following Annual Meeting. The aim of such trials[1] is to encompass the range of plausible scenarios involving *inter alia* stock structure, MSY rates (MSYR), removals and surveys. These trials are used to investigate the implications of various choices of RMP variants such as *catch-cascading* from a risk- and catch-related perspective, with a view to recommending an appropriate variant for implementation of the RMP for a specific species/area.

1.2 Election of Chair and appointment of rapporteurs
The preparatory meeting and the First Intersessional Workshop were chaired by Donovan. Allison, Butterworth, Kelly, Punt and Donovan acted as rapporteurs, with assistance from various other participants as appropriate.

Donovan stressed that after the Workshop, there shall be no changes to the agreed trials structure that implements the agreed plausible hypotheses and that no new data can be considered. However, new analyses of existing data may be presented to the 2011 Annual meeting being held in Tromsø, Norway (hereafter the 'First Annual Meeting'). He also noted that during the *Implementation* process, the Committee has to examine a range of plausible hypotheses to enable it to incorporate the uncertainty around stock structure issues. Achieving this for the present *Implementation Review* is a two-stage process:

(1) review the evidence and, if necessary, eliminate any hypotheses that are shown to be incompatible with the data (this would be undertaken at the present Workshop); and

(2) assign plausibility rankings to the remaining hypotheses (this will be undertaken at the 2011 Annual Meeting).

With respect to (2), he noted that discussions of how to facilitate the consideration of relative plausibility of hypotheses (including, if appropriate, recommending intersessional analyses) would form part of the discussions at the present Workshop.

1.3 Adoption of Agenda
The **agreed** Agenda is given as Annex B.

1.4 Review of documents
The new documents available to the meeting were SC/S10/NPM1-13 and SC/D10/NPM1-16 (see Annex C). Relevant past meeting documents and published papers were made available as necessary. The Chair, on behalf of the meeting, thanked the authors for their efforts during the intersessional period, noting that a substantial amount of work had been conducted, which should simplify the process of developing the *Implementation Simulation Trials*.

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[1] A trial is the combination of a set of 'hypotheses' (e.g. about stock structure, MSYR)

2. HYPOTHESES FOR INCLUSION IN TRIALS

2.1 Stock structure and mixing

2.1.1Brief review of past discussions[2]

The 2003 *Implementation* for the western North Pacific minke whales {IWC, 2004 #31357} considered four major stock structure hypotheses (A, B, C, and D):

- (A) Baseline A: a three-stock scenario (J, O, W), with the W-stock found only in part of sub-area 9 and only sporadically.
- (B) Baseline B: a two-stock scenario (J and O), with no W-stock.
- (C) Baseline C: a four-stock scenario, with J to the west, and OW[3], OE and W to the east of Japan. Boundaries are fixed at 147°E and 157°E and there is no mixing between the stocks.
- (D) Baseline D: a three-stock scenario (J, O, W), with O dominant in the west and W dominant in the east, but mixing across 147°E and 162°E.

Extensive discussion of stock structure for the western North Pacific minke whales has occurred since the 2003 *Implementation*. A number of alternative stock structure hypotheses for the areas to the east and west of Japan have been identified and the support for and against them discussed and the outcome of these discussions occurred during the *pre-Implementation Assessment* completed at the 2010 Annual Meeting {International Whaling Commission, 2011 #44232}. The Committee agreed that the following five stock structure hypotheses were inclusive and sufficiently plausible to take to the next step in the *Implementation* process:

- (1) there is a single J-stock distributed in the Yellow Sea, Sea of Japan, and Pacific side of Japan, and a single O-stock in sub-areas 7, 8, and 9;
- (2) as for hypothesis (1), but there is a W-stock which sporadically intrudes into sub-area 9;
- (3) as for hypothesis (1), but there is a different stock (Y-stock) which resides in the Yellow Sea and overlaps with J-stock in the southern part of sub-area 6;
- (4) as for hypothesis (1), but there is a W[4]-stock which sporadically intrudes into sub-area 9 and a Y-stock which resides in the Yellow Sea and overlaps with J-stock in the southern part of sub-area 6; and
- (5) there are 6 stocks, referred to Y, JW, JE, OW, OE, and C, two of which (Y and JW) occur in the Sea of Japan, and four of which (JE, OW, OE, and C) are found to the east of Japan.

Stock structure hypotheses 1 and 2 are equivalent to the previous baselines A and B, while stock structure hypotheses 3 and 4 mimic some of the aspects of two of the sensitivity tests considered during the 2003 *Implementation* {IWC, 2004 #31357}. Stock structure hypothesis 5 is new, although elements of the hypothesis date back to the 2003 *Implementation* {Baker, 2004 #31374}. An important difference between earlier hypotheses and the five new hypotheses is evidence for an extensive distribution (and bycatch) of 'J-type' whales along the Pacific coast of Japan.

2.1.2 Review of new information

The five hypotheses were not specified to the extent needed to represent them in *Implementation Simulation Trials* during the *pre-Implementation Assessment* - doing so was a major task of the present Workshop. As such, it was **agreed** that modifications could be made to these hypotheses to ensure that they are consistent with the data whilst still retaining the intent of the hypotheses agreed by the Committee (e.g. number of stocks and general locations).

The stock-structure hypotheses specified during the *pre-Implementation Assessment* were all conceptual to some extent and the Workshop consequently focused on how to define these hypotheses so that they can be represented within the *Implementation Simulation Trials*. Representations of stock structure hypotheses in *Implementation Simulation Trials* are necessarily caricatures; it was always anticipated that further refinement of how these hypotheses are specified in trials may be necessary given the results of initial attempts to condition trials.

The reason for considering a C-stock to the west of 170°E is the sporadic presence of heterogeneity in genetics data in sub-area 9W. Recent genetics data {Goto, 2009 #42672} suggest that the frequency with which C-stock (if it is indeed a separate stock) is present in sub-area 9W is lower than was believed to the case during the 2003 *Implementation* because the heterogeneity in genetics data has only been observed in 1 of 6 samples (rather than 3 of 5 when the 2003 *Implementation* took place). The change to the proportion of years in which the C-stock was estimated to occur in sub-area 9W from 3 to 1 was a result of a re-examination of the mtDNA data from sub-area 9W given small sample sizes for some years. Thus, both the probability of a C-stock being present to the west of 170°E, and hence the impact of including a C-stock on trial results, is now smaller. The Workshop therefore **agreed** that trials based on inclusion of a C-stock would represent sensitivity tests, and that there would be three fundamental hypotheses for the current *Implementation*:

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[2] The sub-areas for the earlier trials are defined in Fig. 1a. These sub-areas have been revised for the current *Implementation Review* (see item 3.1).

[3] In the past, this stock has often been named Ow. To avoid confusion with the idea that this is a sub-stock of O rather than a stock, it is referred to as OW in this report. The same is true for Oe, Jw and Je.

[4] In the past, this was called the W-stock. It has been renamed the C-stock for presentational clarity.

(I)   there is a single J-stock distributed in the Yellow Sea, Sea of Japan, and Pacific coast of Japan, and a single O-stock in sub-areas 7, 8, and 9 (i.e. 'old' hypothesis 1);

(II)   as for hypothesis (I), but there is a different stock (Y-stock) which resides in the Yellow Sea and overlaps with J-stock in the southern part of sub-area 6 (i.e. 'old' hypothesis 3); and

(III)   there are five stocks, referred to Y, JW, JE, OW, and OE, two of which (Y and JW) occur in the Sea of Japan, and three of which (JE, OW, and OE) are found to the east of Japan (i.e., 'old' hypothesis 5).

The Workshop **agreed** that the sensitivity tests in which there is a C-stock would be based on stock structure hypotheses I and III where C-stock stock is found in sub-areas 9W, 9E, and 9N for the sensitivity test based on stock structure hypothesis I and in these sub-areas as well as sub-area 12NE for the sensitivity test based on stock structure hypothesis III (i.e. old hypotheses 2 and 4 - thus all of the five hypotheses agreed in IWC {, 2011 #44232} are represented). There is uncertainty regarding whether C-stock is found in sub-area 12NE because of the lack of genetics data for this sub-area.

Preliminary presence-absence tables (by stock and sub-area) for each of these stock structure hypotheses were prepared during the preparatory meeting and refined further during the present Workshop. It was **agreed** that to the extent possible, the presence-absence table for the O-stock (stock hypothesis I and II) would match the sum of those for stocks OW and OE (stock hypothesis III) and that the same would be the case for the presence-absence tables for the J-, JW- and JE-stocks.

A major source of disagreement within the Committee during the 2010 Annual Meeting related to whether common minke whales in sub-areas 7 and 2 (see Fig. 3 for sub-areas) represented a mixture of O- and J-stock animals or a single stock with 'intermediate characteristics'. The Committee consequently agreed that resolving this issue, using genetic and non-genetic data, was a high priority for discussion at the First Intersessional Workshop and beyond {International Whaling Commission, 2011 #44232}.

In general discussion at the preparatory meeting and the workshop, it was **agreed** that rather than analysing data for 'coastal' and 'offshore' operations (as they are termed in the JARPN II programme) as had occurred in some papers in the past, data should be analysed given the strata (sub-areas) on which the stock structure hypotheses are based, in particular because some of the 'offshore' samples are closer to the coast than the 'coastal' samples. It was also noted that fully specifying appropriate sub-areas was one of the tasks of the Workshop (see below).

SC/D10/NPM8 assessed stock structure for North Pacific common minke whales based on the sub-areas defined during the preparatory meeting using genetic as well as non-genetic data collected around Japan. The analysed minke whale samples were from JARPN and JARPNII (1994 to 2007) and from Japanese bycatch (2001 to 2007). The genetic data were obtained by analysing genetic variation at 16 microsatellite loci. Two stock identification procedures were used to assign whales to the J- and O-stocks: a Bayesian clustering method for the microsatellite genotypic data {Kanda, 2009 #42670} and mitochondrial DNA haplogroups (AG, AA, GA, GG) based on the sequence variation at the control region of mtDNA {Baker, 2010 #44151}. There was no evidence of genetic heterogeneity between the J-assigned samples from Sea of Japan and the Pacific coast of Japan (1E, 6E, 10E, 2C, 7CS, and 7CN) and among the O-assigned samples from Pacific side of Japan (2C, 7CS, 7CN, 7WR, 7E, 8, and 9) under the microsatellite stock identification. In contrast, there was evidence for heterogeneity between the samples from Sea of Japan and the Pacific coast of western Japan (6E and 2C) and from the Pacific coast of eastern Japan (7CS and 7CN) using the mtDNA haplogroup identifications. The authors believed that the most likely explanation for the genetic heterogeneity was, however, the incomplete stock ID of the method. No heterogeneity was detected between the samples from the Sea of Japan and from the Pacific side of western Japan in the J-assigned animals (i.e. no JW and JE stocks) and between the samples from the coastal and from offshore areas of Pacific Ocean in the O-assigned animals (i.e. no OW and OE stocks) for either identification method. Therefore, the authors believed that these results were inconsistent with stock structure hypothesis III. Analysis of the non-genetic data, such as fluke color pattern and flipper colour pattern, showed the same pattern as the genetics data. These results support stock structure hypotheses I and II.

Although SC/D10/NPM8 reported that several unique haplotypes in the Pacific side of Japan, each represented by a only few individuals, were not found in animals west of Japan and in the offshore waters of sub-areas 8 and 9, the authors of SC/D10/NPM8 did not believe this was support for stock structure hypothesis III as they believed that those rare haplotypes do not necessarily imply a unique stock.

SC/D10/NPM9 described results of onboard genetic analysis for stock identification of common minke whales using biopsy samples collected during a sighting-biopsy sampling survey conducted using the research vessel *Shonan-maru No. 2*, from 13 July to 26 August, 2010, in the Okhotsk Sea, including the Russian EEZ, although permission was not granted to survey part of the area (Russian territorial waters). A total of 38 schools (42 animals) of common minke whales were encountered during 1,327.7 n.miles of search effort. Of these, 24 schools (28 animals) were targeted for biopsy sampling and the 12 samples were collected from eight individuals using two Larsen guns. Stock identification of the animals was attempted onboard using RFLP analysis of mtDNA extracted from the biopsy samples, using two restriction enzymes (*Psh* B I and *Hae* III). Seven animals were assigned to O-stock and one individual was assigned to J-stock. The animal assigned to J-stock was encountered at the southern end of sub-area 12SW. Sex identification was

also conducted from amplification of the SRY gene located on Y-chromosome using PCR, which indicated that six of the eight animals were males. The presence of cookie cutter shark scars was assessed based on digital photographs of 24 individuals. Examination of photographs revealed that the 13 whales had shark scars on the dorsal and/or lateral aspects of their bodies. Unfortunately, many scars appear to be 'invisible' on the photographs. Therefore, the authors concluded that results of scar examination based on photographs taken at the sea should not be used for stock identification. After the genetic analysis, biopsy samples, DNA extraction, and PCR products were left in the Russian waters.

The Workshop welcomed this paper given the obvious difficulty faced with genetic analyses at sea and for the attempt to collect genetics data from waters that had not previously been sampled.

Two papers focussed primarily on structure within the O-stock. Park *et al*. {, 2010 #44065} examined genetic variation at the mtDNA control region to evaluate the plausibility of proposed stock structure scenarios for the J- and O-stocks. Analyses were based on samples collected during JARPN and JARPN II surveys from 1994 to 2007 off the Pacific side of Japan, from the coast to offshore waters (to 170°E), and from by-catches around Japan and the Korean Peninsula. Analyses were conducted using updated databases (which included corrected versions of the mtDNA data). Scientific Committee quality control guidelines (REF) were followed as far as possible. Samples were first assigned to the J- and O-stocks using microsatellite analysis Kanda *et al*. {, 2010 #44030}, and subsequent mtDNA heterogeneity tests were conducted for different categories of grouping (total samples, 'pure' O or J+ unassigned samples and 'pure' J or O only). Heterogeneity tests were based on the randomised chi-square test and the *Fst* values were calculated to obtain an idea of the effect sizes of the groups compared. For comparisons involving 'pure' J-stock samples: (a) no seasonal significant differences were found in either the Sea of Japan or the Pacific side of Japan; (b) no significant differences were found between whales to the east and west of Japan; (c) a significant difference was found between the Japanese and Korean samples, but the test became insignificant when whales in the Yellow Sea were excluded. *Fst* values in all of these comparisons were very small. Tests examining sub-stock structure in the area occupied by the O-stock followed the four stock structure hypotheses adopted at the final stage of the *Implementation* in 2003. No significant heterogeneity was found when the samples were grouped and tested according to the geographical boundaries of the stock scenarios A, C and D and 'pure' O + unassigned animals were used. Therefore, the present results provide no support for the occurrence of sub-structure within the O-stock. In general, results of these mtDNA analyses, which were based on a very large number of samples, supported the previous view of two stocks of common minke whale in the western North Pacific, the J- and O-stocks. The authors noted that possibility of a different stock in the Yellow Sea should be investigated in the future.

SC/D10/NPM16 was motivated by discussions that took place during 2010 Annual Meeting after Gaggiotti and Durand {, 2010 #44161} was presented. Gaggiotti and Durand {, 2010 #44161} was a direct response to a request by the Committee for repeating (using updated datasets) two types of analyses that were instrumental in erecting some of the existing stock-structure hypotheses: Boundary Rank {BR, \Taylor, 2003 #29537} and empirical Bayesian estimates of migration rates that are consistent with the genetic data {Taylor, 2004 #31463}. In particular, the aim of SC/D10/NPM16 was to explore the genetic structure of western North Pacific minke whales using Principal Component Analysis (PCA) of haplotypic and genotypic data. PCA was used to visualise geographically contiguous patterns of genetic variation because the initial configuration of samples for the original BR analyses could not be recreated. As results presented in Gaggiotti and Durand {, 2010 #44161} were preliminary, SC/D10/NPM16 provided more details of these analyses, in particular, the significance of the principal component axes. Mitochondrial DNA and microsatellite data were used, as provided by the Institute of Cetacean Research (Japan), which corresponded to samples of common minke whales taken by JARPN (1994-99) and JARPNII (2000-07). The samples covered sub-areas 7, 8 and 9. The same four scenarios proposed by Gaggiotti and Durand {, 2010 #44161} were explored, comprising different degrees of purging the samples from J-stock individuals. A genetic cluster in the southwest of the study area (probably J-stock individuals) that is apparent when all individuals are included in the analyses disappears when J-stock individuals are excluded. However, a new cluster appears in the northwest. The genetic pool of this latter cluster is not intermediate between those of J- and O-stocks. Instead, it seems to be closer to that of the O-stock because it becomes apparent when J-stock individuals are removed from the analyses. Since this genetic cluster is found between 142.5°E and 147.5°E it is posited that it may represent the so-called OW-stock. However, the authors noted additional analyses are needed before this hypothesis can be confirmed.

In discussion, a question arose as to why there were no major bimodality features in the histograms of microsatellite PC scores (Fig. 3 of SC/D10/NPM16) when data from J-stock animals were present, given that the genetic signatures of J- and O-stock are different. It was suggested that the proportion of J-assigned animals is not expected to be high as these samples were taken in the Pacific Ocean, away from the coast of Japan. More analyses will be needed to understand why PCA results were not able to distinguish the J-stock animals. The Workshop **recommended** that the PCA results presented in Fig. 3 of SC/D10/NPM16 be colour coded to indicate to which putative stock each animal had been assigned. It also **requested** that the PCA results be placed on a map with coastlines and meridional lines to facilitate interpretation and, in particular, for assigning features to sub-areas.

SC/D10/NMP2 reported on analyses of genetic identity, including mtDNA haplotypes, sex and microsatellite genotypes (up to 11 loci) for 477 samples collected from Korean bycatch of North Pacific minke whales, made available, courtesy

of the Cetacean Research Institute (CRI), National Fisheries Research and Development Institute, Korea, through the IWC Data Availability Group on 15 September 2010 (DAG DNA bycatch.xls). The bycatch database, referred to as KBC, was first reviewed for data quality and internal consistencies. The KBC database was then compared for external consistency to DNA profiles of 90 individual NP minke derived from independent surveys of commercial markets in Busan, Ulsan and Pohang from February 2004 to February 2005. The market database, referred to as Kmk, included mtDNA haplotypes, sex and microsatellite genotypes (5-6 loci), as described in Steel *et al.* {, 2010 #44011}. The 477 KBC samples represented 39 mtDNA haplotypes, 27 of which matched haplotypes from Korean or Japanese market surveys or from ICR samples of Japanese bycatch and scientific hunting. Of the remaining 12 haplotypes, 10 represented potential 'singleton' sequencing artifacts. There was significant disagreement between the data field labeled 'sex' (presumably visual inspection) and the field labeled 'sry sex' (presumably a y chromosome marker), with a greater male bias in the 'sry sex' identification. Internal matching of bycatch genotypes revealed 6 pairs of samples that matched at 9 or 10 of the 11 microsatellite loci, but did not match at mtDNA haplotypes. Given the low probability of identity for 9-10 loci, these 'near matches' are difficult to explain as close relatives, as the mismatching of mtDNA precluded mother/offspring and maternal sibling relationships. Alternatively, the near matches could represent replicate samples of the same individual, with mismatching due to genotype error (e.g. allelic dropout) and sorting error or misallocation of mtDNA. Requests for clarification on these potential quality control issues were communicated by the authors to the data owners on 26 September 2010 and in summary on 27 October 2010.

SC/D10/NPM2 also noted that although microsatellite genotypes in the KBC and Kmk databases overlapped at only 3 loci, the records were sufficient to consider agreement between datasets at two levels: population sampling and individual sampling. At the population level, there were no significant differences in haplotype frequencies or allele frequencies at the three microsatellites (after approximate calibration for allele binning). At the individual level, the DNA profiles of bycatch from the years 2003, 2004 and up until 11 February 2005 were compared to the intensive market survey from February 2004 to February 2005 {Steel, 2010 #44011}. Bycatch for this period was represented by 155 samples, presumably including all of the 148 individuals in national Progress Reports for 2003 and 2004. Market surveys included 160 products of 90 market individuals. A comparison of genotypes resulted in matches of 49 market individuals to one or more bycatch samples at 2 or 3 overlapping loci. These matching genotypes represent 'likely' replicate samples of the same individual as the whale meat is distributed through the market distribution chain. However, 19 of these 49 putative replicates mismatched for mtDNA haplotypes, suggesting that only 30 of the 90 market individuals were represented in samples of the official bycatch. This is likely to be an over-estimate of the number of true matches because of the likelihood of a 'match by chance' at only 3 loci is relatively high. Alternatively, errors in attempts to calibrate allele size bins or misallocation of mtDNA and genotypes in the bycatch records may have resulted in a high rate of false exclusion. The authors of SC/D10/NPM2 concluded that market surveys and official bycatch collections are sampling the same population or stock(s) of minke whales in Korean waters, but not necessarily the same individuals.

SC/D10/NPM3 and SC/D10/NPM4 reported on analyses of genetic information from samples collected in Japanese 'bycatch' and scientific whaling, made available courtesy of the Institute for Cetacean Research of Tokyo (ICR) (with correction in versions 2.0 and 3.0), and in Korean 'bycatch', made available by the Cetacean Research Institute (CRI), National Fisheries Research and Development Institute, Korea.

SC/D10/NPM3 provided an update of previous analyses of mtDNA haplotypes using the corrected records of Japanese haplotypes and the available Korean bycatch dataset in place of the Korean market samples used in Baker *et al.* {, 2010 #44150}. Some analyses also addressed the revised sub-area boundaries arising from the preparatory meeting in September 2010. The combined Japanese and Korean datasets included mtDNA haplotypes from 3,021 samples, representing a total of 130 haplotypes, 118 of which were found in the Japanese dataset, 27 haplotypes found in both Japanese and Korean datasets and 12 found only in the Korean dataset (see SC/SD10/NPM2). Overall, the haplotype results were consistent with haplogroup analyses, showing significant differentiation for almost all comparisons of sub-areas and strata. Initial analyses of regional differentiation and heterogeneity in microsatellite genotypes from the ICR datasets (made available on 23 October 2010) and the CRI dataset are reported in SC/D10/NPM4.

Some members suggested that the haplotype frequencies for bycaught animals in sub-areas 6E and 2 do not seem to differ. The authors of SC/D10/NPM3 suggested that the differences were driven by two alleles (1 and 64). Although the results of SC/D10/NPM3 do not exclude the possibility of some O-stock in sub-area 2, the authors of SC/D10/NPM3 noted that these results were consistent with the haplotype frequency distributions of two closely related stocks rather than a mixing of two stocks with very different haplotype frequencies.

In relation to the location of 'pure' stocks for the purpose of estimating mixing proportions, the authors of SC/D10/NPM3 noted that the OW-stock was found in the offshore area of sub-area 7 in summer under their hypothesis. In relation to interpreting small F_{ST} as indicative of separate stocks, they noted that the genetics tests applied are weak, and that any significant result should be noted in the face of large background variation. This is particularly the case with small sample sizes. Other members referred to the existence of methods to satisfactorily delineate stocks and that these should be used to rank relative plausibilities, this task is appropriate for the First Annual Meeting (see discussion under Items 7 and 8 below).

SC/D10/NPM4 reported on preliminary analyses of microsatellite genotypes at 16 loci for 2,546 samples from the Japanese dataset and 11 loci (a subset of the loci in the Japanese data set) for 477 samples from the Korean dataset. Some analyses address the revised sub-area boundaries arising from the preparatory meeting in September 2010. Overall tests of differentiation were consistent with analyses reported in Baker *et al.* {, 2010 #44150} based on mitochondrial haplogroups and SC/D10/NPM3 based on mtDNA haplotypes, showing significant differentiation for almost all comparisons of sub-areas and strata. Tests for deviation from Hardy-Weinberg equilibria show a pattern of widespread, but inconsistent (by loci and population) heterozygote deficiency, except in the Korean bycatch from subarea 6W (i.e., the Korean bycatch from the East Sea) where a large number of loci showed a significant deficiency. SC/D10/NPM4 concluded that the combined results of the mtDNA haplotype analyses and the initial microsatellite loci analyses are consistent with the predictions of stock structure hypothesis III, showing evidence for differentiation of JE from JW and evidence of differentiation of OW from OE. The authors of SC/D10/NPM4 noted that there were a number of reasons, other than stock mixing for deviations from Hardy-Weinberg equilibrium. In addition, in considering stock structure hypothesis III, they believed that bycaught animals in sub-area 6E represent the best candidate for a pure JW stock.

The Workshop **recommended** that Bonferroni corrections be applied to these analyses for consideration at the First Annual Meeting.

Several papers (e.g. SC/D10/NPM5. SC/D10/NPM7) were prepared related to stock structure but were not discussed. This was because their primary focus related to the relative plausibility of the various stock structure hypotheses. As noted under Item 1.2, this is a task of the First Annual Meeting (and see Items 7 and 8).

2.1.3 Final choice of plausible hypotheses for inclusion in the trials
The conception date distribution for the Yellow Sea inferred from foetal body length data reported in Wang {, 1985 #7679} and the conversion function from SC/S10/NPM10 differs from that for sub-areas 6E and 10E (Annex E). This provides support for the existence of a Y-stock (and against stock structure hypothesis I). However, the Workshop noted that the estimated conception date distribution for the Yellow Sea may be biased by operational effects and lack of information in sub-area 6W. The Workshop **recommended** that a quantitative analysis of such operational and other suggested effects (such as the potential to miss small foetuses) should be presented to the First Annual Meeting. In addition, there is value in the evaluating the biological evidence supporting mixing of a putative Y-stock in sub-area 6W.

In the absence of analyses which unequivocally reject any of the three broad stock structure hypotheses, the Workshop **agreed** that trials should be based on all three of these hypotheses. While recognising that considerable differences of opinion exist over their relative plausibility. These hypotheses, which are summarised in Annex F, are inclusive and sufficiently plausible to take forward to the next step in the *Implementation* process. Annex G lists the stock structure hypotheses in terms of which stocks are found in each sub-area during each month. A major aim of the First Annual Meeting will be to assign plausibility ranks to each stock structure hypothesis and associated sensitivity trials (see Item 7 for suggestions for some ways in which plausibility ranks can be assigned to the stock structure hypotheses).

2.2 $g(0)$
Okamura *et al.* {, 2010 #44029} provides estimates for $g(0)$ obtained from Japanese vessels conducting IO passing mode surveys for common minke whales in sub-areas 10, 11 and 12 during 2003 to 2007 based on a hazard probability model. The Workshop did not have sufficient time to evaluate the methodology used, but suggested that some further diagnostic plots of the fit of the model to the sightings data should be provided, and requested the January IWC Workshop in Bergen, which is to consider abundance estimation for Southern Hemisphere minke whales, to kindly take on this evaluation task.

The Workshop decided that trials should be based on the use of two alternative values for $g(0)$ in the conditioning process: $g(0) = 1$, and $g(0) = 0.798$ as estimated in Okamura *et al.* {, 2010 #44029} for the combination of top barrel and upper bridge. The reasons for this last choice are elaborated in Item 4.1. A range of values is used to conservatively span possibilities pending an evaluation of the methodology used. The range is conservative because the $g(0)$ value is to be applied identically to all surveys, including those by Korean vessels which have lower top barrels, and hence seem likely to miss a greater proportion of minke whales on the trackline. This simple approach to making use of information on $g(0)$ was considered adequate for the purpose of *Implementation Simulation Trials*, but will require reconsideration at the time of adopting abundance estimate inputs for any RMP implementation for this species and region

2.3 Maximum sustainable yield (MSYR)
The previous trials for the western North Pacific minke whales were based on values for MSYR(mat) of 1% and 4%. The Workshop **agreed** that these values would be used in the current set of trials. It was noted that Scientific Committee is currently conducting a review of MSY rates for use in the RMP (Ref). The results of that review may provide information to assign relative plausibility weights to the values for MSYR(mat) at the First Annual Meeting.

2.4 Catch series

2.4.1 Direct catches
Allison reported on progress with the catch series. It was agreed that a 'best' and a 'high' series will be developed to account for uncertainties in the historic catch.

Table 1 summarises the direct catch data from the IWC database for which individual data including position, date, length, sex and foetus details are available by month and sub-area. Further details of the direct catches are given in Annex H.

Japan
Table 2 summarises the direct catches by Japan for which (i) individual data are available (10,902 including 4,105 from Area 7CS); (ii) data are only known by area (~3,100); and (iii) values are estimated (~1,000) – these were almost all taken in Area 7CS.

The 'best' catch series will use the estimated catches from Ohsumi {, 1982 #598} (see Annex H). A 'High' catch series will also be constructed which uses the estimates from Ohsumi multiplied by a factor of 2.

The catches from 1958-63 will be allocated to sub-area using the information from Wada 1988 (which gives the data for the following areas: (i) sub-area 7CS; (ii) sub-areas 11 + 7CN combined; and (iii) sub-areas 6E + 10E combined) and data by sub-area from the years immediately before and after.

Republic of Korea
Table 3 summarises the direct catches off Korea. Further details are given in Annex H.

The level of catches from 1932-39 is unknown but is thought to be small. Brownell {, 1981 #4003} reports that Matsuura {, 1936 #4483} reported catches of minke whales off the coasts of Japan and Korea from January 1932 to March 1935. During this period, minke whales were a by-catch of catcher boats taking larger baleen whales and these figures were not reported officially.

The 'Best' catch series will include a nominal, and arbitrary, annual catch of 2 whales from 1932-1939. The 'High' catch series will include an annual catch of 6 whales in this period.

Catching by Korea commenced in 1946. The level of catches from 1947-56 is unknown but the operations are thought to have increased gradually. The 'Best' catch series will assume a linear increase in catches from 47 whales in 1946 to 249 in 1957. The 'High' catch series assumes an annual catch of 249 minke whales from 1947 to 1956. Catches will be pro-rated to sub-area and month using information from the individual data (1982-85) and information in Gong {, 1988 #37173} and Park 1995.

China
Information on catches from 1955-1980 is given in Appendix 1 of Annex H. There is no evidence of catches prior to 1955.

Other direct catches
A small number of minke whale catches were reported in the official USSR statistics as listed below. There is no information at present on revised minke whale numbers, but in view of the small size of the catches the official numbers will be used in both catch series.

Period	Minke	Notes
1933-42	7	Pelagic catches (by Aleut). Catch numbers only
1949-64	10	Pelagic catches (by Aleut and Dalnij Vostok). Individual data
1948-62	73	Kuril Island catches

There is no information on catches by North Korea.

2.4.2 Incidental catches
It was agreed that both a 'best' and a 'high' by-catch series will be developed as detailed below. The method of setting future by-catches will need to be specified at the First Annual Meeting. See Annex H for details of the incidental catches.

Incidental catches off Japan
Bycatches from 1979-2000 are reported in the Japanese progress reports, and information on bycatches from 2001-9 is given in SC/S10/NPM3 and SC/S10/NPM4. Japan has provided individual records for 1,083 minke whales by caught off Japan with position, date, length and sex from 2001-9. Almost all of the reported bycatch off Japan occurred in setnet fisheries. It has been obligatory to report bycatches since 2001, since when the numbers are thought to be reliable.

Hiruma reported that for fishing gears other than setnets, incidental catch, retention and marketing of whales are prohibited by the 2001 regulations. If baleen whales are entangled/trapped in such fishing gear, they must be released if they are alive, or buried/incinerated if dead. Administrative Instructions are issued to report these incidents to the Minister of Agriculture, Forestry and Fisheries through related prefectural governors. The diagnostic DNA registry is used to deter illegal distribution of whales caught by fishing gear other than setnets. While a small numbers of bycaught animals in other gear have been reported in accordance with the instructions, market monitoring has not produced evidence of unreported bycatches.

Based on the sudden increase in reported catches in 2001, the Workshop **agreed** that catches prior to 2001 were underreported. Hatanaka *et al.* {, 2010 #44056} suggested a method for estimating bycatch levels of minke whales in setnet fisheries for the years before 2001 which was reviewed in IWC/62/Rep 1. Concern had been expressed over the assumption used that the reporting rate was constant over time, particularly for the years before 1994.   The Workshop **agreed** that the available reported bycatch data were sufficiently uncertain to rule out reliable estimation of bycatch, whatever method was employed. Rather, it **agreed** that the only approach that should be considered was to integrate the relationship between bycatch and setnet effort into the conditioning process. The advantage of the integration method is that it is independent of the reporting rate prior to 2001. It was noted that the key assumption used in all methods of extrapolating the historic bycatch series is that the reporting rate since 2001 is constant at 100%.

Baker reviewed previous publications that considered information on genetic identification of market products to estimate true catches. Whale products on the market come from (1) special permit catches which are assumed to be recorded accurately; (2) reported bycatches which may or may not be recorded accurately and (3) other sources, including illegal hunting. In Japan, {Lukoschek, 2009 #42340} used a mixed stock analysis of O-and J-type market products to test for differences in proportions before and after the 2001 change in regulations. A constant proportion before and after this date, suggested that the true level of bycatch was also constant, but historically underreported. Baker suggested the results in this paper may be useful in evaluating those of the proposed method above for extrapolating the historic bycatch, at least for the1998-2001 period.

Three types of setnet are used off Japan: large-scale (excluding salmon nets); salmon nets; and small scale. In order to investigate the different rates of entrapment in these three gear types, the number of nets and the number of catches by year and by net type from 2001-9 will be examined. Assuming that the entrapment rate in salmon and other large-scale nets is similar, these two series can be combined.

Information from Brownell (see Appendix 1) shows that there are records of common minke whale bycatch in setnets as early as 1935. SC/D10/NPM13 provides information on the number of setnets off Japan by sub-area and year from 1979-2006 and {Tobayama, 1992 #8135} gave similar information by area and 5-year period from 1970-1989. Hakamada undertook to look for data prior to 1979 but he thought it unlikely that data would be available prior to 1970. An additional problem is caused by changes in the way large and small scale nets were defined prior to 1969.

The Workshop **agreed** that for the 'best' effort series, the number of nets will be extrapolated from 1946 to 1969 assuming a linear relationship from 0 in 1935 to the known number in 1970 (see Fig 1). Incidental catches before 1946 are ignored as although some setnets were in operation before 1946 the numbers are highly uncertain and are sufficiently small that they are unlikely to effect the implementation.

It was further **agreed** that a 'high' effort series will also generated in which the number of nets is double the best case values from 1946-1969, up to a maximum equal to the number of nets in 1969 (see Fig 1).
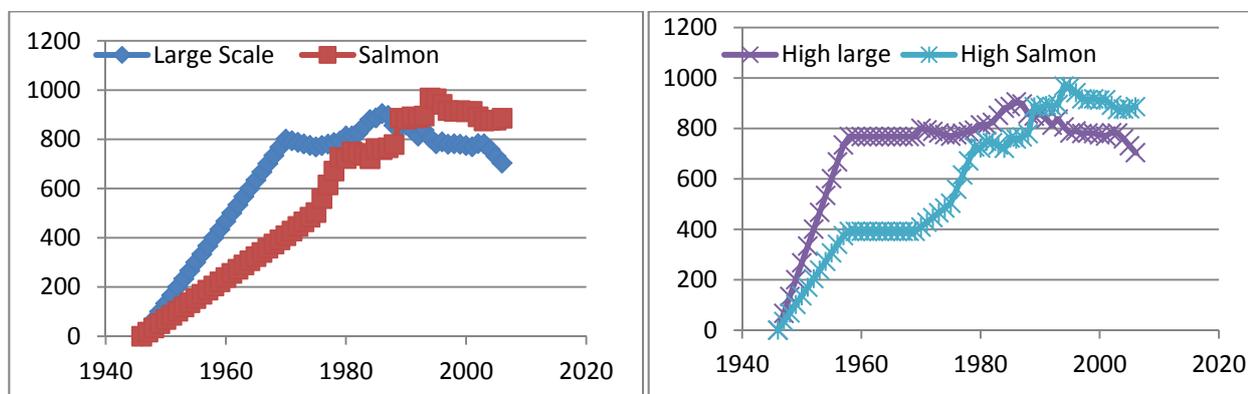

Fig. 1 Plots showing the 'best' and 'high' methods of extrapolating the effort series for large scale and salmon nets off Japan to the years 1946-69.

Incidental catches off the Republic of Korea

The Workshop **agreed** that bycatch should be estimated from fishing effort using the same method proposed for Japan above.

Bycatch in Korean waters is the result of entanglement in a range of gear (setnet, pots, gillnets, trawls, bottom trawls and purse seines - {Song, 2010 #43411}. SC/S10/NPM11 summarised the number of common minke whales caught incidentally by setnets in the East Sea, Korea from 1996-2008 by province together with the number of nets in operation (see Annex H). Kim provided further information on the use of setnets and other fishing gear in the East Sea (see Appendix 2 of Annex H). An noted that the fishery operations in the Yellow Sea are very different from those in the East Sea and that setnets are not used in the Yellow Sea.

The Republic of Korea has provided individual records of 1,146 by-catches off Korea with position, date and gear type from 1996-2009. Lengths and sexes are also given in many cases.

Baker *et al.* {, 2007 #39190} used DNA profiling and a capture-recapture analysis of market products to estimate the total number of whales going through Korean markets as 887 whales from 1999-2003, in comparison to the reported catch of 458 whales, indicating that total takes are underreported by a factor of about 1.8 (with SE) for these years. It was **agreed** that this estimate of underreporting (rounded up to 2) be used as an upward adjustment for the reported bycatch from 1996 to 2006 in the East Sea (Sub-area 6W) to better account for total takes. In the Yellow Sea (sub-area 5) the 'best' effort series will use the reported catch series as the Baker *et al* analysis (Ref) related to East Sea catches and there is no evidence that it also applies to the Yellow Sea. The 'high' Yellow Sea effort series will apply the same estimate of under-reporting as for the East Sea (i.e. a factor of 2).

To account for bycatch prior to 1996, it was suggested that the average for the *adjusted* takes from 1996-2006 be used to extrapolate backwards to 1946 based on fisheries effort. For the East Sea the effort will be based on the numbers of setnets whereas for the Yellow Sea it will be based on the total fisheries effort. Incidental catches before 1946 are ignored as the numbers are highly uncertain but are thought to be sufficiently small that they are unlikely to effect the implementation. Choi **undertook** to be responsible for providing the estimates of fisheries effort.

3. Off China

The meeting received information from Brownell that bycatches of common minke whales are taken off China. In the absence of further information a bycatch series for China will be developed by assuming it is comparable to the Yellow Sea component of the Korean estimated bycatch. In order to produce this bycatch series, Choi **undertook** to provide an estimate of the total fishery effort for China and for Korea in the Yellow Sea.

4. In Russian EEZ

A Japanese salmon driftnet fishery moved into the Russian EEZ after the UN high seas driftnet moratorium in the early 1990s. Yoshida reported that there are bycatches from this fishery but that common minke whales are not taken.

The Workshop received information from Brownell who drew attention to a report from a Russian review of this Japanese fishery (page 201) which included an average incidental catch of one minke whale per year from 1992-2008. A bycatch of 1 minke per year from 1990 to 2010 will be assumed. Japan reserved its right to comment on Brownell's information until it had time to examine the original Russian review.

3. SPECIFICATION OF IMPLEMENTATION SIMULATION TRIALS

3.1 Selection of time-steps and sub-areas

The 2003 *Implementation* was based on six time-steps during the year (January-April; May; June, July; August; September-December). The Workshop noted that given the new stock structure hypotheses, the postulated distribution of minke whales would be changing within the first and last of these time-steps and therefore **agreed** to add additional temporal resolution to the operating model. The time-steps on which the operating models are to be based shall be:

(1) January-March;	(5) July;
(2) April;	(6) August;
(3) May;	(7) September;
(4) June;	(8) October-December.

Sub-areas are areas within which if there are animals from multiple stocks, the probability of catching of an animal belonging to a given stock is proportional to the abundance of animals of that stock in the sub-area (i.e. animals are taken to be randomly distributed within a sub-area). Their primary function is to allow stock structure hypotheses to be adequately specified in space and time i.e. they arise directly from the conceptual representations of the stock structure hypotheses. Selection of the boundaries between sub-areas also takes into account data availability (e.g. the resolution of catch positions, areas for which surveys have been carried out). Sub-areas are not necessarily the same as the *Small Areas* used when applying the RMP although *Small Areas* must comprise either one or more sub-areas. It was **agreed**

that the same sub-areas would be used when modelling each stock structure hypothesis because this eases data analysis as well as coding of the *Implementation Simulation Trials*.
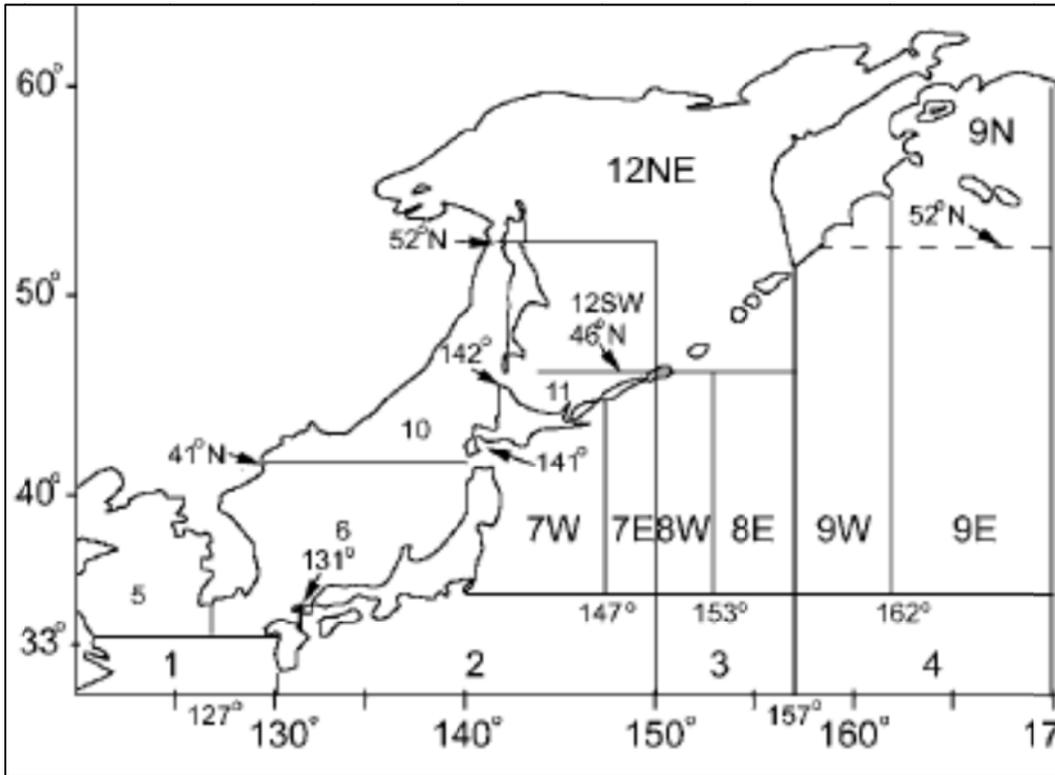
Fig. 2. Sub-areas used in the 2003 *Implementation*.

Fig. 3. Revised sub-areas for the *Implementation Review*.
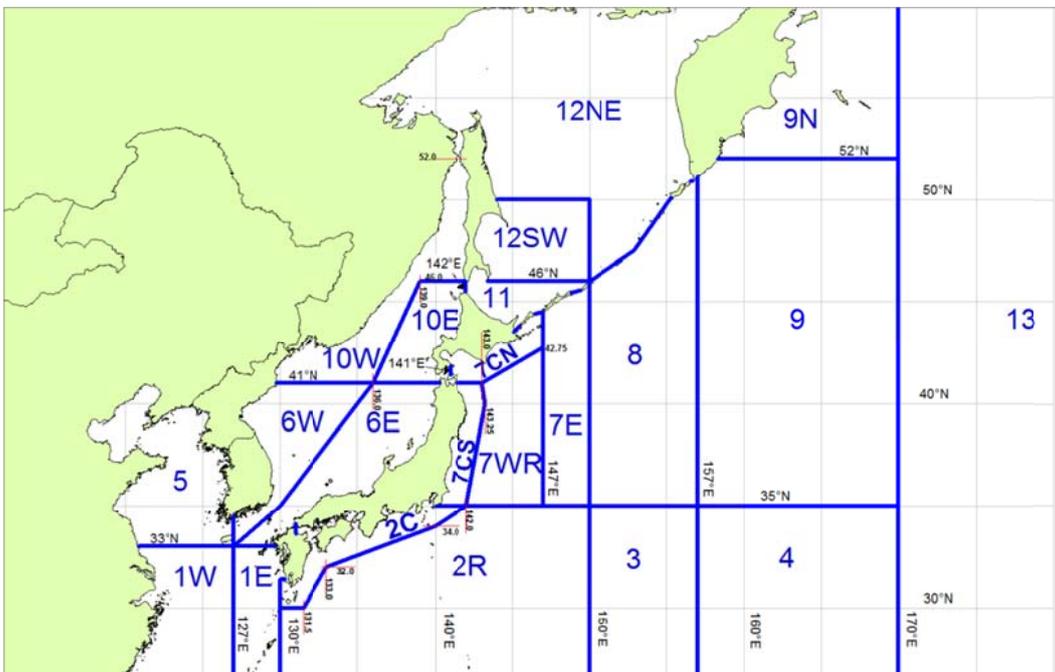
The 2003 *Implementation* was based on 18 sub-areas (Fig. 2). The Workshop considered a number of proposed modifications to the boundaries for these sub-areas as well as the changes needed to implement the stock structure hypotheses. The following changes to the boundaries were agreed (Fig. 3 shows the final set of sub-areas).

(1)   The northern boundary of sub-area 12SW was changed from 52°N to 50°N. There was no direct evidence for the original boundary which was set arbitrarily to capture the hypothesis of a restricted distribution of the J-stock in the Okhotsk Sea {IWC, 2002 #27678}. A northern boundary for sub-area 12SW at 50°N

better matches the area from which the data on conception dates and flipper colour {Kato, 1992 #7677; Kato, 1992 #7676} were obtained,

(2)   The boundary between sub-areas 8W and 8E (153°E) was removed to give a single sub-area 8. This change was made because no stock structure hypothesis postulates that more than one stock is found in these two sub-areas.

(3)   The boundary between sub-areas 9W and 9E (162°E) was removed to give a single sub-area 9. This change was made because all current stock structure hypotheses include C-stock animals in sub-area 9E as well as in 9W, assumed to be in the same proportions.

(4)   The boundary between sub-areas 8 and 12NE was moved from 46°N to a line along the Kuril Islands joining the southern tip of the Kamchatka Peninsula (~157°E; 51°N) with the point (150°E; 46°N). Part of sub-area 12NE was originally outside the Okhotsk Sea, and surveys have generally surveyed this area when surveying sub-area 8, making it more logical to place this area in sub-area 8 rather than sub-area 12NE.

In order to properly represent the hypotheses, it was agreed to split some of the existing sub-areas as summarised below.

(1)   Two new sub-areas were defined within 7W. Sub-areas 7CS and 7CN (7 Coastal South; 7 Coastal North) were defined as being from the coast of Japan out to roughly 60n.miles from the coast (the eastern boundary of these sub-areas is a line from the Kuril Islands at 147°E to (42.75°N; 147°E) then to (41°N; 143°E), to (40°N; 143.25°E), and to (35°N; 142°E). 60 n.miles was selected so that the proportion of J- or JE-stock animals further offshore can be considered to be negligible (e.g. see analyses in SC/S10/NPM9). The boundary between the sub-areas (41°N) was chosen such that whaling ground B is in sub-area 7CN while whaling ground C is in sub-area 7CS (see Fig. 4); detailed positional information is not available for many of the historical catches in these whaling grounds.

(2)   An additional sub-area was defined within 2. Sub-area 2C (2 Coastal) is defined by a line approximating a distance of 60n.miles from the coast of Japan [(35°N; 142°E), to (34°N; 140°E), to (32°N; 133°E) to (30°N; 131.5°E), to (30°N; 130°E)]. The rationale for this sub-area was to separate areas where J- or JE-stock are negligible (offshore regions; sub-area 2R – 2 Remainder) from those where it is non-negligible (sub-area 2C).

(3)   Sub-area 6 was divided into two (6W and 6E). This boundary between these sub-areas (41°N; 136°E – 35°N; 130°E, - 33°N; 127°E) was selected so that the Korean surveys would occur wholly in sub-area 6W while sub-area 6E covers the area where most of the Japanese surveys in the Sea of Japan have taken place. For the hypotheses in which there is a Y-stock, Y-stock animals are found only in sub-area 6W in addition to the Yellow Sea. The Workshop **agreed** that it was not necessary for the survey abundance estimates to be recalculated such that the area used to estimate abundance corresponds exactly with sub-areas 6W and 6E as defined.

(4)   Sub-area 1 was divided into 1W and 1E at 127°E. This boundary was selected so that the bycatch in sub-area 1 could be correctly allocated among the Y- and J-stocks (JW and JE for stock hypothesis III).

(5)   Sub-area 10 was divided into 10W and 10E where the boundary between these sub-areas was a line from (46°N; 142°E) to (41°N; 136°E). This line matches closely (but not exactly) with the offshore strata of the surveys which have occurred in the east of sub-area 10. As for sub-areas 6W and 6E, the Workshop **agreed** that it was not necessary for the survey abundance estimates to be recalculated such that the area used to estimate abundance corresponds exactly with sub-areas 10W and 10E as defined.
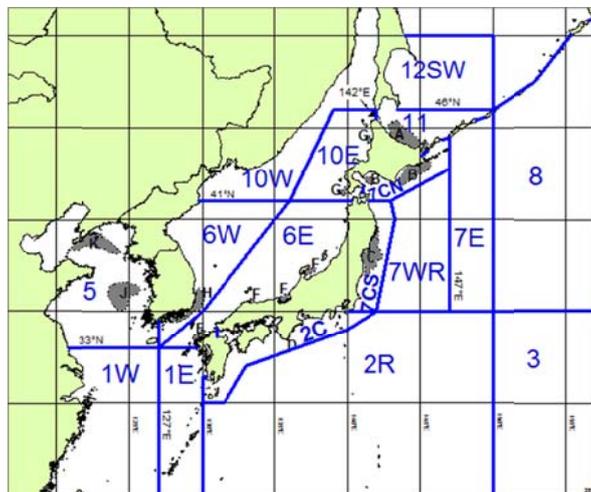

Fig. 4. Past Japanese whaling areas

To avoid a proliferation of sub-areas and to avoid the need for finer time-steps than month, the Workshop **agreed** to model bycatch assuming non-random selection of whales within the sub-area concerned, since bycatches occur on the coast. Thus, while future commercial catches will have the same stock proportions as in the sub-area at the time, the stock proportions for the bycatches can be specified as an input.

3.2 Specification of expected future operations
Hatanaka advised the Workshop that land-based whaling will be conducted by small-type coastal catcher boats in sub-areas 7 and 11. He noted that O-stock minke whales will be targeted by restricting whaling to outside 10 n.miles from the coast of sub-area 7, but that some J-stock animals are expected to be caught. He also advised the Workshop that pelagic whaling will be conducted in sub-areas 7W, 7E, 8, 9, and 11. The season for pelagic whaling will be from April to October in sub-areas 8 and 9 and from August to October in sub-area 11 to avoid catches of J-stock animals.

An advised the meeting that Korean land-based whaling will be conducted by small-type coastal catcher boats in sub-areas 5 and 6W from March to November. Whaling will take place more than 60 n.miles off the coast for sub-area 5 and more than 30 n.miles for sub-area 6.W

3.3 Future survey plans
Sightings surveys (subject to Committee oversight) will be conducted annually by Japan in sub-areas 7, 8 and 9, and every 5 years in sub-areas 11 and 12. Sightings surveys (subject to Committee oversight) will be conducted every 2nd year by Korea from mid-April to late-May in sub-areas 5 and 6W. The surveys by Korea will be conducted in normal closing mode with top barrel and upper bridge.

3.4 Trials structure
The trials structure (see Annex I for the full specifications for the trials) is based on representing the stock structure hypotheses in the form of mixing matrices in which some of the parameters of these matrices are estimated by fitting the operating model to data on absolute abundance and mixing proportions (see Annex J for an outline of the process of conditioning). The Workshop established a small group (Baker, Punt, Wade, An and Butterworth) to finalise the specifications of the mixing matrices (see Item 8). Allison and de Moor will then review the mixing matrices to ensure that there are sufficient data to allow the parameters of the mixing matrices to be estimated during the conditioning process. The Workshop noted that the specifications for the mixing matrices will only be finalised following initial efforts to condition the trials, under the guidance of the group established under Item 8.2.

The Workshop made the following four recommendations in relation to the specifications for the baseline trials.

(1) The mixing proportions for sub-areas 2C (hypotheses I and II), 7CS and 7CN should be set to the weighted average of the mixing proportions based on the bycatch samples and the offshore samples, with weights of 5/60 and 55/60 respectively. Although most of the bycatch occurs within 2 n.miles of the coast, the density of minke whales is highest closest to coast and there will be movement between inshore and offshore. The weight of 5/60 places higher weight on the mixing proportions from the bycatch samples than the area where bycatch occurs would to reflect these considerations. The future commercial catches in these sub-areas will be removed based on the mixing proportions from the offshore samples and future bycatches based on the mixing proportions for the bycatch samples.

(2) Bounds need to be placed on the maximum size of populations in sub-areas 5 and 6W. These bounds will be generated by sampling from the distributions for the minimum estimates of abundance and multiplying these values by 3. The value of 3 is based on the abundance data for sub-areas 6W and 6E. These two sub-areas are approximately the same size, but the minimum abundance estimates (for sub-area 6W) are approximately 1/3 of the abundance estimates for sub-area 6E which are based on 100% coverage of this sub-area.

(3) The proportion of J-stock (JE-stock for hypothesis III) in sub-area 12SW in June is 25%. The value reflects a rough average of the J-stock mixing proportions for sub-area 11 (J-stock animals in sub-area 12SW need to pass through sub-area 11).

(4) The extent of additional survey variance should be estimated using the residuals about the fit to the survey data.

The Workshop **agreed** a set of sensitivity tests (Table 4). These sensitivity tests are based on those considered for the 2003 *Implementation* as well as new sensitivity tests that are specific to the stock structure hypotheses developed for this *Implementation*. The final set of sensitivity tests will be selected during the First Annual Meeting, given the results from the conditioning. The sensitivity tests in Table 4 reflect factors which impact how the trials are conditioned. Other sensitivity tests may be specified during the First Annual Meeting which pertain to assumptions about the future (e.g. levels of additional variance, which areas are open or closed to whaling).

4. CONDITIONING
Conditioning is the process of specifying the values for the parameters of the operating model for a given simulation trial such that the conditioned model is comparable with the available data given the set of hypotheses which define the trial. The data are bootstrapped and the operating model fitted to each bootstrap data set to account for the uncertainty

associated with each datum. Whether conditioning has been achieved successfully is evaluated during the First Annual Meeting.

4.1 Abundance estimates and covariances
In considering which of available sighting survey estimates of abundance might be used for conditioning the trials, the Workshop noted that such estimates were intended to broadly bound the range of plausible past abundance trajectories for the stocks under consideration, and consequently did not need to be as accurate or precise as the estimates to be used for input to the RMP if it is actually implemented. Hence exercising some latitude in making certain limited assumptions in this process is appropriate.

The details of the process used to select estimates suitable for use in the conditioning from the large number of past surveys in the *Region* are set out in Annex K, together with the abundance estimates from those surveys. Hence only a broad summary of the principles applied in this selection is given here.

A primary consideration is that estimates be as comparable as possible to avoid the introduction of spurious trends over time in the values used. Hence a standard approach of basing estimates of abundance from sightings from the top barrel and upper bridge only was adopted. This is because relatively few of the surveys had been conducted including an IO. For those that had, reanalysis would take place to exclude the primary sightings made from the IO platform so as to improve comparability with results from surveys without an IO. (This is the reason for choosing a *g(0)* value based upon sightings from top barrel and upper bridge only – see Item 2.2.)

There are few very high density areas and common minke school sizes are nearly all 1, thus any bias between passing and closing mode estimates of abundance is not expected to be large. Therefore the Workshop **agreed** that for the purpose of developing estimates of abundance for conditioning, estimates from surveys in closing mode and surveys in passing mode would be treated as comparable (including one passing mode survey where delayed closure took place for certain species).

The broad approach adopted for selection was to restrict this to surveys which had covered a large (and nearly the same large) proportion of the sub-area concerned, and had also achieved coverage of a large part of their intended trackline. In some cases, surveys with lesser proportional coverage of the sub-area were also selected, either where other surveys in the same sub-area showed few minke whales sighted in the non-common part of the areas covered, or where extrapolation could be used based of the ratio of abundance in unsurveyed to surveyed parts of the overall area covered in other surveys in that sub-area. While formally such an extrapolation process introduces the need to compute co-variances between different estimates for the same sub-area, the Workshop **agreed** that such co-variances would be unlikely to be large, and could be ignored for conditioning purposes. Where all surveys had covered only a rather small part of the sub-area in question, they were assigned to be treated as providing lower bounds for abundance in the conditioning process, rather than as unbiased estimates included in the likelihood.

Other factors that played a role in the selection process were: exclusion of parts of surveys where the temporal order in which different parts of the sub-area were covered corresponded to the direction of minke whale migration over the survey period, so that double counting may have occurred; and ready availability of results from the survey so that aspects such as achieved coverage of the intended trackline could be checked.

A list of the set of survey estimates of abundance selected for the conditioning is given in Table 5.

4.2 CPUE
It was **agreed** that the Korean CPUE data {Gong, 1987 #298; Gong, 1984 #300; Holt, 1984 #345} were not suitable for use in trials because it has not been possible to obtain the data in a sufficiently disaggregated form.

Three series of CPUE data are available for Japan, two of which were derived from the catch data and the number of catcher boats, with a correction for vessel tonnage. The third series uses catches per operating hour which Anderson {, 1992 #8971} considered more reliable as a measure of effort. The raw catch and effort data (1977-88) are now available at the Secretariat. In principle, these data could be used either to compare with the output from the trials as a 'reality check' or could influence the population model fit by incorporating them into the likelihood calculation. The Workshop **agreed** that as insufficient information on the operational information related to the fisheries concerned are currently available, CPUE data could only be used in the context of a 'reliability check'.

The Workshop **agreed** that a summary of the associated operational information requested by the Comprehensive Assessment workshop on CPUE {IWC, 1989 #23575} as well as a revised analysis of CPUE data needs to be presented to the First Annual Meeting if these data are to be considered as a reliability check and hence to assign plausibility ranks.

4.3 Tagging data
Although eleven discovery-type tags were implanted in western North Pacific minke whales, only one of these was in an animal west of sub-area 13. The Workshop therefore **agreed** that these tagging data could not be used for the *Implementation*.

4.4 Biological and technological parameters

The Workshop **agreed** that the values for the biological parameters (natural mortality, age-at-maturity) and the technological parameters (selectivity) would be the same as for the previous *Implementation* which were based on those for the North Atlantic minke whales.

4.5 Mixing proportions and dispersal rates

'Mixing' differs from 'dispersal' in that 'mixing' refers to the temporary overlap of two (or more) stocks in a sub-area during a given time-step. In contrast, 'dispersal' refers to permanent transfer of individuals between stocks.

4.5.1. Mixing proportions

The Workshop noted that there were potentially several sources of data on mixing proportions (genetics, cookie cutter shark scars, conception dates, flipper colour information). Annex L summarises the sample sizes for each of these sources of data. The Workshop **agreed** that the genetics data (mtDNA and microsatellites) would be used to estimate mixing proportions in different sub-areas x month combinations, under the assumption that frequencies of haplotypes/alleles are multinomially distributed. The general form of the log-likelihood function for microsatellite data is:

$$\ell n L = \sum_i \sum_j n_{i,j} \ell n p_{i,j}$$

where $n_{i,j}$ is the number of type j alleles at locus i in the mixed sample, $p_{i,j}$ is the model-estimate of the proportion of type j alleles at locus i in the mixed sample:

$$p_{i,j} = \sum_{k=1}^{K} \tilde{p}_k I_{k,i,j}$$

where K is the number of stocks represented in the mixed sample (defined by the mixing matrices), $\tilde{p}_k$ is the proportion of stock k individuals in the mixed sample (the estimable parameters of the model), and $I_{k,i,j}$ is the proportion of type j alleles at locus i for stock k. The values for the $I_{k,i,j}$ are defined by the data for combinations of sub-area and month which define 'pure' stocks for each stock-structure hypothesis (Table 6). The Workshop noted that this approach did not account for uncertainty regarding the proportion of alleles in the pure samples and hence that any allele which only appears in the mixed sample cannot be used for parameter estimation purposes. However, it **agreed** that this was not a concern given the need to estimate mixing proportions for the purposes of trials (but see the recommendations related to plausibility of stock-structure hypotheses – item 7). The Workshop **recommended** that the deviance (twice the difference between the negative log-likelihood under the best fit model and that under the saturated model) and hence the extent of overdispersion be reported for each data set.

Conception date and flipper colour data were used to estimate J-O mixing proportions for sub-area 12 SW for the trials on which the 2003 *Implementation* was based, owing to a lack of genetics data for this sub-area. The 2003 *Implementation* did not use cookie cutter shark scars to estimate mixing proportions.

SC/D10/NPM6 used cookie cutter shark-induced scar marks as an ecological marker to determine stock structure in western North Pacific common minke whale. Samples collected by JARPN II surveys during 2002-2007 were used in the analysis. First the samples were assigned to the J- and O-stocks based on a previous microsatellite analysis. Prevalence of scars differed clearly between J- and O-stock assigned animals. However, this ecological marker cannot be considered as an absolute marker to differentiate animals from the two stocks. J-stock animals had fewer scars than O-stock animals. Prevalence increased with body length and almost all animals of more than 7m in body length had scar marks in both stocks. Prevalence of scars in O-stock animals was compared between two Pacific areas off Japan (coastal sub-areas: 7CN and 7CS and offshore sub-areas: 7E, 8 and 9), as a function of body length. No significant differences in scar prevalence were found between these two groups of sub-areas.

The Workshop welcomed this paper which had been written primarily to address questions related to the plausibility of stock-structure hypothesis III. The Workshop **agreed** that cookie cutter shark scars could, in principle, be used to estimate mixing proportions. However, account would need to be taken of several factors, including: (a) the apparent circularity that occurs because the proportions of categories of scars by stock are based on microsatellite data which would also be used to estimate mixing proportions; and (b) the trend in the proportion of scars in putative J-stock animals with increasing size. The Workshop therefore **agreed** that mixing proportions would not be estimated using the data on cookie cutter shark scars for the present *Implementation Review*, but that these data could be considered for a future *Implementation Review* given the development of an appropriate analysis method.

SC/S10/NPM10 examined stock structure of the North Pacific common minke whale using the monthly distribution of conception dates. Samples collected during 1994-2007 by JARPN/JARPN II were used. First, the samples were assigned to J- and O-stock minke whales based on a previous microsatellite analysis. The small number of individuals assigned to J-stock were from sub-areas 11 (n=8) and 7WR (n=3). The conception period of J-assigned animals spread

from August to March suggesting a long breeding (autumn-winter) period while those from the O-assigned animals had unimodal distribution pattern. The long breeding season observed for the J-stock on the Pacific side of Japan was similar to that observed by Kato {, 1992 #7677} in a small sample from the north part of the Sea of Japan. No differences were found in conception date between for O-assigned animals from sub-area 7WR and sub-areas 7E, 8 and 9.

The Workshop also considered Annex E, noting that that the conception dates do not separate putative J- and O-assigned animals absolutely given wide range of conception dates for the J- and O-stocks.

In relation to flipper colour, it was noted that new data which could be used to determine flipper colour had been collected from sub-areas 7CS, 7CN, 7WR, 7E, 8 and 9 (n=1077). These data are now categorised into three classes rather than two, as was the case before. However, only 207 of the photographs had been classified using the criteria of Nagatsuka (2010). Moreover, the criteria applied by Nagatsuka (2010) could not be applied to the data used previously to estimate mixing proportions for sub-area 12SW because those data were based on visual observations by observers rather than using photographs. An additional difficulty using the new data is that there are no photographs for the sub-areas in which is hypothesised that only the J-stock is found while the sample size for the sub-areas in which only O-stock is found (n=27) is very small. A calibration key has been developed (table 7 of SC/D10/NPM9) but this key depends on the assignment of animals to stock using microsatellite analysis (which is an instance of double-use of data). The Workshop therefore **agreed** that while the new data are potentially informative regarding mixing proportions, they would not be used for the current *Implementation Review*. As is the case for cookie cutter shark scar data, data on flipper colour could be used in a future *Implementation Review* given the development of methods for estimating mixing proportions which do not have these problems. A concern with the older data is that assignment of flipper colour categories to stock was based on conception date data and the information in Okamura *et al.* {, 2010 #44029} suggests that conception date is not an absolute marker for J- and O-stocks.

4.5.2 Dispersal rates
The Workshop noted that dispersal has the potential to mitigate the impact of catches from a small stock (the 'rescue effect'). However, the size of this effect depends on the extent of dispersal. A variety of methods for estimating dispersal rates are outlined in Annex M. Dispersal is a difficult parameter to estimate using genetic data owing to uncertainty regarding the correct migration model. Moreover, as dispersal rate is inversely (but not linearly) proportional to a measure of genetic difference (e.g. F_{ST}), the estimate of dispersal rate can be very sensitive to small changes to a low value of, for example, F_{ST}. Finally, there are potentially major computational challenges associated with estimating dispersal rates.

The Workshop **agreed** to include sensitivity tests (Table 4) for stock structure hypothesis III with various levels of dispersal rate between the JW- and JE-stocks and between the OW- and OE-stocks (the base-case models would be based on the assumption of zero dispersal). The Workshop **recommended** that analyses be conducted to estimate the extent of dispersal. The Workshop recognised that if the estimate of dispersal was sufficiently large, it would mean that the bulk of the trials would need to include dispersal (and accounting for its uncertainty). This would mean reconditioning and then re-running all of the trials. The Workshop noted that the possibility of substantial new information becoming available in between the normal *Review* schedule is acknowledged in the Requirements and Guidelines for *Implementations* {Iceland, 2002 #27799}. Specifically, were it to become evident either at the Tromsø meeting or later that dispersal is sufficiently large[5] that the results of trials without dispersal would be an inappropriate basis to provide recommendations related to management options for the western North Pacific minke whales, the Committee would identify the need for an emergency *Implementation Review* to address that specific issue (without re-opening discussions on other specifications of the trials).

5. SPECIFICATION OF MANAGEMENT OPTIONS
The RMP variants include specifications regarding the *Small Areas* (combinations of sub-areas), the use of the capping and cascading options of the RMP, and when and where harvesting will occur. The initial set of RMP variants to be considered in the trials and the sub-areas from which catches are taken when a *Small Area* consists of more than one sub-area are:

1) *Small Areas* equal sub-areas. For this option, the *Small Areas* for which catch limits would be set are 5, 6W, 7CS, 7CN, 7WR, 7E, 8, 9, and 11.
2) 5, 6W, 7+8, 9, and 11 are *Small Areas* and catches are taken from sub-areas 5, 6W, 7CN, 9, and 11.
3) 5, 6W, 7+8, 9, and 11 are *Small Areas* and catches are taken from sub-areas 5, 6W, 7CS, 9, and 11.
4) 5, 6W, 7+8+9+11+12 are *Small Areas* and catches are taken from sub-areas 5, 6W, 11.
5) 5, 6W, 7+8+9+11+12 are *Small Areas* and catches are taken from sub-areas 5, 6W, 7CN.
6) 5, 6W, 7+8+9+11+12 are *Small Areas* and catches are taken from sub-areas 5, 6W, 7CS.

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[5] 'Sufficiently large' being that a different set of management options would be considered 'acceptable' or 'acceptable with research' for that level of dispersal.

7) 5, 6W, 7CN, 7CS, 7WR+7E+8, 9 and 11 are *Small Areas* and catches are taken from sub-areas 5, 6W, 7CN, 7CS, 7WR, 9, and 11.

8) 5, 6W, and 7+8+9+11+12 are combination areas and catches are cascaded to the sub-areas within each combination area. The catch limits for sub-areas 12SW and 12NE are not taken.

9) 5, 6W, 7+8, 9, and 11 are *Small Areas* except that the catches from the 7+8 *Small Area* are taken from sub-areas 7CS, 7CN using catch cascading across those two sub-areas.

10) 5, 6W, 7+8+9+11+12 are *Small Areas* and catches from the 7+8+9+11+12 *Small Area* are taken from sub-areas 7CS, 7CN and 11 using catch cascading across those three sub-areas.

Note that the proportions of the whales in a sub-area that belong to each stock will differ from sub-area to sub-area (as well as from year to year). Thus when a *Small Area* is specified which consists of a number of sub-areas, the impact on the various stocks of the catch allowed under the RMP will differ depending on how this catch is distributed amongst the constituent sub-areas. In such cases trials are specified which attempt to bound the extremes of such catch distributions in terms of their likely impact on stocks. The initials trials above incorporate a first attempt to address this aspect, e.g. trials 2) and 3) reflect likely alternative 'extremes' in this context regarding a catch taken from 7+8.

6. PERFORMANCE STATISTICS AND PRESENTATION OF RESULTS

The Workshop **agreed** that the approach followed during the North Atlantic fin whale and Western North Pacific Bryde's whale *Implementation* {IWC, 2010 #42727, pp. 587-627} was generally appropriate for the present *Implementation*. It **agreed** that the conditioning plots of the style developed for the North Atlantic fin whale *Implementation* should be produced for the current *Implementation Review*. It was **agreed** that the intersessional group established under Item 8.2 would provide guidance regarding the final form for these plots.

7. CONSIDERATION OF WAYS TO DISTINGUISH AMONG COMPETING STOCK HYPOTHESES

The Workshop considered this item with two objectives in mind:

(1) analyses of existing data that will assist discussion of relative plausibility at the First Annual Meeting; and

(2) analyses (including the collection of new data) that may assist in distinguishing amongst stock structure hypotheses in the longer term.

With respect to (1), the difficulties in assigning relative plausibility in a quantitative and fully objective manner are well recognised; stock structure (and the associated uncertainty) is one of the most difficult issues within the *Implementation* process. For example, in both *Implementations* conducted since the adoption of the requirements and guidelines for the *Implementation* process (i.e. western North Pacific Bryde's whales and North Atlantic fin whales, uncertainty around stock structure has led to the need to consider the 'variants with research' options[6] {IWC, 2008 #40149; IWC, 2010 #43204}.

The Workshop recognised that addressing the issue of relative plausibility requires consideration of information from a suite of techniques and usually requires a degree of 'expert' judgement.

Although there was limited time for a full discussion of this issue, the Workshop identified some analyses that could be carried out prior to the First Annual Meeting that may assist in the evaluation of relative plausibility:

(a) an evaluation of the extent to which observed spatial and/or temporal genetic heterogeneity can be explained by different mixture fractions of the same two core stocks or whether an additional stock or stocks is implicated – for details see Annex N, item A (Waples);

(b) additional PCA analyses – for details see Annex N, item B (Gaggioti);

(c) a more detailed consideration of the information on conception dates/foetal length data (see discussion under Item 2.1.3) that addresses potential biases relating to operational factors (e.g. timing, restrictions on catching calves), data collection (e.g. experience of those who examined the carcases, differential missing of foetuses with length), etc.

In addition, the Workshop encouraged review papers for the next meeting (noting that some papers already exist e.g. SC/S10/NPM8-10, SC/D10/NPM5,7) that consider the three hypotheses proposed against available information on biological and ecological information. Such review should also consider the completeness of the hypotheses, including any unexplained issues as well as those that are consistent with the available evidence. The meeting also recognised that the results of conditioning may also be important in the context of relative plausibility.

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[6] If a variant performs 'unacceptably' but only on trials that relate to a contentious hypothesis, then a Government can ask the Committee to investigate the performance of a 'hybrid' variant, i.e. 10 years of the 'unacceptable' variant followed by an acceptable variant. If performance is acceptable then the 'unacceptable' variant can be used if the Committee agrees to a research programme that has a good chance of confirming/refuting the contentious hypothesis with the 10-year period. Depending on the outcome, the 'unacceptable' variant may become acceptable or catch limits revert to being set by the second variant of the hybrid.

With respect to (2) above, the Workshop's initial considerations can be summarised as the need for:
   (a) an evaluation of possible evolutionary pathways - see Annex M, item C (Hoelzel); and
   (b) the importance of obtaining genetic samples from breeding areas to obtain samples from 'pure' stocks; and
   (c) better genetic and biological information from Korean by-catches in the future.

8. WORK REQUIRED PRIOR TO THE 2011 ANNUAL MEETING

8.1 Workplan
A number of recommendations are found throughout the report. Those relevant to the intersessional work for the First Annual Meeting are summarised below.

8.1.1 Work required to enable completion of conditioning
The *Implementation Simulation Trials* in Annex H must be coded and conditioned by the First Annual meeting [Allison and de Moor].

To achieve this, all information to be used in the conditioning process must be available (i.e. submitted to the Secretariat) by 31 January at the latest and ideally by 31 December.

   (1) mixing matrices to be completed (Punt, Butterworth and the hypotheses proponents)
   (2) genetics data:
      (a) a final database (bycatch, scientific permit, commercial) for use in estimating mixing proportions should be compiled [Item 4.5; Japanese and Korean scientists];
      (b) resolution of issues related to data on sex and microsatellite inconsistencies (Park and Baker paragraph]
   (3) abundance estimates (an advisory group under Kitakado has been established):
      (a) update of standard abundance estimates by JARPNII including consideration of covariates related to sighting conditions [Hakamada]
      (b) update standard abundance estimates by Japanese dedicated surveys with IO using only sighting by Top and Upper bridge, including consideration of covariates related to sighting conditions [Miyashita]
      (c) update information on Japanese dedicated surveys in 1990's and prepare the maps [Miyashita]
      (d) prepare abundance estimates for sensitivity exercise [Miyashita]
      (e) further consideration of $g(0)$ [possibly by the Antarctic minke whale abundance workshop in Tromsø in January 2011]

catch series (an advisory group under Allison has been established - Allison, An, Brownell, Kato and Ohsumi = group from Sept meeting + Scott, Choi, Kim and Hakamada

   (4) Catch-related data – commercial, scientific and bycatch (an Advisory Group under Allison has been established)
      (a) the final direct catch series [Allison] [Item 3.4, Allison, NB the final series for use in the *CLA* does not have to be completed by end of January]
      (b) the number of large-scale (excluding salmon nets), salmon nets and small scale setnets and the number of catches by year and by net type for Japan from 2001-9 [Hakamada]
      (c) the number of set-nets (large-scale and small-scale) prior to 1979 (if possible) [Hakamada]
      (d) Estimates of the number of setnets used in the East Sea, Korea prior to 1996 and of total fisheries effort in the Yellow Sea, Korea (all years). [Choi]
      (e) Estimates of total fisheries effort in the Yellow Sea, China (all years). [Choi]
      (f) the individual catch data held by Japan and by the IWC will be compared and discrepancies will be resolved [Allison and Japanese scientists].
      (g) compilation of all available length data [Allison, Korean and Japanese scientists]

   (5) the software for estimating mixing proportions must be extended to handle cases in which more than two stocks are found in a sub-area and this method applied to allow combinations of sub-area and month [Item 4.5; Punt; January 31, 2011]

8.1.2 Work required to assist discussions of relative plausibility and classification of ISTs
The short-term analyses and reviews identified under Item 7 should be submitted to the First Annual Meeting.

In addition, the dispersal rate analyses identified in Annex L should be completed if sufficient funds can be found (see Item 4.5.1)

8.2 Terms of Reference for the intersessional group to facilitate the conduct of the work.
The Workshop **agreed** that it was important to establish an intersessional group (Allison, An, Butterworth, de Moor, Donovan, Kitkado, Miyashita, Pastene, Punt, Wade) to review progress with the conditioning process and to provide advice as necessary. The group will work by email and, if necessary, by conference call.

9. ADOPTION OF REPORT

Most of the Report was adopted during the Workshop. Final editing was undertaken by Punt and Donovan and a revised draft circulated to the participants.

References

Table refs: {Ohsumi, 1982 #598; Gong, 1988 #37173}

[Missing refs: Wada, 1988; Park 1995; Park 1987]

Table 1.

Direct catches of western North Pacific minke whales from the IWC individual database including data on position and date summed over all years. Commercial, research catches, infractions and whales of unknown sex are included.

Area	Jan-Mar	Apr	May	Jun	Jul	Aug	Sep	Oct-Dec	Total
1W	0	0	0	0	0	0	0	0	0
1E	28	0	0	0	1	0	0	0	29
2C	5	4	2	3	3	0	1	0	18
2R	2	1	0	0	0	0	1	0	4
3 & 4	0	0	0	0	0	0	0	0	0
5	112	173	95	51	131	55	52	0	669
6W	8	37	281	154	58	25	182	151	896
6E	248	324	189	22	24	0	14	3	824
7CS	145	1441	1795	708	94	9	1	0	4193
7CN	0	12	64	313	486	490	879	170	2414
7W	0	1	54	31	6	1	1	0	94
7E	0	0	37	12	2	0	21	1	73
8	0	0	51	108	117	31	19	15	341
9	0	0	41	91	185	207	10	0	534
9N	0	0	0	3	2	18	0	1	24
10W	0	0	6	21	1	0	2	0	30
10E	2	26	66	171	101	35	12	3	416
11	2	405	846	958	742	323	186	34	3496
12SW	0	0	0	6	25	33	5	0	69
12NE	0	0	0	0	60	21	16	0	97
13	0	0	0	0	1	4	0	0	5
Total	552	2424	3527	2652	2039	1252	1402	378	14226

Table 2.

Direct Catches by Japan and data types

Period	Catch Type	Total	Data Available
1930-47	Commercial coastal catches	981	Numbers unknown & have been estimated by Area and year (Ohsumi 1982, Wada 1988)
1948-57	Commercial coastal catches	3,673	Individual data
		+ 5	Numbers only known by area (Wada 1988) and by month (IWS)
1958-63	Commercial coastal catches	1,835	Numbers only known by area* and year (Wada 1988) and by month (IWS)
1964-75	Commercial coastal catches	2,434	Individual data
		+ 1,274	Numbers known by sub-area and year (Wada 1988) and by month (IWS)
1976-1987	Commercial coastal catches	4,091	Individual data.
2002-2009	Coastal Scientific Permit catches	720	Individual data.
1969-76	Commercial Pelagic catches	24	Individual data.
1973-75	Catches by Miwa Maru	279	Individual data. Miwa Maru was a combined factory/catcher.
1994-2009	Scientific Permit Pelagic catches	1,344	Individual data.

* Wada 1988 gives the catch for i) sub-area 7CS ii) sub-areas 11 + 7CN combined and iii) sub-areas 6E + 10E

Table 3

Summary of the direct catches of minke whales taken off Korea

Period	Total	Notes
1932-39	?	Small numbers of minke whales were taken as a by-catch of catcher boats taking larger baleen whales
1940-45	878	Pre-war catches by Japan off Korea (Park 1995)
1946	47	Catching by Korea commenced in 1946. (Park 1995)
1947-56	?	Catches taken but numbers are unknown
1957	249	Catch from Park 1995
1958-71	4,777	From official statistics (= Park 1987 & Gong 1988). Catches by month given in Park 1987.
1972-76	4,734	True numbers from Park 1995 p443 who says the official numbers were under-reported. 3,270 whales given in the official statistics which are given by month in Park 1987 & Gong 1988.
1977-81	4,642	From official statistics (= Park 1987 & Gong 1988). Catches by month known with 1979-83 catches plotted by 0.5°square (Gong 1988).
1982-85	1,898	From official statistics (= Gong 1988). Individual data for 1,491 whales (submitted for Data Inventory)
1986	69	Special permit catch. Individual data
2000-09	66	Infractions (taken deliberately)

Table 4

The sensitivity tests which will involve conditioning the operating model

Trial No. NPM-	Sensitivity trial no.	MSYR	Description
A	A01-1 & A01-4	1% & 4%	2 stocks ('J' and 'O'); g(0) = 0.8
B	B01-1 & 4	1% & 4%	3 stocks ('J', 'O', and 'Y'); g(0) = 0.8
C	C01-1 & 4	1% & 4%	5 stocks ('Jw', 'Je', 'Ow', 'Oe', and 'Y'); g(0) = 0.8
Baseline		MSYR	Description
AC	A02-1 etc	1% / 4%	With a 'C' stock
ABC	A03-1 etc	1% / 4%	Assume g(0) = 1
ABC	A04-1 etc	1% / 4%	High direct catches + alternative Korean & Japanese bycatch level
ABC	A05-1 etc	1% / 4%	Double all A values
ABC	A06-1 etc	1% / 4%	Halve all A values
ABC	A07-1 etc	1% / 4%	Some 'O' ['Oe'] animals in sub-area 10E
ABC	A08-1 etc	1% / 4%	Fraction in bycatch areas of 2C [hypotheses II and III only], 7CS, 7CN = 2/60
ABC	A09-1 etc	1% / 4%	Fraction in bycatch areas of 2C [hypotheses II and III only], 7CS, 7CN = 10/60
ABC	A10-1 etc	1% / 4%	Assign the catches by Korea in sub-area 6E to sub-area 6W.
ABC	A11-1 etc	1% / 4%	Alternative split of Korean catches between 5 and 6W.
ABC	A12-1 etc	1% / 4%	12.5% J-stock in 12SW / 0% J-stock in 12NE
ABC	A13-1 etc	1% / 4%	37.5% J-stock in 12SW / 10% J-stock in 12NE
C	C14-1 & 4	1% / 4%	Include 'Y' and 'Jw' in 1W and 1E in Aug – Sept
C	C15-1 & 4	1% / 4%	Some 'C' animals in sub-area 12NE
C	C16-1 & 4	1% / 4%	No 'Ow' in 11 or 12 SW.
C	C17-1 & 4	1% / 4%	No 'Oe' in 11 or 12 SW
C	C18-1 & 4	1% / 4%	No 'Oe' in 7WR
C	C19-1 & 4	1% / 4%	With 'Je' in 2R iJ-M and O-D
C	C20-1 & 4	1% / 4%	Dispersal rate of 0.0025 between the Ow and Oe & Jw and Je stocks
C	C21-1 & 4	1% / 4%	Dispersal rate of 0.005 between the Ow and Oe & Jw and Je stocks
C	C22-1 & 4	1% / 4%	Dispersal rate of 0.01 between the Ow and Oe & Jw and Je stocks
C	C23-1 & 4	1% / 4%	Dispersal rate of 0.02 between the Ow and Oe & Jw and Je stocks

Table 5

The abundance estimates for use when conditioning the trials (taken from Kitakado Email of Feb 2nd 2011)

Sub-area	Year	Season	Survey type[7]	Mode[8]	Areal coverage (%)	STD estimate[9]	CV[10]	Conditioning	Source
5	2001	Apr-May	KD	NC	13.0	1,534	0.523	Min	SC/D10/NPM15
	2004	Apr-May	KD	NC	13.0	799	0.321	Min	ditto
	2008	Apr-May	KD	NC	13.0	680	0.372	Min	ditto
6W	2000	Apr-May	KD	NC	14.3	549	0.419	Min	ditto
	2002	Apr-May	KD	NC	14.3	391	0.614	Min	ditto
	2003	Apr-May	KD	NC	14.3	485	0.343	Min	ditto
	2005	Apr-May	KD	NC	14.3	336	0.317	Min	ditto
	2006	Apr-May	KD	NC	14.3	459	0.516	Min	ditto
	2007	Apr-May	KD	NC	14.3	574	0.437	Min	ditto
	2009	Apr-May	KD	NC	14.3	884	0.286	Min	ditto
6E	2002	May-Jun	JD	NC	79.1	891	0.608	Yes(#1)	SC/D10/NPM11
	2003	May-Jun	JD	NC	79.1	935	0.357	Yes(#1)	ditto
	2004	May-Jun	JD	NC	79.1	727	0.372	Yes(#1)	ditto
7CS	2004	May	JR	NC	100.0	886	0.502	Yes	SC/D10/NPM12(rev)
	2006	Jun - Jul	JR	NC	100.0	3,690	1.199	Yes	SC/D10/NPM12(rev)
7CN	2003	May	JR	NC	75.4	184	0.805	Yes	SC/D10/NPM12(rev)
7W	2003	May - Jun	JR	NC	54.2	524	0.700	Min	SC/D10/NPM12(rev)
	2004	May - Jun	JR	NC	88.8	863	0.648	Yes	SC/D10/NPM12(rev)
	2007	Jun - Jul	JR	NC	88.8	546	0.953	Yes	SC/D10/NPM12(rev)
7E	2004	May - Jun	JR	NC	57.1	440	0.779	Yes	SC/D10/NPM12(rev)
	2006	May - Jun	JR	NC	57.1	247	0.892	Yes	SC/D10/NPM12(rev)
	2007	Jun - Jul	JR	NC	57.1	0	-	Yes	SC/D10/NPM12(rev)
8	1990	Aug-Sep	JD	NC	61.8	1,057	0.705	Yes	From Miyashita
	2002	Jun - Jul	JR	NC	65.0	0	-	Yes	SC/D10/NPM12(rev)
	2004	Jun	JR	NC	40.5	1,093	0.576	Yes	ditto
	2005	May - Jul	JR	NC	65.0	132	1.047	Yes	ditto
	2006	May - Jul	JR	NC	65.0	309	0.677	Yes	ditto
	2007	Jun - Jul	JR	NC	65.0	391	1.013	Yes	ditto
9	1990	Aug-Sep	JD	NC	35.0	8,264	0.396	Yes	JCRM 6: 124
	2003	Jul-Sep	JR	NC	33.2	2,546	0.276	Min	SC/D10/NPM12(rev)
9N	2005	Aug-Sep	JD	IO-PS	67.8	420	0.969	Yes	From Miyashita
10W	2006	May-Jun	JD	IO-PS	59.9	2,476	0.312	Yes	From Miyashita
10E	2002	May-Jun	JD	NC	100.0	816	0.658	Yes	SC/D10/NPM11
	2003	May-Jun	JD	NC	100.0	405	0.566	Yes	ditto
	2004	May-Jun	JD	NC	100.0	474	0.537	Yes	ditto
	2005	May-Jun	JD	NC	100.0	666	0.444	Yes	ditto
11	1990	Aug-Sep	JD	NC	100.0	2,120	0.449	Yes	JCRM 6: 124
	1999	Aug-Sep	JD	NC	100.0	1,456	0.565	Yes	ditto
	2003	Aug-Sep	JD	IO-AC	33.9	882	0.820	Yes	From Miyashita
	2007	Aug-Sep	JD	IO-PS	20.2	377	0.389	Min	From Miyashita
12SW	1990	Aug-Sep	JD	NC	100.0	5,244	0.806	Yes	JCRM 6: 124
	2003	Aug-Sep	JD	IO-AC	100.0	3,401	0.409	Yes	From Miyashita
12NE	1990	Aug-Sep	JD	NC	100.0	10,397	0.364	Yes	JCRM 6: 124
	1999	Aug-Sep	JD	NC	89.4	11,544	0.380	Yes	ditto
	2003	Aug-Sep	JD	IO-AC	46.0	13,067	0.287	Yes	From Miyashita

Sensitivity 1: Use estimates in full area in 2002 & 2003 (originally 100% coverage) and one extrapolated to the full area in 2004 (79.1% coverage)

6E	2002	May-Jun	JD	NC	100.0	1,795	0.458	Yes	SC/D10/NPM11
	2003	May-Jun	JD	NC	100.0	1,059	0.322	Yes	ditto
	2004	May-Jun	JD	NC	100.0	919	0.372	Yes	ditto

Sensitivity 2: Use only in sensitivity as an estimate extrapolated to the full area

10E	2007	May-Jun	JD	IO-PS	100.0	552	0.159	Yes	From Miyashita

#Sensitivity: Did we agree these – they are not in table 4.

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[7] KD=Korean dedicated survey, JD=Japanese dedicated survey, JR=JARPNII
[8] NC=Normal-closing, IO-PS=Passing with IO mode, IO-AC=Abeam-closing with IO mode. (STD estimates by different modes, NC, IO-AC, IO-NC, are considered comparable.)
[9] Standard (STD) estimate based on "Top and Upper bridge", which will be corrected by estimate of g(0) for the combined platform "Top and Upper bridge"
[10] CV does not consider any process errors

Table 6

The nomination of samples representative of 'pure' stocks for the purpose of estimating mixing proportions

Hypotheses I & II		Hypothesis III	
Stock	Location / months to define pure sample	Stock	Location / months to define pure sample
Y-stock	5 (all months)	Y-stock	5 (all months)
J-stock	6E (all months)	JW-stock	6E (all months)
O-stock	7WR, 7E, 8 (all months)[1]	JE-stock	2C (all months)
		OW-stock	7CS [April and May] & 7CN [Sept. and Oct.] [>10NM]
		OE-stock	8 & 9 (all months) [excluding 9W in 1995]

1 (a)Under Hypotheses I and II only O stock occur in these sub-areas, (b) There is some genetic heterogeneity in sub-area 9 that is different from the heterogeneity between J and O stock animals (see Table 5 of SC/61/JR7 for mtDNA and Table 7 of SC/61/JR8 for microsatellite). This was the rational for proposing the former W stock (currently C stock). The source of such heterogeneity is not well understood yet, but it seems to occur temporarily (e.g. the sample from 9W in 1995 remain as a source of mtDNA heterogeneity). In the case of the microsatellite the source is not well understood. The genetic differences in sa 9 appear to be small and the heterogeneity only of a sporadic nature. However we want to avoid any bias in the estimation of mixing proportion derived from any heterogeneity in sa 9. (c) Sample sizes for sa 7WR+7E and 8 is reasonably large: 341 for mtDNA and 342 for STR.

Annex A

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Annex B

Agenda

1.   INTRODUCTORY ITEMS

1.1 Convenor's opening remarks
1.2 Election of Chair and appointment of rapporteurs
1.3 Adoption of Agenda
1.4 Review of documents

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2.1.3   Final choice of plausible hypotheses for inclusion in the trials
2.2 $g(0)$
2.2.1 Direct catches
2.2.2 Incidental catches

3. SPECIFICATION OF IMPLEMENTATION SIMULATION TRIALS

3.1 Selection of time-steps and sub-areas
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8. WORK REQUIRED PRIOR TO THE 2011 ANNUAL MEETING

8.1 Workplan
8.1.1 Work required to enable completion of conditioning
8.1.2 Work required to assist discussions of relative plausibility and classification of ISTs
8.2 Terms of Reference for the intersessional group to facilitate the conduct of the work.

9. ADOPTION OF REPORT

Annex C

List of Documents

Preparatory meeting

SC/S10/NPM1	Pastene, L.A., Goto, M. and Kanda, N. Specifications of plausible stock structure hypotheses for western North Pacific common minke whales.
SC/S10/NPM2	Bando, T. Biological data of western North Pacific common minke whales collected by JARPN (1994-1999) and JARPN II (2000-2009).
SC/S10/NPM3	Goto, M. Biological data collected from by-caught western North Pacific common minke whales in Japan (2001-2009).
SC/S10/NPM4	Hakamada, T. and Goto, M. Some information on statistics of the incidental catches of North Pacific common minke whales including the 'effort' expressed by the numbers of the setnets in the coast of Japan.
SC/S10/NPM5	Hakamada, T. and Miyashita, T. Summary information on sighting surveys undertaken by Japan during JARPN/JARPNII that are intended for consideration for use in the *Implementation Simulation Trials* for the RMP and the RMP itself.
SC/S10/NPM6	Miyashita, T. Summary information on the Japanese dedicated sighting surveys for western North Pacific common minke whales that is intended for consideration for use in the *Implementation Simulation Trials* for the RMP and the RMP itself.
SC/S10/NPM7	Miyashita, T and Hakamada, T. Results of a validation exercise of abundance data obtained by Japan that are intended for consideration for use in the *Implementation Simulation Trials* for the RMP and the RMP itself.
SC/S10/NPM8	Pastene, L.A. and Hatanaka, H. Non-genetic data provide little support for additional structure in the J and O stocks common minke whales.
SC/S10/NPM9	Kanda, N., Goto. M., Nagatsuka, S., Kato, H., Pastene. L.A. and Hatanaka, H. Analyses of genetic and non-genetic data do not support the hypothesis of an intermediate stock in sub-area 7.
SC/S10/NPM10	Bando, T., Miyashita. T., Kishiro T., Yoshida H. and Hatanaka. H. An analysis of conception date of common minke whales sampled by JARPN and JARPN II in the context of stock structure hypotheses.
SC/S10/NPM11	Yong-Rock AN and Ji-Eun Park Annual variations in the number of common minke whales incidentally caught by setnets in the East Sea, Korea.
SC/S10/NPM12	Yong-Rock AN and Jung-Youn Park Biological data collected from by-caught common minke whales in Korean waters from 1996 to 2008.
SC/S10/NPM13	Yong-Rock AN and Kyum-Joon Park Summary information on the Korean sighting surveys for common minke whales and results of a validation exercise of abundance data for the Implementation Simulation Trials for the RMP and RMP itself.

First Intersessional Workshop

SC/D10/NPM1	Wade, P.R. and Baker, C.S. Evidence for Stock Structure Hypothesis III for Implementation Simulation Trials for western North Pacific minke whales
SC/D10/NPM2	Steel, D and Baker, CS. Genetic identity of North Pacific minke whales from Korean bycatch and market surveys
SC/D10/NPM3	Baker, C.S., Slikas, B., Brownell R.L. and Wade, P.R. Stock structure of western North Pacific minke whales based on mtDNA haplotypes from Korean 'bycatch' and Japanese 'bycatch' and scientific whaling
SC/D10/NPM4	Baker, C.S. and Slikas, B. Hardy Weinberg in NPminke populations
SC/D10/NPM5	Pastene, L.A. and Hatanaka, H. Non-genetic data are not consistent with sub-division of J and O stocks common minke whales
SC/D10/NPM6	Bando, T. Kanda, N., Pastene, L.A, Kishiro, T., Yoshida, H. and Hatanaka, H. An analysis of cookie cutter shark-induced body scar marks of common minke whales in the context of stock structure hypotheses
SC/D10/NPM7	Kanda, N., Pastene, L.A. and Hatanka, H. Length composition and sex ratio of western North Pacific minke whales and their consistencies with stock structure hypotheses
SC/D10/NPM8	Kanda, N., Goto, M., Nagatuka, S., Kato, H., Pastene, L.A. and Hatanka, H. Genetic and non-genetic analyses of North Pacific common minke whales under the newly defined sub-areas
SC/D10/NPM9	Yoshida, H., Nozawa, A., Kanda, N., Kishiro, T. and Miyashita, T. Results of onboard genetic analysis of common minke whale biopsy samples collected in the Okhotsk Sea, summer 2010
SC/D10/NPM10	Pastene, LA., Kanda, N. and Hatanaka, H. Summary of scientific evidence supporting stock structure Hypotheses I and II for western North Pacific common minke whales.
SC/D10/NPM11	Miyashita, T. Summary of the information on Japanese dedicated sighting surveys for abundance estimation
SC/D10/NPM12	Hakamada, T. Summary of the information on dedicated sighting surveys for abundance estimation in JARPN and JARPN II
SC/D10/NPM13	Hakamada, T. The number of setnets in the coast of Japan by sub-areas and years during 1979-2006.
SC/D10/NPM14	Allison, C and de Moor, C. NPM Mixing Matrices – A Strawman
SC/D10/NPM15	An, Y-R, Choi, C-D, Moon, D-Y and Park, K-H. Summary of the information on Korean dedicated sighting surveys for abundance stimates of common minke whales
SC/D10/NPM16	Gaggiott, O and Gascuel, F. Apparent substructuring within the O stock of North Pacific minke whales

Annex D

The following is an extract from 'Requirements and Guidelines for Implementations' {IWC, 2005 #32809}.

2. First intersessional Workshop

The primary objective of the first intersessional workshop is to develop an appropriate *Implementation Simulation Trials* structure and to specify the associated conditioning so that it can be carried out before the following Annual Meeting. The aim of such trials[1] is to encompass the range of plausible scenarios involving *inter alia* stock structure, MSY rates (*MSYR*), removals and surveys. These trials are used to investigate the implications of various choices of RMP variants such as *Catch-cascading* from a risk- and catch-related perspective, with a view to recommending an appropriate variant for implementation of the RMP for a specific species/area.

Workshop discussions will include the items listed below.

(1) A final review of the plausible hypotheses arising from the *pre-Implementation assessment* (and, if appropriate, elimination of any hypotheses that are inconsistent with the data) – this will take into account the probable management implications of such hypotheses to try to avoid unnecessary work in the precise specifications of hypotheses for which these are very similar;

(2) An examination of more detailed information in expected operations, including whether coastal, pelagic, on migration, on feeding, on breeding or combinations of these. When providing such information, users and scientists may provide options or suggest modifications to the pattern of operations;

(3) The determination of the small geographical areas ('sub-areas') that will be used in specifying the stock structure hypotheses and operational pattern;

(4) The development of (options for) potential *Small Areas*[2] and management variants;

(5) The specification of the data and methods for conditioning the trials that will be carried out before the next annual meeting (an e-mail correspondence group will be established to make revisions should any problems arise);

(6) Further consideration of experimental ways to distinguish amongst competing stock hypotheses.

It is **important** to note that after this stage:

(1) there shall be no changes to the agreed trials structure that implements the agreed plausible hypotheses;

(2) no new data will be considered, although new analyses of existing data may be presented to the First Annual Meeting (see below).

REFERENCE

[FOOTNOTES]

[1] A trial is the combination of a set of 'hypotheses' (e.g. about stock structure, *MSYR*).

[2] *Small Areas* cannot be smaller than sub-areas.

Annex E

Summary of conception data from the IWC individual database and Wang (1985)

de Moor CL

Using the formula for number of days from conception as a function of foetal body length from SC/S10/NPM10, conception dates were calculated from the monthly body length of embryos of Yellow Sea minke whales from table 4 of Wang {, 1985 #7679}. This distribution is plotted in Fig. 1, compared to that of the distribution of the data in the IWC database plotted in Fig. 2. A single sample from the Yellow Sea in 2003, provided by Korea is included in Fig. 1. The data plotted in Fig. 2 are plotted separately by areas in Figs 3-9.

Fig. 10 plots the relative number of embryos for which body length data are available by month for the Yellow Sea {Wang, 1985 #7679}. The mean lengths of these data by month do not conflict with those predicted by the formula of Bando et al. (2010) – see Fig. 11.
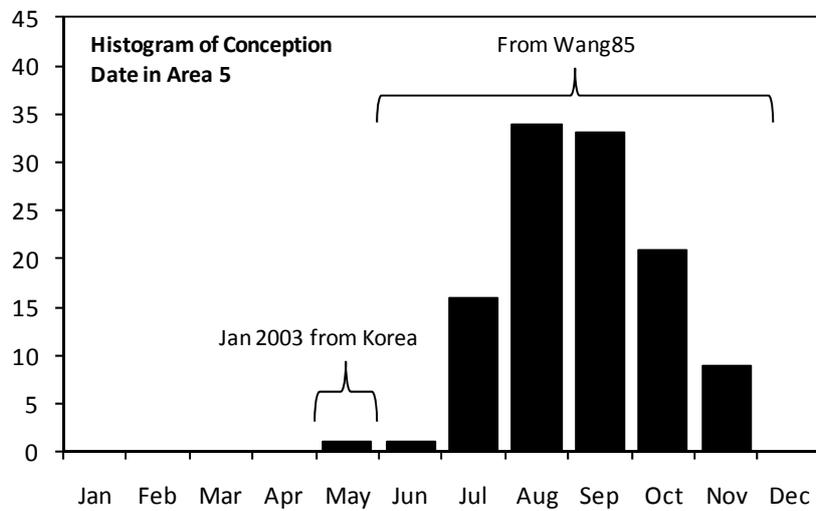
Fig. 1. Histogram of conception date in Area 5 (Yellow Sea).[11]
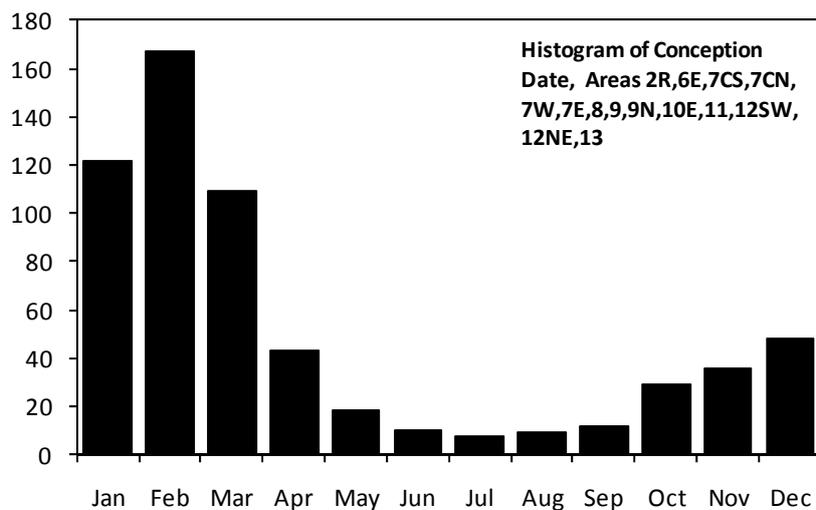
Fig. 2. Histogram of conception date from IWC database.

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[11] The assumption was made that the embryo lengths corresponded to the median of the length groups.
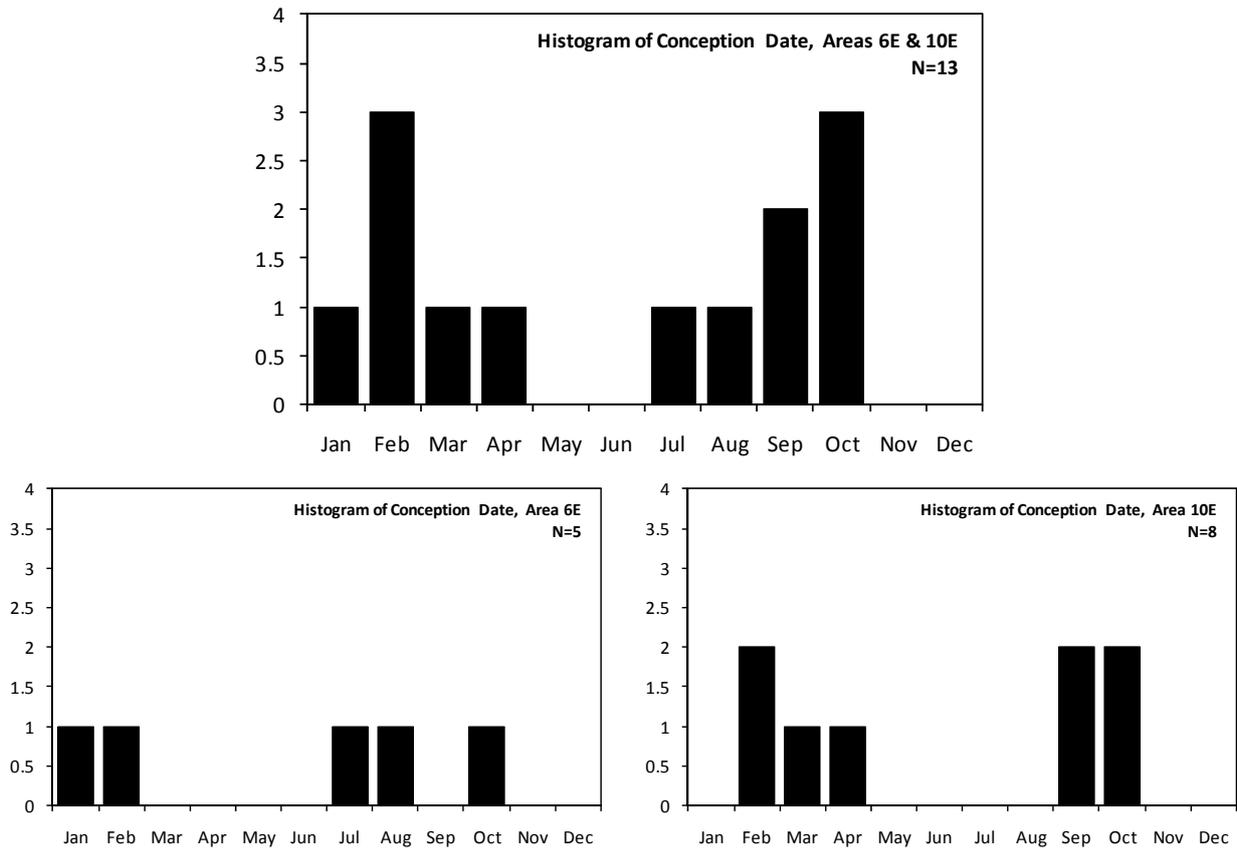
Fig. 3. Histograms of conception date from IWC database for areas 6E and 10E only.
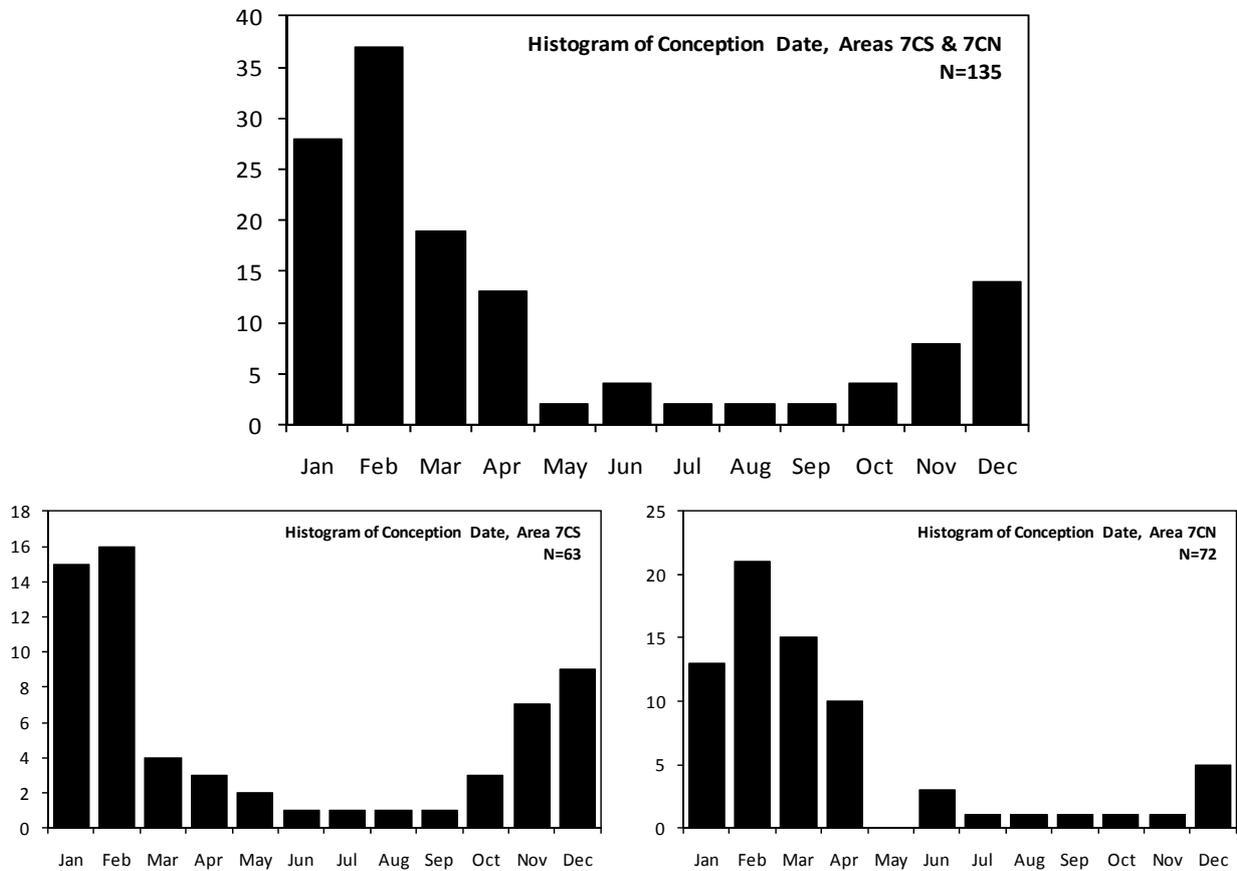
Fig. 4. Histograms of conception date from IWC database for areas 7CN and 7CS only.
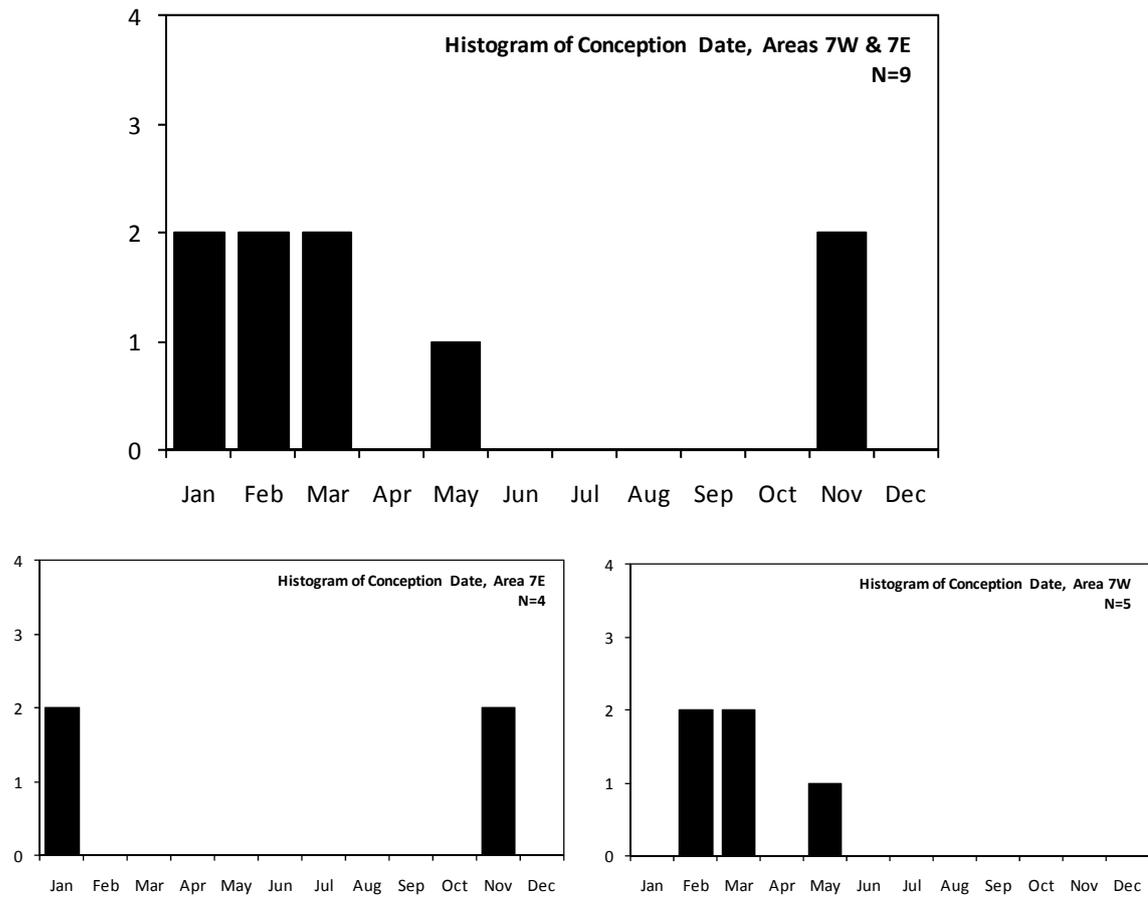
Fig. 5. Histograms of conception date from IWC database for areas 7W and 7E only.
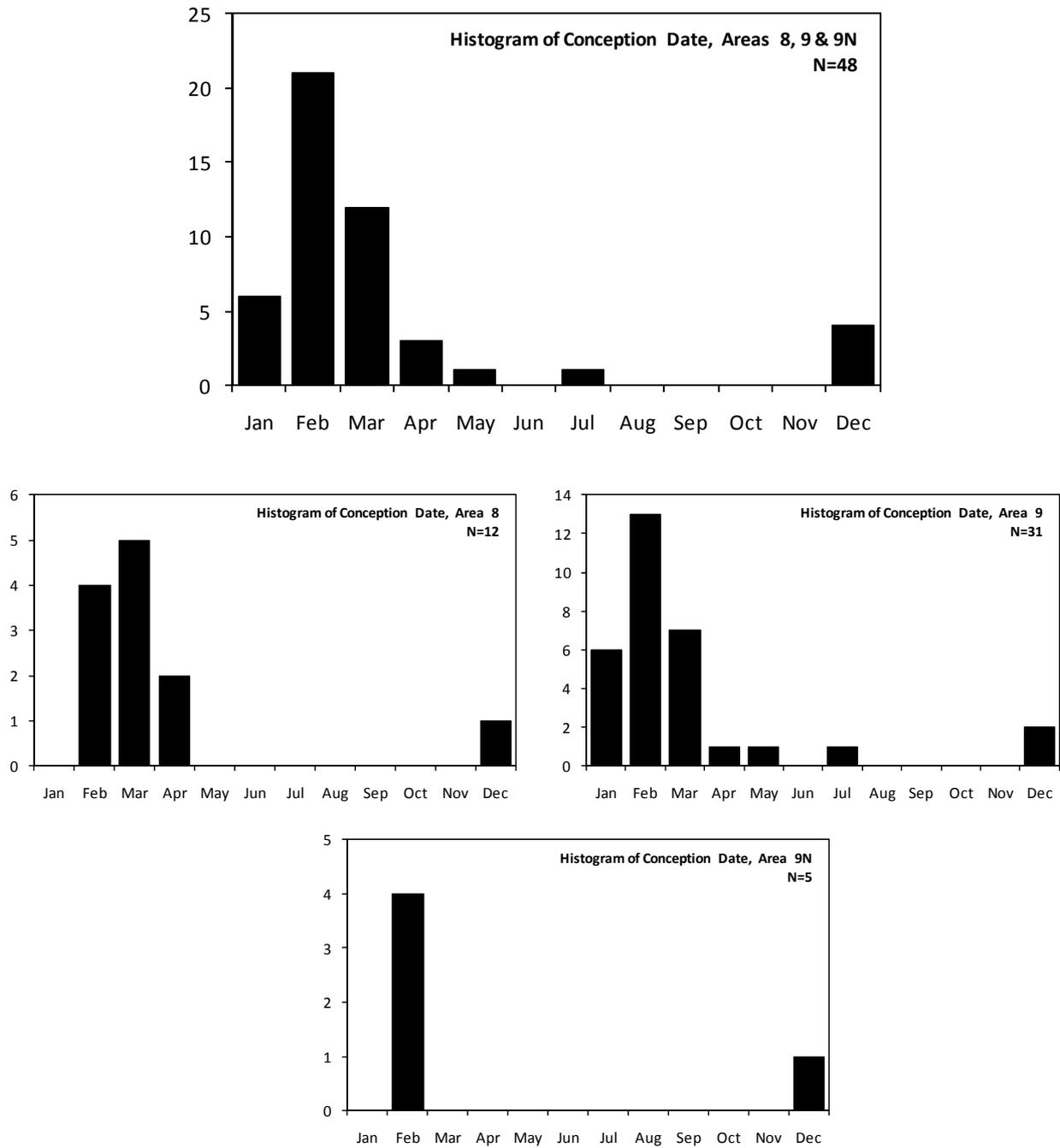
Fig. 6. Histograms of conception date from IWC database for areas 8, 9 and 9N only.
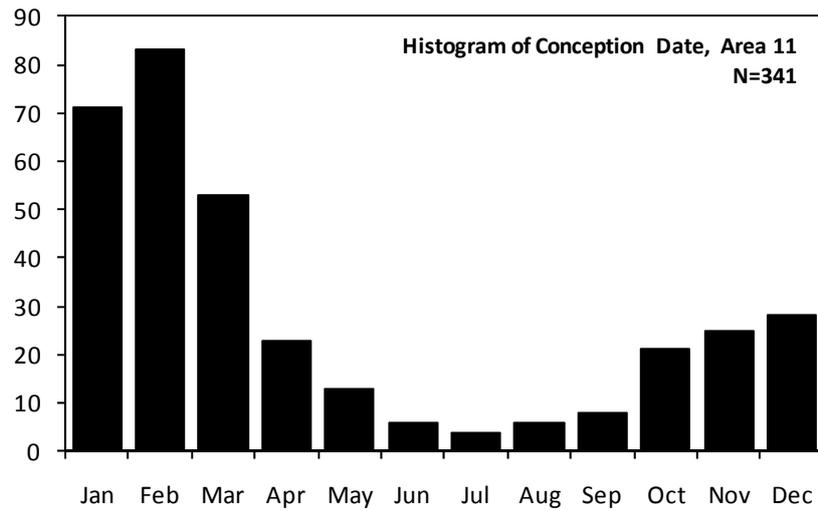
Fig. 7. Histogram of conception date from IWC database for area 11 only.
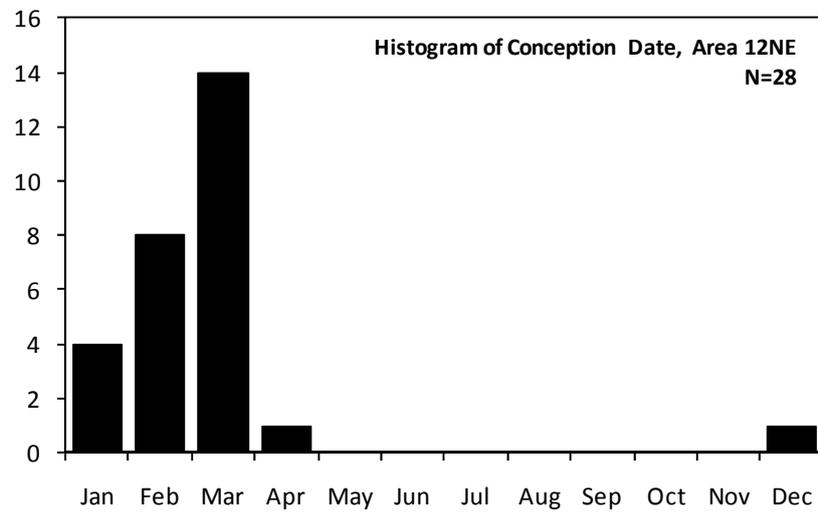
Fig. 8. Histogram of conception date from IWC database for area 12NE only.
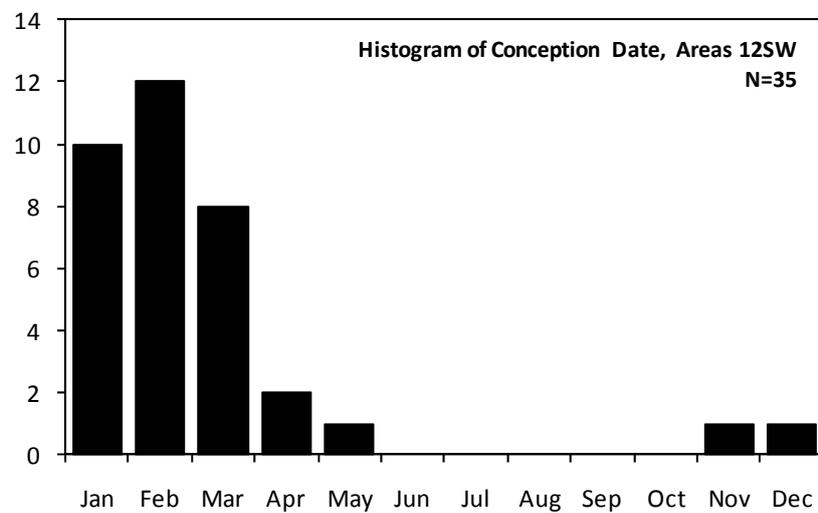
Fig. 9. Histogram of conception date from IWC database for area 12SW only.
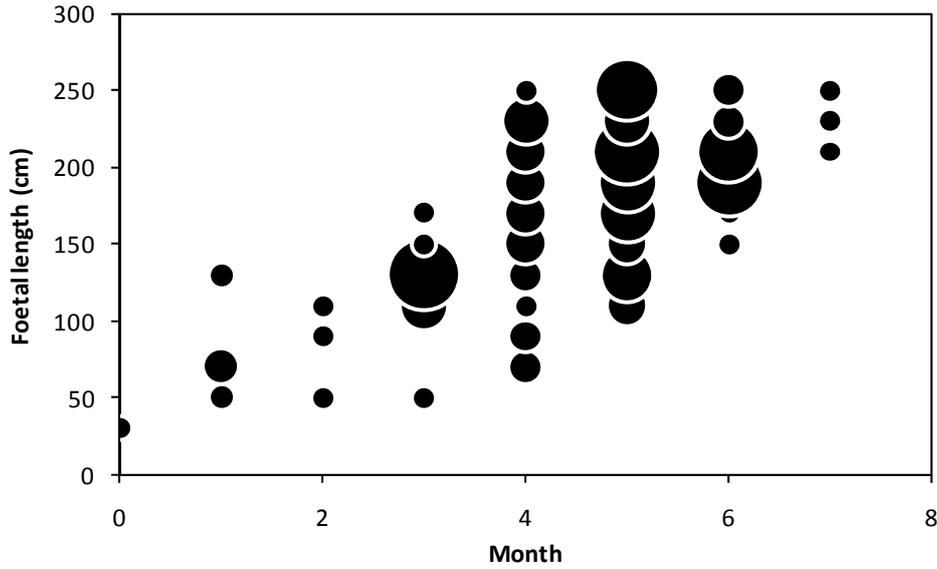
Fig. 10. The number of observations of foetuses from the Yellow Sea for which length class data is available, by month {Wang, 1985 #7679}.
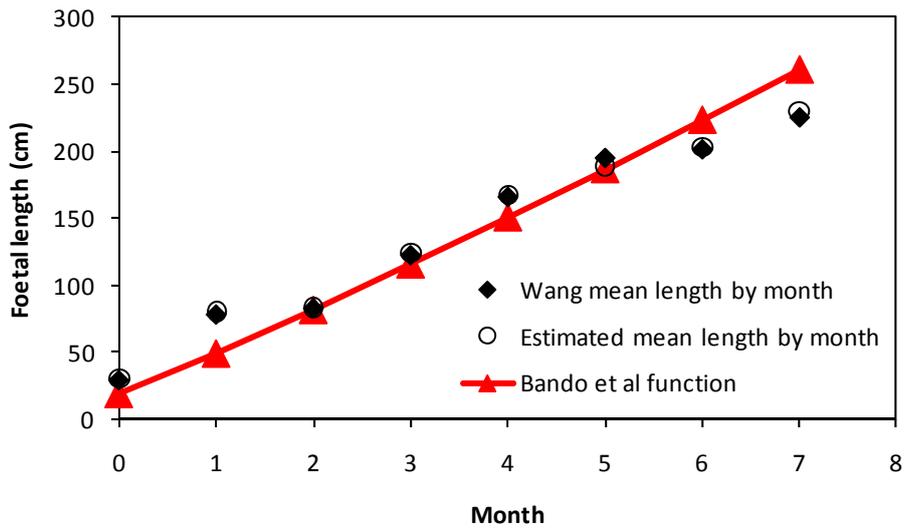
Fig. 11. The estimated mean length by month from Wang {, 1985 #7679} compared to the estimated foetal length, given conception date from the formula provided by Bando et al. (2010). (Bando *et al.* curve conception date chosen so that curve goes through centroid of Wang data.)

References

Annex F

Descriptions of the Three Stock-Structure Hypotheses[1]

Appendix F-1. Description and summary of evidence supporting stock structure Hypotheses I and II for western North Pacific common minke whales

Luis A. Pastene, Naohisa Kanda and Hiroshi Hatanaka

DESCRIPTION OF STOCK STRUCTURE HYPOTHESES

Hypothesis I (Fig. 1)
A single J stock is distributed in the Yellow Sea, Sea of Japan and the Pacific side of Japan. A single O stock occurs in sub-areas 7, 8 and 9, which migrates in summer mainly to the Okhotsk Sea (sub-areas 12SW and 12NE). Both J and O stocks overlap temporally along the Pacific coast (sub-areas 7CS and 7CN) and the southern part of the Okhotsk Sea (sub-areas 11 and 12SW).

Hypothesis II (Fig. 2)
As Hypothesis I except that a Y stock resides in the Yellow Sea and overlaps temporarily with the J stock in the southern part of sub-area 6W.

HYPOTHESISED MIGRATION PATTERN OF STOCKS J, O AND Y

The migration pattern of J-stock adults and juveniles is as suggested by Hatanaka *et al.* {, 2010 #43242} and Goto *et al.* {, 2010 #44039}. The migration of O-stock adults and juveniles is as suggested by Hatanaka and Miyashita {, 1997 #14887}. The temporal and spatial overlap between J and O stocks along the Japanese coast is as proposed by Kanda *et al.* {, 2009 #42670}.

Pattern of migration of J stock
The migratory pattern of J-stock has the following characteristics:

    (1) the northward (feeding) migration begins in January-February;
    (2) pregnant females migrate into the southern part of Okhotsk Sea in April, following the retreat of sea ice;
    (3) the main feeding season is April-June;
    (4) the southward (breeding) migration starts in July;
    (5) segregation by sex and maturity occurs

    (a) pregnant females migrate to the northernmost distribution area
    (b) in general, adult animals migrate and are found in offshore waters in the Sea of Japan
    (c) the migration of juveniles is different from adult animals and they stay close to the coast of Japan and Korea almost year around.

Goto *et al.* {, 2010 #44039} showed that this hypothesis was consistent with several kinds of data.

Pattern of migration of O stock
The migratory pattern of O stock has the following characteristics:

    (1) immature animals migrate into the coastal area of southern sub-area 7 (7CS) in April and then disperse to northern sub-area 7 (7CN) and the southern Okhotsk Sea (11);
    (2) mature males occur widely from coastal waters to offshore waters in May;
    (3) mature females enter the Okhotsk Sea (11) in April and May and then move further to the middle (12SW) and northern (12NE) Okhotsk Sea.

Spatial and temporal overlap of J and O stocks in the Pacific side of Japan
In sub-areas 7CS and 7CN, J stock animals occur mainly within 10 n.miles of the coast {Kanda, 2011 #44233}. Kanda *et al.* {, 2009 #42670} showed the relative occurrence of J and O stocks in sub-area 7 by month. The general pattern is that J stocks animals are more frequent in autumn/winter and O stock animals in spring/summer {see table 6 in \Kanda, 2009 #42670}. We consider that this information is the most useful to elucidate the pattern of spatial and temporal overlap of J and O stocks in sub-areas 7CS and 7CN.

Pattern of migration of Y stock

There is insufficient information to specify the occurrence and migration of Y stock. We assume that it is mainly a resident stock in the Yellow Sea with all sexual classes occurring there through the year. A small component of that stock would carry out a short seasonal migration in summer (July-October) to the southern part of the Sea of Japan (6W), mixing there with the J stock.

SUPPORTING EVIDENCE FOR HYPOTHESES I AND II

Genetic markers

Genetic analyses based on Japanese samples

Previous genetic analyses were presented and discussed to the JARPN Review Workshop {IWC, 2001 #35253}. The only evidence for genetic heterogeneity on the Pacific side of Japan (other than J stock) came from the mtDNA analysis. Based on this analysis, the Workshop did not discard the hypothesis of occurrence of C stock in offshore areas in the Pacific side of Japan (sub-area 9W), at least in some years of the period of JARPN. The Workshop recommended that further research was necessary to examine the hypothesis of the C stock {IWC, 2001 #35253}.

The most recent genetic analyses were based on a larger set of samples collected by JARPN and JARPN II in the period 1994-2007 and from bycaught animals around the Japanese coast in the period 2001-2007. These analyses have been valuable to examine stock structure hypotheses of common minke whales in the western North Pacific. Papers containing these analyses were presented to the JARPN II review meeting {IWC, 2010 #42725} and subsequently revised versions of those papers that responded to some of the suggestions of the JARPN II review meeting were presented to the IWC SC meeting in 2009 {IWC, 2010 #43209}.

One of the most valuable pieces of information was the work on microsatellites to assign individuals to J and O stocks {Kanda, 2009 #42670}. The Scientific Committee had recommended several times in the past to carry out hypothesis testing analyses separately for O and J stocks {e.g. \IWC, 2003 #27779}, and this microsatellite work was in direct response to those Committee recommendations.

Kanda *et al.* {, 2009 #42670} used 16 microsatellite loci to examine samples taken by JARPN and JARPN II in sub-areas 7 (7CN, 7CS, 7WR, 7E), 8 and 9 between 1994 and 2007 and samples from bycaught animals along the Japanese coast between 2001 and 2007. A Bayesian clustering approach was implemented with the microsatellite data in the STRUCTURE (version 2.0) to determine the most likely number of genetically distinct stocks present in the samples. Bayesian clustering analyses conducted on the total samples of 2,542 animals presented the highest likelihood probability at K= 2 (J and O stocks). The animals with the membership probability of over 90% for either of the two stocks were assigned as 'pure' individuals. A total of 2,302 animals (91%) were assigned as the pure individual to the either stock (770 to J stock and 1,532 to O stock). There were 9% unassigned animals.

The authors used these data to study the pattern of geographical and temporal distribution of J and O stocks around Japan {see figs 4, 5 and 6 of \Kanda, 2009 #42670}.

There were some Committee discussions on the effect of unassigned individuals and on how these samples can affect the conclusion of the stock structure. The unassigned individuals could be whales from some other additional weakly differentiated stocks or simply could be whales that could not be assigned to J and O stocks simply due to the low statistical power of the STRUCTURE analysis. The Committee provided some useful suggestions to elucidate this problem {IWC, 2010 #43209}. Some of those suggestions were responded by Kanda *et al.* {, 2010 #44030}. Following the recommendations these authors conducted some additional STRUCTURE runs and Principal Component Analysis (PCA). Results of these additional analyses failed to detect evidence of a third stock in the Pacific side of Japan and the authors concluded that the unassigned animals were either J or O stock animals.

Subsequently, hypothesis testing analyses based on mtDNA and microsatellites were carried out separately for J and O stock animals in sub-area 7W (this includes 7CS, 7CN and 7WR at the present sub-division), as recommended by the Committee in the past. Hypothesis testing analyses were conducted for the samples collected by JARPN and JARPN II in 1994-2007 and bycaught animals in Japan between 2001 and 2007.

Goto *et al.* {, 2009 #42672} conducted a mtDNA analysis for O stock animals sampled in sub-areas 7, 8 and 9. A total of 1,639 samples were used. No significant mtDNA heterogeneity was found except in the western part of sub-area 9, which was attributed to the samples taken in 1995. Kanda *et al.* {, 2009 #42673} conducted a microsatellite analysis for O stock animals sampled in sub-areas 7, 8 and 9. A total of 1,631 sampled were used. Results were very similar to those from the mtDNA analysis. No significant microsatellite heterogeneity was found for O stock animals except in sub-area 9.

The microsatellite analyses on O stock animals by Kanda *et al.* {, 2009 #42673} included an analysis of statistical power {see table 12 of \Kanda, 2009 #42673 for details}. The study suggested high statistical power providing

confidence to the conclusion of single O stock scenario. Consideration of the statistical power of genetic analyses has been recommended by the Committee several times in the past. This study was in direct response to those recommendations.

As noted above, the microsatellite analysis found significant differences between western and eastern sectors of sub-area 9 {Kanda, 2009 #42673} while the mtDNA analysis found significant differences between those sectors using *Fst* for a particular year (1995) {Goto, 2009 #42672}. These results were consistent with the sporadic intrusion of an offshore stock into sub-area 9 ('C' stock).

Regarding the analyses on J stock, Goto *et al* {, 2009 #42678} found no significant mtDNA differences among animals in the sub-areas surrounding Japan (2, 6, 7, 10, 11).

Genetic analyses including Korean by-catch samples
The most recent analyses have involved both Japanese (1994-2007 JARPN+JARPN II; bycatches 2001-2007) and Korean (bycatches 1999-2007) common minke whales.

Park *et al.* {, 2010 #44065} conducted a mtDNA analysis on common minke whales from Japan and Korea. Regarding the J stock no significant heterogeneity was found except in the comparison between Japanese and Korean minke whales. No significant heterogeneity was observed when the sample from the Yellow Sea (5) was excluded from the comparison. Regarding the O stock, no significant heterogeneity was found in sub-areas 7, 8 and 9 based on the chi-square test.

Kanda *et al.* {, 2010 #44030} used 16 microsatellite loci to examine a similar set of samples, but the analysis was focused on J stock animals. This microsatellite analyses suggested some levels of seasonal genetic differentiation in the Korean samples but not in the Japanese sample. Yearly heterogeneity and the very weak heterogeneity between the Japanese and Korean samples from sub-area 6 could be due to a different stock in the Yellow Sea (Y stock) moving north at some extent along the Korean coast in summer (July-October) mixing there with the J stock {Kanda, 2010 #44030}.

Non-genetic markers
Non-genetic information is limited for J and Y stocks. The non-genetic information presented to the JARPN review meeting provided no evidence for a separate C stock in offshore waters (sub-area 9).

Regarding the O stock, the Committee reviewed the results on stock structure based on analyses of non-genetic markers during the JARPN Workshop {IWC, 2001 #35253}. The information based on morphometric {Hakamada, 2000 #37257}, pollutant burden {Fujise, 2000 #37255}, parasite load (Kuramochi *et al.*, 2000) and biological parameters {Zenitani, 2000 #37267; Zenitani, 2002 #28338} was not contradictory with the view of a single O stock scenario in sub-areas 7, 8 and 9 {see also \Pastene, 2000 #37264}.

Okamura *et al.* {, 2001 #26838} studied the density of minke whales in the western North Pacific using a generalised additive model (GAM) and JARPN sightings data obtained in sub-areas 7, 8 and 9 between 1994 and 1999. The aim of the study was to investigate spatial and temporal distribution and followed a Committee recommendation. The trend surface of the transformed density predicted by each month revealed no clear gaps. The authors concluded that the density distribution suggested the northward seasonal feeding migration of the minke whales. Therefore, the density distribution provided no evidence of sub-divisions of the O stock.

As noted above, the microsatellite analyses by Kanda *et al.* {, 2009 #42670} made possible the assignment of animals to either J or O stocks. Therefore the analyses based on non-genetic markers could be conducted separately for both stocks. The most recent non-genetic information on the O stock structure is summarised below.

Hakamada and Bando {, 2009 #41904} conducted a study on stock structure based on ten external measurements. Common minke whales sampled by JARPN II in sub-areas 7CN, 7CS, 7WR, 7E, 8 and 9 between 2000 and 2007, were used in the analysis. In the sample, two J stock animals and 118 O stock animals were identified. Results of the analysis of covariance (ANCOVA) showed significant differences in morphometric measurements between J and O stock animals. No significant differences were found among O stock animals grouped under several geographical divisions in the Pacific side of Japan.

SC/S10/NPM10 examined conception date in minke whales sampled by JARPN and JARPN II in sub-areas 7CN, 7CS, 7WR, 7E, 8, 9 and 11 between 1994 and 2007. A total of 107 animals was analysed. A total of 11 J-stock animals was identified, three in sub-area 7 and eight in sub-area 11. The conception period of the J stock spread from August to March. O stock animals had a single winter peak of conception. No differences were found in conception dates among O-stock animals from sub-areas 7, 8 and 9.

SC/D10/NPM6 examined cookie cutter shark-induced body scar marks in 1,069 minke whales sampled by JARPN II in sub-areas 7CN, 7CS, 7WR, 7E, 8 and 9. In those sub-areas, a total of 862 and 97 animals was assigned to the O and J stocks, respectively. Three types of scars were defined. There were clear differences in the occurrence of these scar types between J and O stocks, and in both stocks scar numbers increased with body length. No differences in scar types were found between O stock animals from sub-areas 7CN+7CS and sub-areas 7E+8+9.

SC/D10/NPM8 examined flipper and fluke color pattern in 189 (flipper) and 178 (fluke) minke whales sampled by JARPN II in 2007 in sub-areas 7CS, 7CN, 7WR, 8 and 9. Three types of flipper and three type of fluke color pattern were defined. For both traits differences were observed between J and O stock animals. However no differences were observed among O stock animals from those sub-areas in the Pacific side of Japan.

SC/D10/NPM7 examined length composition and sex ratio data of minke whales bycaught along the Japanese coast in the period 2001-2007, and minke whales sampled by JARPN and JARPN II between 1994 and 2007. J stock animals from the Sea of Japan and Pacific coast showed quite similar characteristics. On the Pacific side of Japan, immature O stock animals were found mainly in coastal areas whereas mature animals were found mainly in offshore areas. This distribution pattern can be explained only when a single O stock, not two stocks, is found in the area.

Table 1 presents our summary of the most recent information on stock structure in the western North Pacific common minke whale. The most parsimonious interpretation of the available genetic and non-genetic data suggests a single O stock (Table 1)

DISCUSSION AND CONCLUSIONS

The target of the RMP *Implementation* is the O stock common minke whale. Sub-structure within the O stock had been proposed and discussed by the Committee since 1993. The Committee proposed a complicated sub-stock scenario with several sub-stocks composing the O stock and hypothesised a western stock ('C' stock) in offshore areas in the Pacific side of Japan {IWC, 1994 #20517}.

The issue of stock structure was discussed again by the Committee in 1996. During that meeting, the new scientific information derived from JARPN was examined and the Commitee concluded that the sub-stock scenario proposed in 1993 was not plausible {IWC, 1997 #16683}.
The Committee reviewed the results on stock structure during the JARPN Workshop conducted in 2000. The information based on genetics, morphometric, ecological markers, biological parameters was not contradictory with the view of a single O stock scenario in sub-areas 7, 8 and 9 {Pastene, 2000 #37264}. Based on the mtDNA information, the Workshop did not discard the hypothesis of occurrence of C stock in offshore areas in the Pacific side of Japan, at least in some years of the period of JARPN. The Workshop recommended that further research was necessary to examine the hypothesis of the C stock {IWC, 2001 #35253}.

The only previous evidence suggesting further division of the O stock (apart from the C stock) comes from the application of the Boundary Rank Algorithm (BRA) to mtDNA data. This resulted in the proposal of two O stocks, O_w and O_e, separated at 147°E. Re-run of the BRA on a larger number of samples provided no support for the division of O_w and O_e stocks {Gaggiotti, 2010 #44161}.

Recent genetic and non-genetic evidence is consistent with what the Committee sponsored JARPN review workshop agreed in 2000: a single O stock scenario and the possibility of a sporadic intrusion of a different stock (C stock) in sub-area 9. This is supported by the best available genetic and non-genetic evidence. The current genetic evidence suggests a single J stock (the degree of genetic heterogeneity in the Yellow Sea is considered weak). These results-most of them emerging from analyses recommended by the Committee through the years-support Hypothesis I.

The possibility of a separated Y stock (Hypothesis II) suggested by some genetic analyses should be confirmed by additional genetic and non-genetic analyses.

REFERENCES

Table refs: {Kanda, 2010 #44030; Goto, 2009 #42672; Park, 2010 #44065; Okamura, 2001 #26838; Hakamada, 2009 #41904}

Table 1. Summary of the most recent information on stock structure in the western North Pacific common minke whale.

Marker	Result	Reference
Microsatellite	Analyses conducted separately for J and O stock animals. Weak differences between Japanese and Korean J stock animals attributed to whales in the Yellow Sea (Y stock). Apart from sub-area 9, no heterogeneity was found among the O stock in the Pacific side.	Kanda *et al*. (2010b); SC/D10/NPM8
Mitochondrial DNA	Analyses conducted separately for J and O stocks. Weak differences between Japanese and Korean J stock animals attributed to whales in the Yellow Sea. Apart from a sporadic heterogeneity found in sub-area 9W, no other heterogeneity was found among the O stock in the Pacific side.	Goto *et al*. (2009a); Park *et al*. (2010)
Whale density	The trend surface of the transformed density predicted by each month revealed no clear gaps in the Pacific side of Japan (sub-areas 7, 8 and 9).	Okamura *et al*. (2001)
Morphometric	Analyses conducted separately for J and O stocks. Significant differences in morphometric measurements between J and O stocks. No significant differences were found among O stock animals from sub-areas 7 8 and 9.	Hakamada and Bando (2009)
Conception date	Analyses conducted separately for J and O stocks. Differences between J and O stock animals. No differences among O stock animals from sub-areas 7, 8 and 9.	SC/S10/NPM10
Cookie cutter shark scars	Analyses conducted separately for J and O stocks. Differences between J and O stock animals. No differences between 7CN+7CS and 7E+8+9 O stock animals.	SC/D10/NPM6
Flipper color pattern	Analyses conducted separately for J and O stocks. Differences between J and O stock animals. No differences between 7CN, 7CS, 7WR, 8, and 9 O stock animals.	SC/D10/NPM8
Fluke color pattern	Analyses conducted separately for J and O stocks. Differences between J and O stock animals. No differences between 7CN, 7CS, 7WR, 8, and 9 O stock animals.	SC/D10/NPM8
Length composition and sex ratio	Analyses conducted separately for J and O stocks. Pattern of distribution by sex and body length in sub-areas 7, 8 and 9 was consistent with a single O stock in the Pacific side. J stock animals from the Sea of Japan and Pacific coast showed quite similar characteristics in the data.	SC/D10/NPM7
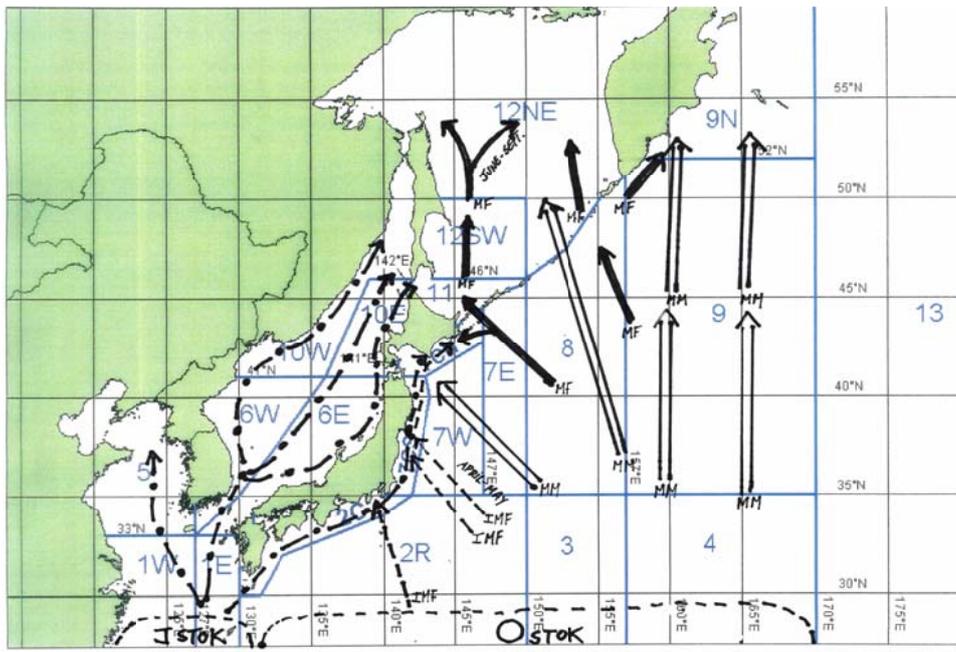
Fig. 1. Schematic representation of Hypothesis I {modified from \Hatanaka, 1997 #14887}.

MM=mature males, MF=mature females, IMF=immature males and females.
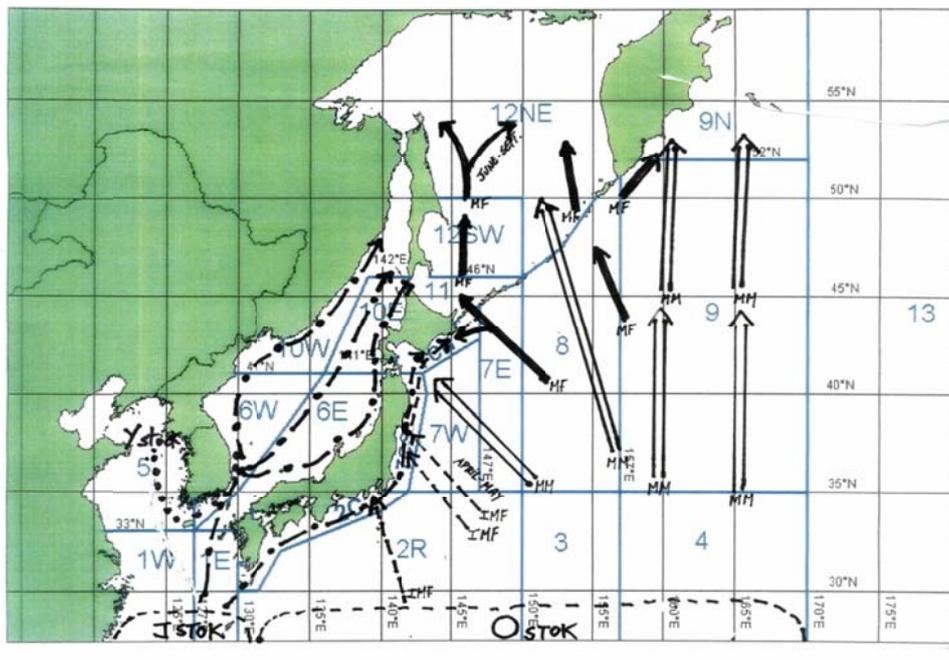
Fig. 2. Schematic representation of Hypothesis II {modified from \Hatanaka, 1997 #14887}.

MM=mature males, MF=mature females, IMF=immature males and females. Y stock residing in the Yellow Sea and mixing with the J stock in the southern part of sub-area 6W in summer.

Appendix F-2. Description and summary of evidence supporting stock structure Hypothesis III for western North Pacific common minke whales

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SUMMARY OF THE EVIDENCE FOR EACH STOCK

In Stock Structure Hypothesis III there are five stocks, referred to as Y, JW, JE, OW, and OE, one of which (Y) occurs primarily in the Yellow Sea, one of which (JW) occurs in the Sea of Japan, and three of which (JE, OW, and OE) occur to the east of Japan. The most important evidence regarding stock structure comes from pair-wise tests of mtDNA and microsatellite DNA, tests for Hardy-Weinberg disequilibrium in microsatellite DNA, and biological data on conception dates. A summary of the most important evidence for each stock division is as follows.

1. The Yellow Sea stock (Y-stock)

- There are microsatellite DNA genetic differences between the Yellow Sea and Sea of Japan (in winter) based on bycatch samples.
- Whales in the Yellow Sea have only autumn conception dates.
- There is substantial evidence for Hardy-Weinberg disequilibrium along the Korean coast of the Sea of Japan in summer suggesting the Yellow Sea stock mixes with the Sea of Japan stock.

2. The Sea of Japan stock (JW-stock)

- There are microsatellite DNA genetic differences between the Yellow Sea and Sea of Japan (in winter) based on bycatch samples.
- There are differences in mtDNA and microsatellite DNA between the Sea of Japan and all areas in the Pacific (including coastal waters).
- Whales in the Sea of Japan have a mixture of autumn and winter conception dates.

3. A 'J-like' stock along the Pacific coast of Japan (JE-stock)

- There are differences in mtDNA and microsatellite DNA between coastal bycatch samples and nearshore whaling samples in the Pacific.
- The bycatch samples along the Pacific coast are significantly different from Sea of Japan bycatch samples but have similar haplotype fequencies, suggesting they are also a 'J-type' stock (as compared to 'O-type' stocks further offshore).
- There are unique haplotypes found along the Pacific coast of Japan that are not found in the Sea of Japan or further offshore.
- There is no Hardy-Weinberg disequilibrium along the southern Pacific coast of Japan, thus no evidence for a mixture of two stocks there.

4. Two 'O-like' stocks in the Pacific Ocean, one of which is more 'nearshore' (OW) and one of which is found further offshore to the east (OE).

- There are differences in mtDNA and microsatellite DNA between coastal bycatch samples and 'nearshore' whaling samples (7CS and 7CN) in the Pacific.
- There are differences in mtDNA and microsatellite DNA between nearshore whaling samples (7CS and 7CN) and offshore whaling samples (8 and 9) in the Pacific.
- There is no significant Hardy-Weinberg disequilibrium in samples collected during commercial whaling operations from coastal stations along the Pacific coast of Japan (e.g., Kushiro and Sanriku) based on allozyme loci, consistent with a single stock in nearshore waters.
- There is no significant Hardy-Weinberg disequilibrium based on microsatellite DNA in areas 7CS, 7CN, 7WR+7E, or 8+9, thus providing no evidence for a mixture of two strongly differentiated stocks, such as O and J, in the areas where 'O-type' whales primarily occur.
- Whales in the Pacific Ocean have only winter conception dates (except in the coastal sub-areas 7CS and 7CN).

DESCRIPTION OF THE HYPOTHESIZED MIGRATION PATTERN OF EACH STOCK

The hypothesised migration patterns for each stock are summarised below.

(1) Y-stock is found year round in sub-area 5 (the Yellow Sea), and also partially migrates south into 1W in winter. Y-stock also potentially migrates into sub-area 6W (along the Korean coast of the East Sea/Sea of Japan) in spring and summer.

(2) JW-stock is found year round in sub-areas 6W and 6E (southern East Sea/Sea of Japan) and 10W and 10E (northern East Sea/Sea of Japan) but migrates into sub-areas 10 and 11 (northern East Sea/Sea of Japan) during April and then

into sub-area 12SW before later migrating south during winter. This stock is assumed to migrate south into sub-area 1E in winter.

(3) JE-stock is found along the east coast of Japan year round in sub-areas 2C, 7CS, and 7CN. This stock may be found in sub-area 2R during October- March which is consistent with the assumption the animals from the JE-stock migrate from breeding grounds that are to the south of sub-area 2. If they occur in sub-area 2R, it may only be in the western-most section of 2R.

(4) OW-stock is migratory and found in the Pacific Ocean off Japan. It moves along the east coast of Japan from sub-area 2R to sub-area 12SW by May and returns to the southerly sub-areas (e.g. 7CS, 7CN and 7WR) by October. It may also occur further offshore in sub-areas 7E and 2R.

(5) OE-stock is also migratory and found in the Pacific Ocean. It occurs further offshore (east) than the OW-stock and so is not found in the coastal sub-areas (2C, 7CS, and 7CN). It is thought to migrate further north than the OW-stock, being found in sub-areas 9N and 12NE during the summer. The proportion of the OE-stock in sub-area 9N is assumed to be low to avoid having part of this stock in a Residual Area when the surveys are undertaken.

(6) As a sensitivity test, a further stock (W-stock) is hypothesized that is sporadically found in sub-areas 9 and 9N (and perhaps 12NE).

DETAILS OF THE EVIDENCE FOR EACH STOCK

Detailed evidence for each stock proposed in stock structure hypothesis III is presented below. We reiterate that finding conclusive evidence to fully resolve the stock structure of western North Pacific minke whales is unlikely given   that no samples have been collected on the breeding grounds in winter when presumably "pure" stocks would exist.

(1) Evidence for a Yellow Sea stock (Y-stock)

The so-called "J-stock" was originally assumed to occur in both the Sea of Japan and the Yellow Sea, but a re-examination of available evidence suggests the possibility of a separate stock in the Yellow Sea. Minke whales are found year-round in the Yellow Sea, and mature whales and cow/calf pairs are seen in the Yellow Sea in summer, indicating the possibility of a separate stock there. Evidence for a separate stock comes from both biological and genetic data.

The most significant biological data comes from information on conception dates. From a large sample (n=158), Wang (1985) reported that pregnant minke whales caught in the northern Yellow Sea all had estimated conception dates between June and August. Wang (1985) also reported seeing cows with young calves in summer (May-July) in the Yellow Sea, consistent with an autumn conception and a gestation of ~10 months.

In contrast, Kato (1992) noted that the timing of conception in North Pacific minke whales was not uniform geographically, where samples from the Pacific Ocean (Sanriku and east of Hokkaido) had a peak of conception in winter, the northeastern Sea of Japan (east coast of Hokkaido) had a bimodal distribution with the largest peak in autumn and a smaller peak in winter (from a small sample), and the southern Sea of Okhotsk (north coast of Hokkaido) also had a bi-modal distribution with a large winter peak and a smaller autumn peak. If there was a single stock throughout the Yellow Sea and Sea of Japan, the whales in the northeastern Sea of Japan should only have autumn conception dates. The only other explanation for the observation of both autumn and winter conception dates in the northeastern Sea of Japan would require hypothesizing that whales from the Okhotsk Sea (an "O-stock"), which have winter conception dates, move into the northeastern Sea of Japan and the small sample of mixed conception dates represents a mixture of two stocks. There is no evidence for movements of O-stock whales from the Okhotsk Sea into the Sea of Japan, and no obvious explanation for such a movement pattern (which would represent a migration north from the Pacific Ocean into the Okhotsk Sea, and then a migration west and then south into the Sea of Japan). Moreover, a small sample (n=5) from sub-area 6E (the southwest coast of Japan) also supports the idea of a mix of winter (n=3) and summer (n=2) conception dates in the Sea of Japan (Annex E, this report). Omura and Sakiura (1956) indicate that North Pacific minke whale data support the possibility of two breeding seasons within single stocks.

Microsatellite DNA showed differences between winter Sea of Japan samples and the Yellow Sea but not between summer Sea of Japan samples and the Yellow Sea (Kanda et al. 2010a). This could be explained by a Yellow Sea stock moving northward along the Korean coast of the Sea of Japan in summer. Haplotype frequencies along the East Sea coast of Korea show a substantial amount of homozygous excess (6 out of 11 loci), consistent with a mixture of two stocks or some technical artefact (e.g., null alleles) (Baker et al. 2010b). Park et al. (2010) did not find differences in mtDNA between the Yellow Sea and Sea of Japan, but no comparison was done between the Yellow Sea and only winter Sea of Japan samples.

In conclusion, minke whales from this stock occur year round in the Yellow Sea, but it is also assumed there is some north-south migration, such that minke whales from the Yellow Sea (sub-area 5) move south into sub-area 1W in winter, and that some whales from this stock move into sub-area 6W (the Korean coast in the East Sea/Sea of Japan) in spring and summer. **Consequently**, samples from sub-area 5 represent the best proxy for "pure" Y-stock.

(2) Evidence for a Sea of Japan stock (JW stock)

The so-called "J-stock" was originally hypothesized as a stock that occurred in the East Sea/Sea of Japan. As discussed above in the previous section, under hypothesis III there is a separate stock in the Yellow Sea. Therefore, discussions in this section only refer to the Sea of Japan and adjacent waters to the east.

Numerous studies have found strong genetic differences between the Sea of Japan and Pacific Ocean, and there is no dispute about whether there are at least two stocks in these regions. The main areas of uncertainty are whether there are more than two stocks, and whether some of these stocks overlap in distribution in certain areas.

Korean versus Japanese coasts of the Sea of Japan
Survey data show minke whales distributed throughout the Sea of Japan with no obvious hiatus in distribution between the two coasts. Whales in the northeast and southeast Sea of Japan appear (from a relatively small sample) to have a bimodal distribution of conception dates, with peaks in both autumn and winter (Kato 1992, Annex E this report). Two different flipper colour patterns are also seen in the northeast Sea of Japan. For both the conception date and flipper colour pattern, the data could represent a mixture of two stocks from either side of the Sea of Japan. Genetic differences were found between bycatch samples from Korea and Japan in both mtDNA (Park et al. 2010) and microsatellite DNA (Kanda et al. 2010a), though in the case of the mtDNA the Korean dataset included samples from the Yellow Sea. In contrast, no genetic differences were found in a haplogroup analysis (Baker et al. 2010). As mentioned above, there is some evidence for a mixture of two stocks along the Korean coast of the Sea of Japan, which could be explained by Yellow Sea whales appearing there in summer. No sex bias or haplogroup-by-sex differences were found for Japanese Sea of Japan bycatch, suggesting a possible year-round presence of a non-migratory coastal stock (Baker et al. 2010). In summary, it is plausible there are different stocks on either side of the Sea of Japan, but the data are somewhat contradictory or are lacking in sufficient resolution or spatial extent to make definitive conclusions. Therefore we assume there is only one stock that occurs throughout the Sea of Japan, but note that this assumption may need to be revised if further data suggest differences between the two coasts.

Sea of Japan versus Pacific Ocean/Okhotsk Sea
As mentioned above, in a broad sense there are clear genetic differences between the Sea of Japan and the Pacific Ocean/Okhotsk Sea, but the detailed picture is more complex. For example, in stock structure hypotheses I and II it is proposed that whales from a so-called Sea of Japan stock ("J-stock") also occur along the Pacific (east) coast of Japan, and are distinct from the Pacific Ocean stock (called "O-stock"). While it is clear that there are whales along the Pacific coast of Japan that are genetically similar to Sea of Japan whales (a "J-like" stock), evidence is presented below that they actually represent a distinct stock (JE stock) from the Sea of Japan whales (JW stock). The most direct evidence for this comes from observed genetic differences between sub-areas 6E (Japanese coast in the Sea of Japan) and 2C (the southern Pacific coast of Japan). These areas should only contain "J-stock" animals (meaning it is not hypothesized that any O-stock animals mix into 2C from the offshore Pacific Ocean), so these genetic differences represent two "J-like" stocks. Oceanographic differences between the two coasts of Japan lend further plausibility to the existence of these two stocks.

Sub-areas 11 (Wada 1991) and 12SW in the Okhotsk Sea appear to have a mixture of stocks from the Sea of Japan and Pacific Ocean. This is reasonable as this would represent a convergence of whales migrating on either side of Japan, as suggested by many authors.

In conclusion, under stock structure hypothesis III, there is a single stock throughout the Sea of Japan found year-round. This stock does not move into the Pacific Ocean, but it may move into sub-areas 11 and 12 SW in the Okhotsk Sea in spring and summer. There is mixing of a Yellow Sea stock with this stock along the coast of Korea in summer. **Consequently**, sub-area 6E represents the best proxy for "pure" JW-stock (Baker et al. 2010b).

(3) Evidence for a coastal 'J-like' stock on the Pacific-side of Japan (JE stock)

There are many studies showing significant genetic differences between coastal and offshore waters on the Pacific-side of Japan when all samples are included (Park et al. 2010, Kanda et al. 2010a, Baker et al. 2010, Gaggiota and Durand 2010). The genetic signal in Pacific coastal waters off northern Honshu and Hokkaido (sub-area 7CN and 7CS) has been interpreted by some to be a mixture of 'J-type' whales from the Sea of Japan and 'O-type' whales (e.g., Kanda et al. 2010a, Park et al. 2010). However, there is no direct evidence (e.g., satellite tagging data) for movements of individual whales from the Sea of Japan into the Pacific Ocean. An alternate view is that this area contains a distinct stock characterised by intermediate haplotype frequencies (Baker et al. 2010). Stocks characterized by intermediate haplotype frequencies are well described in, for example, humpback whales, where stock divisions are supported by multiple lines of evidence (e.g., photo-ID records). Pairwise tests of differentiation for mtDNA haplogroups and haplotypes from different sample sets showed significant differences between most comparisons (Baker et al. 2010a, 2010b). These include bycatch samples from the northern Pacific coast of Japan (7BC), bycatch samples from the

southern Pacific coast of Japan (sub-area 2C), samples from the "coastal" whaling operation at Kushiro, samples from the "coastal" whaling operation at Sanriku, samples from the "offshore" whaling operation in the old sub-area 7W, and samples from whaling operations in sub-areas 8 and 9 (the eastern portion of old sub-area 7 (7E) did not have a large sample size which likely explains why this area was not significantly different from any other area in that analysis). The only pair-wise comparison with an adequate sample size that **did not** show a significant difference was the comparison between sub-areas 8 and 9. These genetic differences show a gradient with an increasing proportion of the AG haplogroup (depicted in the color green in Fig. 1) moving from the Sea of Japan, to the bycatch sample along the Pacific coast, to the coastal whaling operations, then to the offshore whaling operation in old sub-area 7, then to the offshore whaling operations in sub-areas 8 and 9 (Baker et al. 2010). This fits a model of "isolation-by-distance", with the most extreme genetic differences seen between the Sea of Japan and the offshore samples in sub-areas 8 and 9. The large degree of spatial genetic heterogeneity cannot be easily explained by a hypothesis of different mixing proportions of just two stocks. Further consideration of stocks in this area are discussed below in section 4.

As mentioned above, it is seen from the bycatch samples that whales along the southern Pacific coast of Japan (sub-area 2C) look most genetically similar to whales from the Sea of Japan (as seen by the prevalence of the GG and GA haplogroups), but they are significantly different in haplotype frequencies from whales along the Sea of Japan coast of Japan. This suggests there is a "J-like" stock on the southern Pacific coast of Japan, called here the JE stock. The bycatch samples represent samples collected closest to the coast (as the set nets are generally thought to be set within a few miles of the coast, and are often within a mile of the coast).

Bycatch samples from sub-area 2C were significantly different from all other sub-areas in the Pacific in both mtDNA and microsatellite DNA (Baker et al. 2010b, Slikas and Baker 2010), with one important exception – summer samples from 2C were not different from winter bycatch samples in sub-areas 7CS and 7CN in haplotype frequencies. This indicates the JE-stock occurs year-round along the Pacific coast of Japan, with apparent mixing in the north in summer from the influx of OW-stock (because samples from 2C are significantly different from summer bycatch samples in 7CS and 7CN). Baker et al. 2010b also provides further evidence for the existence of the JE-stock from the fact that the significant difference seen between sub-areas 6E and 2C appears to be primarily due to different frequencies of two shared haplotypes (#1 and #64). A frequency-based difference in shared haplotypes is consistent with the hypothesis of two related stocks (i.e, JW and JE), meaning these are both "J-type" stocks. Further evidence for a separate stock along the coast of Japan comes from the occurrence of many unique haplotypes in sub-areas 2C, 7CS, and 7CN that are not found in either the Sea of Japan or the offshore Pacific (Kanda et al. 2010b, this report), indicating there is a unique stock there rather than a mix of stocks from other areas.

Available biological data in the Pacific were not necessarily collected from locations that provide good evidence to resolve stock structure questions. In the study by Kato (1992) whales from Sanriku and Kuroshiro along the Pacific coast of Japan had only winter conception dates, whereas minke whales in the northeast Sea of Japan appear (from a small sample) to have a bimodal distribution of conception dates, with peaks in both autumn and winter. A re-analysis of conception data in the Pacific by spatial areas shows there are a mix of autumn and winter conception dates along the coast of Japan (sub-areas 7CS and 7CN), but only winter conception dates away from the coast (sub-areas 7WR, 7E, 8, and 9) (Annex E, this report). Given that whales from the Sea of Japan show both autumn and winter conception dates, this supports the hypothesis of a 'J-type' stock along the Pacific coast of Japan, with genetic differences between the coasts of Japan supporting the hypothesis there are two J-type stocks, one along the Sea of Japan coast of Japan and one along the Pacific coast of Japan. Additionally, the proportions of flipper colour type in the Sea of Japan whales were significantly different from the proportions seen in the coastal-based Sanriku catches (Kato et al. 1992). Unfortunately, no conception date data are available from sub-area 2C.

In conclusion, under hypothesis III, this stock is resident year-round in sub-areas 2C, 7CS, and 7CN. It is not clear whether part of this stock migrates, but it is possible that part of the stock migrates south into sub-area 2R in winter. Significant differences were found between the two coasts of Japan (sub-areas 2C versus 6E) in mtDNA (Baker et al. 2010) and in microsatellite DNA (Kanda et al. 2010a, using all samples), providing evidence that the whales in sub-area 2C represent a separate stock. **Consequently**, the bycatch samples from sub-area 2C are thought to represent the "pure" signal of the JE stock as there is no evidence for mixing of another stock in sub-area 2C.

(4) Evidence for two 'O-like' stocks in the Pacific Ocean (OW and OE)

The hypothesis of two 'O-like' stocks in the Pacific Ocean, one closer to Japan and one further offshore of Japan, is confounded by the presence of a coastal 'J-like' stock (JE) along the Pacific coast of Japan. Under hypothesis III, the JE stock only occurs in significant numbers very close to shore, and is best represented by data from bycatch samples. Therefore, evidence for the possibility of multiple 'O-like' stocks comes from comparing nearshore samples (meaning >10nm from land rather than coastal samples collected within a few nm of the coast) with areas farther offshore. As discussed above, there are pair-wise genetic differences in haplogroup proportions between samples from the "coastal" whaling operation at Kushiro, samples from the "coastal" whaling operation at Sanriku, samples from the "offshore" whaling operation in sub-area 7, and samples from whaling operations well offshore in sub-areas 8 and 9, indicating

there is genetic heterogeneity in areas away from the coast (Baker et al. 2010a). In a revised analysis using haplotype frequencies (Baker et al. 2010b), a better spatial stratification of the samples in the Pacific Ocean was used to examine this question more directly. The coastal bycatch samples (7BC) were significantly different from all areas further offshore. Samples from nearshore waters (7CS and 7CN) were significantly different from both the coastal bycatch samples (7BC) and from offshore waters (sub-areas 8 and 9). The sample size in sub-areas 7WR and 7E was small, but this area was also significantly different from the coastal sample (7BC). These genetic differences indicate there is a coastal stock along the Pacific coast of Japan represented by the 7BC samples (the "J-type" stock called JE), a nearshore stock in the Pacific represented by the 7CS and 7CN samples (an "O-type" stock called OW), and an offshore stock represented by the 8 and 9 samples (an "O-type" stock called OE). The sample sizes in sub-areas 7WR and 7E are not large enough to be able to resolve whether those areas are part of the OW stock, the OE stock, or both.

The samples from the coastal Sanriku and Kushiro hunts appear to represent the best proxy for the OW-stock, particularly after removal of samples collected within 10nm of the coast. The individual and combined samples from these two seasonal hunts show significant differences in both haplotypes and microsatellite loci with almost all other sub-areas and strata, including comparisons to 7BC, 8, and 9. However, samples from these two hunts show no differences with each other, at either mtDNA (Baker et al. 2010b) or microsatellite loci (Slikas and Baker 2010). The combined sample of Sanriku and Kushiro shows no difference between sexes for mtDNA (microsatellite analyses are in progress). These differences, and absence of differences, are consistent with seasonal hunting (spring for Sanriku and autumn for Kushiro) from a single migratory stock that is differentiated from the more coastal JE stock and the more offshore OE stock.

Although it has been proposed that the substantial heterogeneity in haplotype frequencies seen in the Pacific Ocean can be explained by a complex seasonal, sex- and age-biased mixing of 2 stocks, e.g., a 'core J' and a 'core O', we consider this less parsimonious than the hypothesis of 3 stocks, with one "J-like" stock (JE), and two "O-like" stocks (OE and OW), where OW shows haplogroup frequencies that are intermediate to JE and OE. The absence of a strong haplogroup (or haplotype)-by-sex interaction in coastal waters is inconsistent with the prediction of a sex-biased mixing of just two stocks (Baker et al. 2010, Baker et al. 2010b). In support of this ieda, the analysis of Gaggiota and Durand (2010) concludes there is genetic heterogeneity in the Pacific Ocean, and their conclusions still hold when the analysis is restricted to what are thought to be 'O-only' type whales.

Additional evidence against a complex mixing of two distinct stocks comes from genetic analyses of catches from commercial whaling before the moratorium, as a test of Hardy-Weinberg disequilibrium can be used to examine whether there is evidence for mixing of two stocks in an area. Wada (1984) provided the first genetic evidence for a distinct stock of minke whales in the Sea of Japan, based on a comparison of allele frequencies of the Adh-1 allozyme locus. Wada (1991) updated this analysis comparing the genotype frequencies of n=903 whales taken by Japanese small-type coastal whaling north of Hokkaido (area A), in Kuroshiro (area B), Sanriku (area C) and southeast of Honshu (area D). In sub-area 11 (north of Hokkaido), the results showed a significantly higher frequency of the Adh-1D allele and a deviation of genotype frequencies from Hardy-Weinberg (an excess of homozygotes), particularly in the month of April, compared to sub-area 7CS (Sanriku) and sub-area 7CN (Kuroshiro). Wada (1991) attributed the deviation in sub-area 11 to a mixing of whales from the Sea of Japan, where the frequency of Adh-1D is nearly fixed (Adh-1D = 0.93, with whales from the Pacific coast, where Adh-1D = 0.31. In Sanriku and Kuroshiro, Wada (1991) found no evidence of deviation from Hardy-Weinberg equilibrium in analyses of the total sample, or in stratification by year, month, sex or age class. In summary, the allele frequencies and Hardy-Weinberg equilibrium of the Adh-1 locus in the small-type coastal whaling on the Pacific side of Japan in sub-areas 7CN, as reported by Wada (1991), are inconsistent with the simple mixing of two strongly differentiated stocks (e.g., J and O), but are consistent with the occurrence of a third stock with intermediate haplotype frequencies (e.g., OW).

Microsatellite DNA data can also be used to examine evidence for mixing of two stocks. Kanda et al. (2009) suggested that the existence of deviation from Hardy-Weinberg equilibrium found in some microsattelite loci in the combined samples from all Pacific areas is evidence for the mixing of core J and O stocks in that large area. However, that result is consistent with our hypothesis, as Kanda et al. (2009) pooled samples from the coast (now sub-areas 7CS and 7CN) to far offshore in sub-areas 8 and 9, which includes samples from 3 stocks under Hypothesis III (JE, OW, and OE). Tests for Hardy-Weinberg disequilibrium were done on a finer spatial scale in Slikas and Baker (2010). Because tests for Hardy-Weinberg deviation are applied independently at each loci, it is appropriate to use a simple Bonferroni correction for testing significance. For the tests performed in Table 4 of Slikas and Baker (2010), the critical value becomes 0.003 (a significance level of 0.05 divided by 16 loci). Therefore, using that critical value there is no evidence for deviation from Hardy-Weinberg equilibrium in population strata 2BC, 7CS, 7CN, 7WR+7E, and 8+9. One out of 16 loci (GT509) shows deviation in 7BC; this could be the result of mixing between the JE and OW stocks in summer that is indicated by the significant difference in haplotype frequencies seen between winter and summer samples in 7BC (Baker et al. 2010b). The one population stratum that shows substantial disequilibrium (6 out of 11 loci, using a critical value of 0.0045 from 0.05 divided by 11 loci) is 6W, the east coast of Korea. Therefore, there is no evidence that the significant genetic differences seen between the Pacific coast (7BC), the nearshore Pacific (7CN and 7CN), and the offshore Pacific (8 and 9) are explained by these areas containing different mixtures of just two stocks. Instead, these three areas represent three stocks, JE, OW, and OE.

In conclusion, stock structure hypothesis III includes two "O-like" stocks, in addition to the coastal JE stock. OW-stock is migratory and found in the Pacific Ocean off Japan. It appears to seasonally occur in Pacific coastal waters of Japan in spring and summer during migration, as it moves north from sub-areas 2R, passing through sub-areas 7CS and 7CN. Part of the stock may stay offshore and moves into sub-areas 7WR and possibly 7E. Some portion of the stock, likely to be mostly mature whales, appears to move north into the Okhotsk Sea in spring and summer, arriving in sub-areas 11 and 12SW by May, and returns to the southerly sub-areas by October. **Consequently**, samples from sub-areas 7CS (April and May) and 7CN (Sept. and Oct.) excluding samples within 10nm of the coast, represent the best proxy for the OW-stock, as this essentially represents the migratory pulse with samples from the spring Sanriku hunt and the autumn Kushiro hunt. Excluding samples within 10nm of the coast essentially excludes bycatch samples from close to the coast that contain individuals from JE-stock.

OE-stock is also migratory and found in the Pacific Ocean. It occurs further offshore (east) than the OW-stock in sub-areas 8, 9, and possibly 7E and 7WR, but is not found in the coastal sub-areas (2C, 7CS, and 7CN). It is hypothesized to migrate further north than the OW-stock, being found in sub-areas 9N and 12NE during the summer. The proportion of the OE-stock in sub-area 9N is assumed to be low to avoid having part of this stock in a Residual Area when the surveys are undertaken. Sub-areas 8 and 9 do not differ from each other at either mtDNA haplotypes or microsatellite loci, but do differ from all other sub-areas or strata, except for the relatively small sample from the adjacent 7WR and 7E. **Consequently**, sub-areas 8 and 9 represent the best proxy for the OE-stock (excluding samples from the old 9W sub-area in 1995).

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Annex G

NPM Mixing Matrices

Notes:

- Where there are X's in the tables from the September meeting, the entries are shown in brackets.
- For the C-stock sensitivity test to hypothesis III in 12NE, the entries for the C stock are shown in grey (i.e. C)

Hypothesis I

'J' indicates the presence of J-stock and 'O' indicates the presence of O-stock

Table 1a. The distribution of stocks by sub-area and month for age 4 juveniles {and ages 5-9 in brackets}.

Mon Juv	1W	1E	2C	2R	3	4	5	6W	6E	7CS	7CN	7WR	7E	8	9	9N	10W	10E	11	12SW	12NE	13
J-M	J	J	JO	O	O	O	J	J	J	JO	JO						J	J				
Apr	J	J	JO	O	O	O	J	J	J	JO	JO	O	O				J	J	JO			
May	J	J	JO				J	J	J	JO	JO	O	O				J	J	JO	O	O	
Jun	J	J	JO				J	J	J	JO	JO	O	O				J	J	JO	O	O	
Jul	J	J	JO				J	J	J	JO	JO	O	O				J	J	JO	O	O	
Aug	J	J	JO				J	J	J	JO	JO	O	O				J	J	JO	O	O	
Sep	J	J	JO				J	J	J	JO	JO	O	O				J	J	JO	J		
O-D	J	J	JO	O	O	O	J	J	J	JO	JO						J	J	J			

Table 1b. The distribution of stocks by sub-area and month for adult males

Mon M	1W	1E	2C	2R	3	4	5	6W	6E	7CS	7CN	7WR	7E	8	9	9N	10W	10E	11	12SW	12NE	13
J-M	J	J	JO	O	O	O	J	J	J	JO	JO						J	J				
Apr			JO	O	O	O	J	J	J	JO	JO	O	O	O	O		J	J	JO	JO		
May			J				J	J	J	JO	JO	O	O	O	O	O	J	J	JO	JO	O	
Jun			J				J	J	J	JO	JO	O	O	O	O	O	J	J	JO	JO	O	
Jul			J				J	J	J	JO	JO	O	O	O	O	O	J	J	JO	JO	O	
Aug			J				J	J	J	JO	JO	O	O	O	O	O	J	J	JO	JO	O	
Sep	J	J	J				J	J	J	JO	JO	O	O	O	O	O	J	J	O	O	O	
O-D	J	J	JO	O	O	O	J	J		JO	JO											

Table 1c. The distribution of stocks by sub-area and month for adult females.

Mon F	1W	1E	2C	2R	3	4	5	6W	6E	7CS	7CN	7WR	7E	8	9	9N	10W	10E	11	12SW	12NE	13
J-M	J	J	JO	O	O	O	J	J	J	JO	JO						J	J				
Apr			JO	O	O	O	J	J	J	JO	JO	O	O	O	O		J	J	JO	JO		
May			J				J	J	J	JO	JO	O	O	O	O	O	J	J	JO	JO	O	
Jun			J				J	J	J	JO	JO	O	O	O	O	O	J	J	JO	JO	O	
Jul			J				J	J	J	JO	JO	O	O	O	O	O	J	J	JO	JO	O	
Aug			J				J	J	J	JO	JO	O	O	O	O	O	J	J	JO	JO	O	
Sep	J	J	J				J	J	J	JO	JO	O	O	O	O	O	J	J	O	O	O	
O-D	J	J	JO	O	O	O	J	J		JO	JO											

Hypothesis I Sensitivity test including C-stock

'J' indicates the presence of J-stock, 'O' indicates the presence of O-stock, and 'C' indicates the presence of C-stock.

Table 2a. The distribution of stocks by sub-area and month for age 4 juveniles (and ages 5-9 in brackets).

Mon Juv	1W	1E	2C	2R	3	4	5	6W	6E	7CS	7CN	7WR	7E	8	9	9N	10W	10E	11	12SW	12NE	13
J-M	J	J	JO	O	O	O	J	J	J	JO	JO						J	J				C
Apr	J	J	JO	O	O	O	J	J	J	JO	JO	O	O				J	J	JO			C
May	J	J	JO				J	J	J	JO	JO	O	O				J	J	JO	O	O	C
Jun	J	J	JO				J	J	J	JO	JO	O	O				J	J	JO	O	O	C
Jul	J	J	JO				J	J	J	JO	JO	O	O				J	J	JO	O	O	C
Aug	J	J	JO				J	J	J	JO	JO	O	O				J	J	JO	O	O	C
Sep	J	J	JO				J	J	J	JO	JO	O	O				J	J	JO	J		C
O-D	J	J	JO	O	O	O	J	J	J	JO	JO						J	J	J			C

Table 2b. The distribution of stocks by sub-area and month for adult males.

Mon M	1W	1E	2C	2R	3	4	5	6W	6E	7CS	7CN	7WR	7E	8	9	9N	10W	10E	11	12SW	12NE	13
J-M	J	J	JO	O	O	O	J	J	J	JO	JO						J	J				C
Apr			JO	O	O	O	J	J	J	JO	JO	O	O	O	OC		J	J	JO	JO		C
May			J				J	J	J	JO	JO	O	O	O	OC	OC	J	J	JO	JO	O	C
Jun			J				J	J	J	JO	JO	O	O	O	OC	OC	J	J	JO	JO	O	C
Jul			J				J	J	J	JO	JO	O	O	O	OC	OC	J	J	JO	JO	O	C
Aug			J				J	J	J	JO	JO	O	O	O	OC	OC	J	J	JO	JO	O	C
Sep	J	J	J				J	J	J	JO	JO	O	O	O	OC	OC	J	J	O	O	O	C
O-D	J	J	JO	O	O	O	J	J		JO	JO											C

Table 2c. The distribution of stocks by sub-area and month for adult females.

Mon F	1W	1E	2C	2R	3	4	5	6W	6E	7CS	7CN	7WR	7E	8	9	9N	10W	10E	11	12SW	12NE	13
J-M	J	J	JO	O	O	O	J	J	J	JO	JO						J	J				C
Apr			JO	O	O	O	J	J	J	JO	JO	O	O	O	OC		J	J	JO	JO		C
May			J				J	J	J	JO	JO	O	O	O	OC	OC	J	J	JO	JO	O	C
Jun			J				J	J	J	JO	JO	O	O	O	OC	OC	J	J	JO	JO	O	C
Jul			J				J	J	J	JO	JO	O	O	O	OC	OC	J	J	JO	JO	O	C
Aug			J				J	J	J	JO	JO	O	O	O	OC	OC	J	J	JO	JO	O	C
Sep	J	J	J				J	J	J	JO	JO	O	O	O	OC	OC	J	J	O	O	O	C
O-D	J	J	JO	O	O	O	J	J		JO	JO											C

Hypothesis II

'Y' indicates the presence of Y-stock, 'J' indicates the presence of J-stock and 'O' indicates the presence of O-stock

Table 3a. The distribution of stocks by sub-area and month for age 4 juveniles (and ages 5-9 in brackets).

Mon Juv	1W	1E	2C	2R	3	4	5	6W	6E	7CS	7CN	7WR	7E	8	9	9N	10W	10E	11	12SW	12NE	13
J-M	Y	J	JO	O	O	O	Y	J	J	JO	JO						J	J				
Apr	Y	J	JO	O	O	O	Y	J	J	JO	JO	O	O				J	J	JO			
May	Y	J	JO				Y	J	J	JO	JO	O	O				J	J	JO	O	O	
Jun	Y	J	JO				Y	J	J	JO	JO	O	O				J	J	JO	O	O	
Jul	Y	J	JO				Y	YJ	J	JO	JO	O	O				J	J	JO	O	O	
Aug	Y	J	JO				Y	YJ	J	JO	JO	O	O				J	J	JO	O	O	
Sep	Y	J	JO				Y	YJ	J	JO	JO	O	O				J	J	JO	J		
O-D	Y	J	JO	O	O	O	Y	J	J	JO	JO						J	J	J			

Table 3b. The distribution of stocks by sub-area and month for adult males.

Mon M	1W	1E	2C	2R	3	4	5	6W	6E	7CS	7CN	7WR	7E	8	9	9N	10W	10E	11	12SW	12NE	13
J-M	Y	J	JO	O	O	O	Y	J	J	JO	JO						J	J				
Apr	Y		JO	O	O	O	Y	J	J	JO	JO	O	O	O	O		J	J	JO	JO		
May	Y		J				Y	J	J	JO	JO	O	O	O	O	O	J	J	JO	JO	O	
Jun	Y		J				Y	J	J	JO	JO	O	O	O	O	O	J	J	JO	JO	O	
Jul	Y		J				Y	YJ	J	JO	JO	O	O	O	O	O	J	J	JO	JO	O	
Aug	Y		J				Y	YJ	J	JO	JO	O	O	O	O	O	J	J	JO	JO	O	
Sep	Y	J	J				Y	YJ	J	JO	JO	O	O	O	O	O	J	J	O	O	O	
O-D	Y	J	JO	O	O	O	Y	J		JO	JO											

Table 3c. The distribution of stocks by sub-area and month for adult females.

Mon F	1W	1E	2C	2R	3	4	5	6W	6E	7CS	7CN	7WR	7E	8	9	9N	10W	10E	11	12SW	12NE	13
J-M	Y	J	JO	O	O	O	Y	J	J	JO	JO						J	J				
Apr	Y		JO	O	O	O	Y	J	J	JO	JO	O	O	O	O		J	J	JO	JO	O	
May	Y		J				Y	J	J	JO	JO	O	O	O	O	O	J	J	JO	JO	O	
Jun	Y		J				Y	J	J	JO	JO	O	O	O	O	O	J	J	JO	JO	O	
Jul	Y		J				Y	YJ	J	JO	JO	O	O	O	O	O	J	J	JO	JO	O	
Aug	Y		J				Y	YJ	J	JO	JO	O	O	O	O	O	J	J	JO	JO	O	
Sep	Y	J	J				Y	YJ	J	JO	JO	O	O	O	O	O	J	J	O	O	O	
O-D	Y	J	JO	O	O	O	Y	J		JO	JO											

Hypothesis III

'Y' indicates the presence of Y-stock, 'Jw' indicates the presence of JW-stock, 'Je' indicates the presence of   JE-stock,'Ow' indicates the presence of OW-stock, and 'Oe' indicates the presence of OE-stock.

Table 4a. The distribution of stocks by sub-area and month for age 4 juveniles (and ages 5-9 in brackets).

Mon											Sub - Area											
	1W	1E	2C	2R	3	4	5	6W	6E	7CS	7CN	7WR	7E	8	9	9N	10W	10E	11	12SW	12NE	13
J-M	Y	Jw	Je	OwOe	Oe	Oe	Y	Jw	Jw	Je	Je	Ow					Jw	Jw				
Apr	Y	Jw	Je	OwOe	Oe	Oe	Y	Jw	Jw	JeOw	JeOw	OwOe	Oe	Oe	Oe		Jw	Jw	JwOwOe			
May	Y	Jw	Je				Y	Jw	Jw	JeOw	JeOw	OwOe	Oe	Oe	Oe	Oe	Jw	Jw	JwOwOe	OwOe		Oe
Jun	Y	Jw	Je				Y	Jw	Jw	JeOw	JeOw	OwOe	Oe	Oe	Oe	Oe	Jw	Jw	JwOwOe	OwOe		Oe
Jul	(Y)	(Jw)	Je				Y	YJw	Jw	JeOw	JeOw	OwOe	Oe	Oe	Oe	Oe	Jw	Jw	JwOwOe	OwOe		Oe
Aug	(Y)	(Jw)	Je				Y	YJw	Jw	JeOw	JeOw	OwOe	Oe	Oe	Oe	Oe	Jw	Jw	JwOwOe	OwOe		Oe
Sep	(Y)	(Jw)	Je				Y	YJw	Jw	JeOw	JeOw	OwOe	Oe	Oe	Oe	Oe	Jw	Jw	JwOwOe			
O-D	Y	Jw	Je	OwOe	Oe	Oe	Y	Jw	Jw	Je	Je	Ow					Jw	Jw	Jw			

Table 4b. The distribution of stocks by sub-area and month for adult males.

Mon											Sub - Area											
	1W	1E	2C	2R	3	4	5	6W	6E	7CS	7CN	7WR	7E	8	9	9N	10W	10E	11	12SW	12NE	13
J-M	Y	Jw	Je	(Je)OwOe	Oe	Oe	Y	Jw	Jw	Je	Je	Ow					Jw	Jw				
Apr	Y	Jw	Je	OwOe	Oe	Oe	Y	Jw	Jw	JeOw	JeOw	OwOe	Oe	Oe	Oe		Jw	Jw	JwOwOe			
May	Y	Jw	Je				Y	Jw	Jw	JeOw	JeOw	OwOe	Oe	Oe	Oe	Oe	Jw	Jw	JwOwOe	JwOwOe		Oe
Jun	Y	Jw	Je				Y	Jw	Jw	JeOw	JeOw	OwOe	Oe	Oe	Oe	Oe	Jw	Jw	JwOwOe	JwOwOe		Oe
Jul	(Y)	(Jw)	Je				Y	YJw	Jw	JeOw	JeOw	OwOe	Oe	Oe	Oe	Oe	Jw	Jw	JwOwOe	JwOwOe		Oe
Aug	(Y)	(Jw)	Je				Y	YJw	Jw	JeOw	JeOw	OwOe	Oe	Oe	Oe	Oe	Jw	Jw	JwOwOe	JwOwOe		Oe
Sep	(Y)	(Jw)	Je				Y	YJw	Jw	JeOw	JeOw	OwOe	Oe	Oe	Oe	Oe	Jw	Jw	JwOwOe	OwOe		Oe
O-D	Y	Jw	Je	(Je)OwOe	Oe	Oe	Y	?		Je	Je	Ow										

Table 4c. The distribution of stocks by sub-area and month for adult females.

Mon											Sub - Area											
	1W	1E	2C	2R	3	4	5	6W	6E	7CS	7CN	7WR	7E	8	9	9N	10W	10E	11	12SW	12NE	13
J-M	Y	Jw	Je	(Je)OwOe	Oe	Oe	Y	Jw	Jw	Je	Je	Ow					Jw	Jw				
Apr	Y	Jw	Je	OwOe	Oe	Oe	Y	Jw	Jw	JeOw	JeOw	OwOe	Oe	Oe	Oe		Jw	Jw	JwOwOe	OwOe		Oe
May	Y	Jw	Je				Y	Jw	Jw	JeOw	JeOw	OwOe	Oe	Oe	Oe	Oe	Jw	Jw	JwOwOe	JwOwOe		Oe
Jun	Y	Jw	Je				Y	Jw	Jw	JeOw	JeOw	OwOe	Oe	Oe	Oe	Oe	Jw	Jw	JwOwOe	JwOwOe		Oe
Jul	(Y)	(Jw)	Je				Y	YJw	Jw	JeOw	JeOw	OwOe	Oe	Oe	Oe	Oe	Jw	Jw	JwOwOe	JwOwOe		Oe
Aug	(Y)	(Jw)	Je				Y	YJw	Jw	JeOw	JeOw	OwOe	Oe	Oe	Oe	Oe	Jw	Jw	JwOwOe	JwOwOe		Oe
Sep	(Y)	(Jw)	Je				Y	YJw	Jw	JeOw	JeOw	OwOe	Oe	Oe	Oe	Oe	Jw	Jw	JwOwOe	OwOe		Oe
O-D	Y	Jw	Je	(Je)OwOe	Oe	Oe	Y	?		Je	Je	Ow										

Annex H
Catch Appendix
[See separate copy]

Annex I
The Specifications for the Trials
[See separate copy]

Annex J

An example of the use of mixing matrices

André E. Punt, Toshihide Kitakado, Cherry Allison & Carryn de Moor

Consider the case in which there are three stocks (A, B and C) and two areas (I and II). It is postulated that (a) stock A is only found in Area I, (b) stock B is found in areas I and II and (c) stock C is only found in area II. i.e. the Distribution matrix is

Area	Stocks
I	A B
II	B C

This leads to the presence absence matrix in Table 1.

Table 1. Presence-absence matrix for the example.

Stock	Area	
	I	II
A	1	0
B	1	1
C	0	1

Now, assume that the available data are (a) abundance estimates for areas I and II (from surveys) and (b) mixing proportions (proportions of stock B in areas I and II). The data are summarised in Table 2.

Table 2. The data for the example.

Datum	Value
Proportion of Stock B in area I	0.2
Proportion of Stock B in area II	0.6
Abundance in area I	1000
Abundance in area II	2000

The presence-absence matrix can be represented as a mixing matrix (Table 3), which indicates the estimable parameters (in this case only one). There is a '1' for stock B in area II to ensure that all of the parameters are identifiable (there must be a '1' in each row, i.e. for each stock).

Table 3. Mixing matrix for the example.

Stock	Area	
	I	II
A	1	0
B	γ	1
C	0	1

The 'unknowns' are therefore N_A, N_B, and N_C, the numbers in stocks A, B and C (these would normally be predicted by the operating model but lets just assume that the populations are constant over time) and γ. The values for these parameters are obtained by solving the equations:

$$1000 = N_A + \tfrac{\gamma}{1+\gamma} N_B \qquad \text{Abundance in area I}$$

$$2000 = N_C + \tfrac{1}{1+\gamma} N_B \qquad \text{Abundance in area II}$$

$$0.2 = \tfrac{\gamma}{1+\gamma} N_B / (N_A + \tfrac{\gamma}{1+\gamma} N_B) \qquad \text{Proportion of Stock B in area I}$$

$$0.6 = \tfrac{1}{1+\gamma} N_B / (N_C + \tfrac{1}{1+\gamma} N_B) \qquad \text{Proportion of Stock B in area II}$$

Solving these equations leads to the following estimates: N_A=800, N_B=1400, N_C=800, γ=1/6. The predictions by stock and area based on these estimates are listed in Table 4. It is easily show that the predictions satisfy the data in Table 2.

Table 4. Number of animals by stock and area based on the estimates for the parameters.

Stock	Area		Stock Total
	I	II	
A	800	0	800
B	200	1200	1400
C	0	800	800
Area Total	1000	2000	

Note: the number of fixed values (e.g. '1' in Table 3) depends on the number of areas in which each stock is found). Also, given the very simple set up here, the model mimics the data exactly. This will not be true in general.

Note: If there was a third area (III) in which stocks B and C are found, and there was an abundance estimate and stock B mixing proportion, the mixing matrix would be modified to:

Stock	Area		
	I	II	III
A	1	0	0
B	γ_1	0	γ_2
C	0	1	γ_3

Annex K

Availability of abundance estimates for Implementation process

AN, BUTTERWORTH, HAKAMADA, MIYASHITA, WADE AND KITAKADO (CHAIR)

This is a compilation of the three different types of surveys which have been conducted so far by Japan and Korea (the details are shown in their original primary papers, SC/D10/NPM 11, 12 and 15) to show when and where the surveys were done. Abbreviations used in the tables below are as follows:

KD: Korean dedicated survey,

JD: Japanese dedicated survey,

JR: JARPN and JARPN II.

Table 1. Overview of availability of abundance estimates 'subarea-by-year' 'and 'subarea-by-month'

Year	Sub-area																					
	1W	1E	2C	2R	3	4	5	6W	6E	7CS	7CN	7W	7E	8	9	9N	10W	10E	11	12SW	12NE	13
1990													JD	JD	JD				JD	JD	JD	
1991											JD											
1992																					JD	
1993																						
1994															JR							
1995															JR							
1996																						
1997																						
1998																						
1999																			JD			
2000								KD (N2)														
2001							KD (N1)															
2002								KD (N2)	JD			JR	JR	JR	JR			JD				
2003								KD (N2)	JD	JR	JR	JR	JR	JR	JR			JD	JD (N4)	JD	JD (N5)	
2004							KD (N1)		JD	JR		JR	JR	JR	JR			JD				
2005								KD (N2)						JD/JR*	JD/JR*	JD (N3)		JD				
2006								KD (N2)		JR		JR	JR	JR	JR		JD					
2007								KD (N2)		JR		JR	JR	JR	JR			JD	JD (N4)			
2008							KD (N1)			JR	JR	JR	JR	JR	JR							
2009								KD (N2)						JR	JR							
2010					JD	JD		KD (N2)				JR	JR	JR	JR							JD

Month	Sub-area																					
	1W	1E	2C	2R	3	4	5	6W	6E	7CS	7CN	7W	7E	8	9	9N	10W	10E	11	12SW	12NE	13
Jan-Mar																						
Apr							KD (N1)	KD (N2)														
May									JD	JR	JR	JR	JR	JR	JR		JD	JD				
Jun										JR		JR	JR	JR	JR							JD
Jul					JD	JD				JR	JR	JR	JR	JR	JR							JD
Aug												JR	JR	JD/JR*	JD/JR*	JD			JD(N4)	JD	JD (N5)	
Sep														JD/JR*	JD/JR*							
Oct-Dec																						

Note 1: 13% of 5
Note 2: 14% of 6W
Note 3: 68% of 9N
Note 4: 20~34% of 11
Note 5: 46% of 12
*JD/JR: coverage by JD is poor

Remark:

1) In sub-areas 5, 6W, 6E, 9N, 10W, 10E, 11, 12SW and 12NE, independent abundance etimates are not available for two consecutive months. This is the case for other sub-areas (see Table 2).
2) In sub-area 5 and 6W, although the area coverage are small (at most 14%), the tracklines of surveys were allocated in a good manner in their predetermined survey blocks.

Table 2. Abundance estimates and their associated CVs with information on the survey coverage

SA	Year	Season	Survey type[1]	Mode[2]	Areal coverage (%)	STD estimate[3]	CV[4]	Conditioning	Rationale	Source
1W	NA									
1E	NA									
2C	NA									
2R	NA									
3	2010	Jul-Aug	JD					No at this time	Not available yet	
4	2010	Jul-Aug	JD					No at this time	Not available yet	
5	2000									
	2001	Apr-May	KD	NC	13.0	1,534	0.523	Min	Low area coverage	SC/D10/NPM15
	2002									
	2003									
	2004	Apr-May	KD	NC	13.0	799	0.321	Min	Low area coverage	ditto
	2005									
	2006									
	2007									
	2008	Apr-May	KD	NC	13.0	680	0.372	Min	Low area coverage	ditto
	2009									
	2010									
6W	2000	Apr-May	KD	NC	14.3	549	0.419	Min	Low area coverage	SC/D10/NPM15
	2001									
	2002	Apr-May	KD	NC	14.3	391	0.614	Min	Low area coverage	ditto
	2003	Apr-May	KD	NC	14.3	485	0.343	Min	Low area coverage	ditto
	2004									
	2005	Apr-May	KD	NC	14.3	336	0.317	Min	Low area coverage	ditto
	2006	Apr-May	KD	NC	14.3	459	0.516	Min	Low area coverage	ditto
	2007	Apr-May	KD	NC	14.3	574	0.437	Min	Low area coverage	ditto
	2008									
	2009	Apr-May	KD	NC	14.3	884	0.286	Min	Low area coverage	ditto
	2010	Apr-May	KD		14.3			No at this time	Not available yet	
6E	2000									
	2001									
	2002	May-Jun	JD	NC	100.0	1,795	0.458	Yes	Use only northern part due to possible double counting*	SC/D10/NPM11
	2003	May-Jun	JD	NC	100.0	1,059	0.322	Yes	Use only northern part due to possible double counting*	ditto
	2004	May-Jun	JD	NC	79.1	727	0.372	Yes	Use only northern part due to possible double counting*	ditto
	2005									
	2006								*Sentivity:	
	2007								Use 2002 and 2003 with 2004 extrapolated to full area	
	2008								using a ratio approach (see Section 4.1)	
	2009									
	2010									
7CS	2000									
	2001									
	2002									
	2003	May	JR	NC	62.6	335	0.683	No	Low coverage of intended trackline	SC/D10/NPM12
	2004	May	JR	NC	100.0	736	0.447	Yes		ditto
	2005									ditto
	2006	Jun - Jul	JR	NC	100.0	2,391	1.080	Yes		
	2007	Jun - Jul	JR	NC	100.0	0	-	No	Less on-effort trackline than planned	ditto
	2008	Jul	JR					No at this time	Not available yet	
	2009		JR							
	2010		JR							
7CN	1991	Aug-Sep	JD	NC				No	Not available yet	
	2003	May	JR	NC	75.4	270	0.71	Yes		SC/D10/NPM12
	2008	Jul	JR	NC				No at this time	Not available yet	

Table 2 (continued)

SA	Year	Season	Survey type[1]	Mode[2]	Areal coverage (%)	STD estimate[3]	CV[4]	Conditioning	Rationale	Source
7W	2000									
	2001									
	2002	Aug	JR	NC	30.5	0	-	No	Low area coverage and; low coverage on intended trackline	SC/D10/NPM12
	2003	May - Jun	JR	NC	54.2	551	0.374	Min	Low area coverage	ditto
	2004	May - Jun	JR	NC	88.8	506	0.404	Yes		ditto
	2005									
	2006	Jun - Jul	JR	NC	88.8	0	-	No	Low area coverage and; low coverage on intended trackline	ditto
	2007	Jun - Jul	JR	NC	88.8	368	0.834	Yes		ditto
	2008	Jul	JR	NC				No at this time	Not available yet	
	2009		JR							
	2010	Jul	JR	NC				No at this time	Not available yet	
7E	1990	Aug-Sep	JD	NC	?	791	1.848	No	CV too high to be meaningful	JCRM 6: 124
	2000									
	2001									
	2002									
	2003	May - Jun	JR	NC	26.3	303	0.842	No	Low area coverage	SC/D10/NPM12
	2004	May - Jun	JR	NC	57.1	290	0.577	Yes		ditto
	2005									
	2006	May - Jun	JR	NC	57.1	438	0.917	Yes		ditto
	2007	Jun - Jul	JR	NC	57.1	0	-	Yes		ditto
	2008	Jul	JR	NC				No at this time	Not available yet	
	2009		JR							
	2010	Jul	JR	NC				No at this time	Not available yet	
8	1990	Aug-Sep	JD	NC	To come	1,057	To come	Yes	In other years, no whales observed in area not covered	JCRM 6: 124
	2000									
	2001									
	2002	Jun - Jul	JR	NC	65.0	0	-	Yes		SC/D10/NPM12
	2003	Jul	JR	NC	13.1	147	0.843	No	Low area coverage	ditto
	2004	Jun	JR	NC	40.5	691	0.496	Yes	In other years, no whales observed in area not covered	ditto
	2005	May - Jul	JR	NC	65.0	177	0.749	Yes		ditto
	2006	May - Jul	JR	NC	65.0	481	0.650	Yes		ditto
	2007	Jun - Jul	JR	NC	65.0	278	0.983	Yes		ditto
	2008	Jul-Aug	JR	NC				No at this time	Not available yet	
	2009	May-Jun	JR	NC				No at this time	Not available yet	
	2010	Jul-Aug	JR	NC				No at this time	Not available yet	
	2005	Aug.-Sep.	JD	IO-PS	27.3			No at this time	Low area coverage	
9	1990	Aug-Sep	JD	NC	35.0	8264	0.396	Yes		JCRM 6: 124
	1994	Jul-Aug	JR	NC	42.5	3065	0.423	No	Low area coverage	SC/D10/NPM12
	1994	Aug-Sep	JR	NC	32.9	973	0.628	No	Low area coverage	ditto
	1995	Jun	JR	NC	54.7	1348	0.272	No	Low area coverage	ditto
	1995	Jul-Aug	JR	NC	13.2	994	0.396	No	Low area coverage	ditto
	1995	Aug	JR	NC	28.5	399	0.636	No	Low area coverage	ditto
	2000									
	2001									
	2002	Jun- Jul	JR	NC	62.4	702	0.806	No	Dense northern area not covered; low coverage of intended trackline in south	SC/D10/NPM12
	2003	Jul-Sep	JR	NC	33.2	3670	0.282	Min	Survey not co-incident with density peak in Aug-Sep	ditto
	2004	Jun-Jul	JR	NC	42.6	496	0.649	No	Dense northern area not covered; low coverage of intended trackline in south	ditto
	2005	May-Aug	JR	NC	63.0	970	0.610	No	Time gap during the period of survey, hence linkage to month unclear	ditto
	2006	May-Aug	JR	NC	86.9	2680	0.437	No	Time gap during the period of survey, hence linkage to month unclear	ditto
	2007	May-Jul	JR	NC	86.9	189	1.439	No	CV too high to be meaningful	ditto
	2008	Aug	JR					No at this time	Not available yet	
	2009	May-Jun	JR					No at this time	Not available yet	
	2010	Jun-Aug	JR					No at this time	Not available yet	
	2005	Aug.-Sep.	JD	IO-PS	23.7			No	Low area coverage	
9N	2005	Aug-Sep	JD	IO-PS	67.8	To come		Yes		From Miyashita

Table 2 (continued)

SA	Year	Season	Survey type[1]	Mode[2]	Areal coverage (%)	STD estimate[3]	CV[4]	Conditioning	Rationale	Source
10W	2006	May-Jun	JD	IO-PS	59.9	To come		Yes		From Miyashita
10E	2000									
	2001									
	2002	May-Jun	JD	NC	100.0	816	0.658	Yes		SC/D10/NPM11
	2003	May-Jun	JD	NC	100.0	405	0.566	Yes		ditto
	2004	May-Jun	JD	NC	100.0	474	0.537	Yes		ditto
	2005	May-Jun	JD	NC	100.0	666	0.444	Yes		ditto
	2006									
	2007	May-Jun	JD	IO-PS	80.1	575	0.327	No*	*Sensitivity: extrapolate to full area	SC/62/NPM9
	2008									
	2009									
	2010									
11	1990	Aug-Sep	JD	NC	100.0	2,120	0.449	Yes		JCRM 6: 124
	1999	Aug-Sep	JD	NC	Mostly	1,456	0.565	Yes*	*Check the map to make sure	ditto
	2003	Aug-Sep	JD	IO-AC	33.9	To come		Yes		
	2007	Aug-Sep	JD	IO-PS	20.2	To come		Min	Low area coverage	
12SW	1990	Aug-Sep	JD	NC	100.0	5,244	0.806	Yes		JCRM 6: 124
	2003	Aug-Sep	JD	IO-AC	100.0	To come		Yes		
12NE	1990	Aug-Sep	JD	NC	100.0	10,397	0.364	Yes		JCRM 6: 124
	1999	Aug-Sep	JD	NC	89.4	11,544	0.38	Yes*	*Check the map to make sure	ditto
	2003	Aug-Sep	JD	IO-AC	46.0	To come		Yes		
13	2010	Jun-Aug	JD	NC				No at this time	Not available yet	

(1) KD=Korean dedicated survey, JD=Japanese dedicated survey, JR=JARPNII
(2) NC=Normal-closing, IO-PS=Passing with IO mode, IO-AC=Abeam-closing with IO mode
(3) Standard (STD) estimate based on "Top and Upper bridge", which will be corrected by estimate of g(0) for the combined platform "Top and Upper bridge"
(4) CV does not consider any process errors
Remark 1. STD estimates by different modes, NC, IO-AC, IO-NC, are considered comparable
Remark 2. JAPRNII estimates may change after model selection considering inclusion of covariates
Remark 3. Variance-covariance matrix should be provided soon after the meeting
Remark 4. Estimates with "No at this time" at "Conditioning" column will be able to be considered at the stage of CLA application

Note:

1) No extrapolations have been made for abundance estimates.
2) Survey seasons used in the tables such as 'Apr-May' do not necessarily mean 'April 1st to May 31th'. In some cases, coverages of months is only partial.

Annex L

Sample sizes for different biological, ecological and genetic markers for the estimation of stocks mixing rates (Korean data)

	Sub-areas											
	1E	2C	6E	7CS	7CN	7W	7E	8	9	10E	11	Total
Conception date				45	14	4	1	11	32		17	124
Cookie cutter shark scars[1]				299	398	23	9	110	238			1077
Flipper color pattern[2]				442	619	78	52	246	533		80	2050
mtDNA[3]	22	180	393	437	599	70	48	223	467	9	269	2717
Microsatellite	22	180	392	437	598	70	48	224	466	9	96	2542

Footnote 1: this information was obtained from sampled whales. In addition there are some observations made from vessels as follow:
Sub-area 12NE: 19 in 2009 (17 in July, 2 in August); 20 in 2010 (17 in July, 3 in August)
Sub-area 12SW: 3 in 2009 (3 in August); 4 in 2010 (2 in July, 2 in August)

Footnote 2: these figures correspond to number of photographs and are available under request. In addition there are some data classified under the criteria of Nagatsuka (2010) and used by Kanda *et al*. in SC/S10/NPM9 as follow:
Sub-area 7CN: 90
Sub-area 7CS: 90
Sub-area 7W: 6
Sub-area 8: 15
Sub-area 9: 6

Footnote 3: these correspond to mtDNA control region sequences. In addition there are some mtDNA RFLP data as follow:
Sub-area 12NE: 7 in 2010 (6 in July, 1 in August)
Sub-area 12SW: 1 in 2010 (1 in August)

Sample size of non-genetic data of north Pacific common minke whales in each new sub-area.

	Month	Sub-areas											
		1E	2C	6E	7CS	7CN	7W	7E	8	9	10E	11	Total
Conception date	April				26								26
	May				12		3			4			19
	June				6	2		1	5	4			18
	July					2	1		6	11		12	32
	August				1					13		5	19
	September					9							9
	October					1							1
	Total				45	14	4	1	11	32		17	124
Cookie cutter shark scars[*1]	April				110								110
	May				141		8	5	30	11			195
	June				48	42	12	2	56	29			189
	July					27	2	2	16	62			109
	August					5	1		7	130			143
	September					220			1	6			227
	October					104							104
	Total				299	398	23	9	110	238			1077
Flipper color pattern[*2]	April				162								162
	May				225		46	40	39	41			391
	June				50	101	28	10	99	90			378
	July					31	3	2	95	184		50	365
	August				4	22	1		12	208		30	277
	September				1	318			1	10			330
	October					147							147
	Total				442	619	78	52	246	533		80	2050
Flipper color pattern Criteria of Nagatsuka (2010)[*2]	April				10								10
	May				47				1	1			49
	June				40	33	6		14	5			98
	July												0
	August												0
	September					21							21
	October					29							29
	Total				97	83	6		15	6			207

		1E	2C	6E	7CS	7CN	7W	7E	8	9	10E	11
mtDNA		22	180	393	437	599	70	48	223	467	9	269
microsatellites		22	180	392	437	598	70	48	224	466	9	96

		1E	2C	6E	7CS	7CN	7W	7E	8	9	10E	11
mtDNA	January	2	31	60	6	4	0	0	0	0	0	0
	February	3	25	33	4	1	0	0	0	0	0	0
	March	6	12	34	7	1	0	0	0	0	0	0
	April	5	8	55	129	10	0	0	0	0	0	57
	May	3	15	45	181	16	46	36	37	37	0	65
	June	1	6	25	67	121	20	10	94	83	0	34
	July	0	13	16	6	40	3	2	79	154	0	54
	August	0	5	24	8	27	1	0	12	183	0	38
	September	0	0	14	3	255	0	0	1	10	0	7
	October	0	5	14	3	108	0	0	0	0	1	6
	November	1	18	30	11	8	0	0	0	0	6	8
	December	1	42	43	12	8	0	0	0	0	2	0
microsatellite	January	2	31	60	6	4	0	0	0	0	0	0
	February	3	25	33	4	1	0	0	0	0	0	0
	March	6	12	34	7	1	0	0	0	0	0	0
	April	5	8	55	129	10	0	0	0	0	0	0
	May	3	15	45	181	16	46	36	38	37	0	0
	June	1	6	25	67	121	20	10	94	83	0	1
	July	0	13	16	6	40	3	2	79	154	0	50
	August	0	5	24	8	27	1	0	12	182	0	30
	September	0	0	13	3	255	0	0	1	10	0	1
	October	0	5	14	3	107	0	0	0	0	1	6
	November	1	18	30	11	8	0	0	0	0	6	8
	December	1	42	43	12	8	0	0	0	0	2	0

Annex M

Potential methods for the estimation of migration rates and prospects for their application to the North Pacific common minke whales

Oscar E. Gaggiotti

There are many methods that can be used for the estimation of migration rates. This Annex briefly explains their basic assumptions and evaluates their usefulness for the estimation of migration rates among putative populations of North Pacific common minke whales in an RMP context.

One general remark should be made: the fact that two populations are genetically similar does not necessarily imply that they exchange migrants. Indeed, genetic similarity can also be explained by a scenario where the two populations have diverged in the recent past from a single ancestral population (Fig. 1a). This is the so-called 'fission' or 'isolation' model in which the two main processes controlling genetic divergence are mutation and genetic drift. The alternative standard model that is considered for the estimation of migration rates assumes that two (or more) populations have persisted for a very long time and have reached an equilibrium between migration and genetic drift (Fig. 1b); the 'pure island model (PIM)'. Obviously, real subdivided populations lie somewhere along a continuum determined by these two extreme scenarios of population subdivision and would be better described by a so-called 'isolation with migration' model (IMM, Fig. 1c).

There are methods for the estimation of migration rates under both scenarios (pure island and isolation with migration models), recognising that there are two types of migration rate estimates:

(a) long-term or equilibrium estimates that assume that no significant demographic changes have taken place (local population sizes and migration rates more or less constant through time) and furthermore that the time since divergence from the ancestral population is so large that there is a migration-drift equilibrium – they are in this case, rates averaged over evolutionary time and use allele frequency data;

(b) short-term estimates that assume a very long divergence time but allow for some recent changes in demographic conditions - in this case, they are recent migration rates, i.e. migration events that took place one or two generations back in time and are based on multilocus-genotype data.

The remainder of the Annex describes the available models according to their underlying demographic assumptions and the type of estimate they provide.

1 Pure island models
1.1 Long-term/equilibrium estimates
F_{ST}: this is the oldest method and is no longer considered as a proper method for estimating migration rates. It assumes that population sizes and migration rates are all constant and equal across populations. It is based on the well know equation relating F_{ST} and effective number of migrants: $F_{ST} = 1/(1 + 4Nm)$.

Migrate: estimates the effective population sizes and migration rates of n constant populations using non-recombining sequences, microsatellite data or enzyme electrophoretic data. It is based on coalescent theory and allows ML and Bayesian estimation implemented using MCMC. Not the best choice for minke whales because of its equilibrium assumption and the amount of time each run takes (fifteen days or more in some cases).

Website: *http://popgen.sc.fsu.edu/Migrate/Migrate-n.html*

Lamarc: estimates the effective population sizes and migration rates, per-site recombination rate of n constant or exponentially growing/shrinking populations using sequence data or microsatellite data. Also based on coalescent theory and allowing for ML and Bayesian estimation implemented using MCMC. It allows for non-constant population sizes but each run can take a very long time particularly when using microsatellite data.

Website: *http://evolution.genetics.washington.edu/lamarc/index.html*

1.2 Recent migration
BayesAss: estimates recent migration rates between populations from multilocus genotype data. It allows for asymmetric migration between populations. Assumes co-dominant unlinked markers, and sampling of source populations of the immigrants; allows for missing data. Estimates each individual's immigrant ancestry, the generation in which immigration occurred, and inbreeding levels within populations. Uses a Bayesian approach implemented using MCMC. Less time consuming than Lamarc and Migrate but it has serious convergence problems when Fst is very low.

Website: *http://sites.google.com/site/rannalaorg/software*

BIMr: very much like BayesAss but it allows for simultaneous use of genetic and non-genetic data in order to identify factors controlling migration. It also allows for correlated allele frequencies. Less convergence problems than BayesAss but they are still present.

Website: *http://www-leca.ujf-grenoble.fr/logiciels.htm*
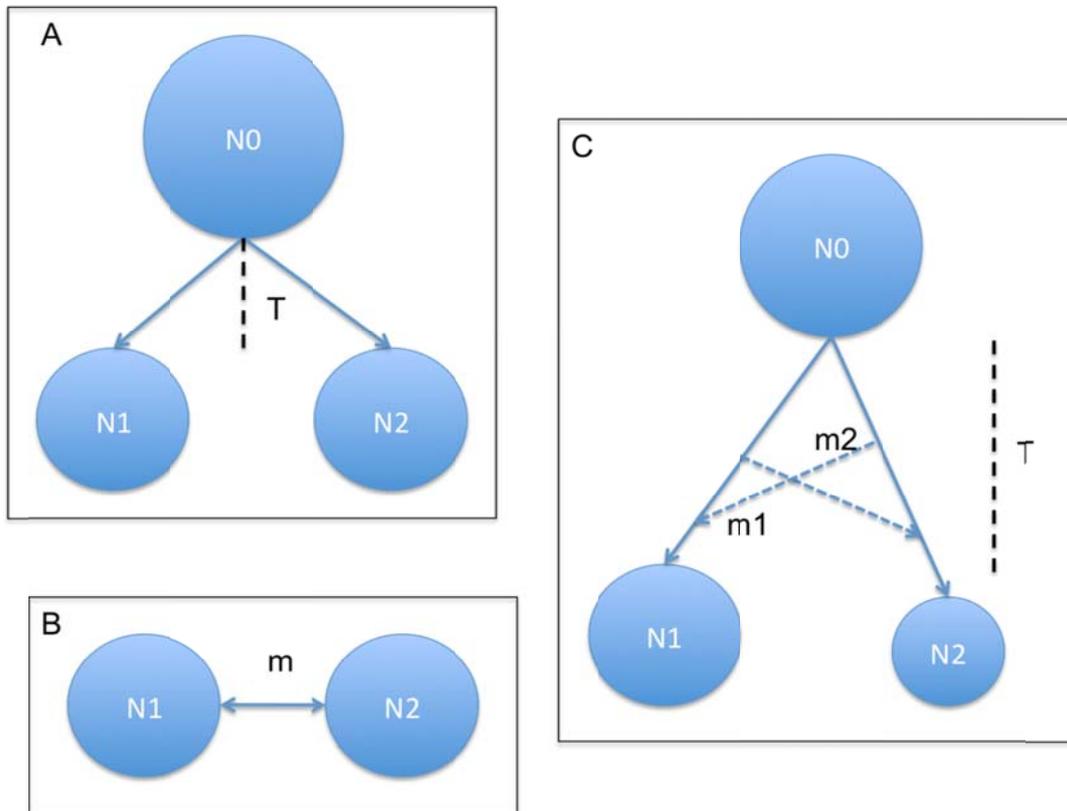
Fig. 1. Alternative population models that could explain genetic similarity between populations.

2 Isolation with migration model

IM, IMa: Estimate the divergence time and the migrations having occurred in the ancestry of two populations. Reports the posterior distributions of the ancestral population size, the divergence time, the relative initial population sizes, the growth rates and potentially asymmetrical migration rates between populations. Assumes that there are no other populations exchanging migrants with the sampled populations, no linkage between loci, and no recombination within loci. It can use DNA sequence and microsatellite data. It uses a Bayesian approach implemented with MCMC. A single run can take weeks specially if using microsatellites.

Website: *http://genfaculty.rutgers.edu/hey/software#IMFIG*

IM2: pretty much like IMa but it allows for up to 10 populations.

Website: *http://genfaculty.rutgers.edu/hey/software#IMa2*

Final remark

All the above-mentioned estimation methods face real difficulties when genetic differentiation among populations is low ($F_{ST} < 0.01$). Thus, they are unlikely to give reliable estimates in the case of minke whales.

A not-so-quick but dirty alternative method for minke whales

In Agadir, Gaggiotti and Durand (2010) described a method based on coalescent simulations for the estimation of the migration rate between the OW and OE putative stocks. Using this method we obtained estimates between 0.033 and 0.05. The migration rate that best fit the observed F_{ST} is m = 0.049 per generation. This estimate assumes migration-drift equilibrium but it allows for mutations. The details are presented in Appendix 1.

Appendix 1: Simulation study to infer migration rates between OW and OE stocks using the newly available microsatellite data

In order to comply with the terms of the contract, a simulation study similar to that of Taylor and Martien (2004) was undertaken. More specifically, we aimed at inferring the range of migration rates that are consistent with the degree of genetic differentiation observed between the putative stocks OE, OW and W. Note, however, that the results obtained using Boundary Rank analysis and PCA do not support this stock structure.

Methods

MS (Hudson, 2002) is a computer program for generating samples under neutral models. The program MS can be used to generate many independent replicate samples under a variety of assumptions about migration and population size to aid in the interpretation of polymorphism studies. The samples are generated using the now standard coalescent approach in which the random genealogy of the sample is first generated and then mutations are randomly place on the genealogy (Hudson, 1990).

MS was used to generate samples for 16 independent loci under a three islands model. A mutation rate of 0.0001 for each locus was used. We assumed that the diploid population sizes in the three islands were equal to 3400 x 2, 1600 x 2 and 5165 x 2, which corresponded to the estimated number of female alleles in the populations OW, OE and W respectively (see Taylor and Martien 2004). For each locus, we drew 894 x 2, 270 x 2 and 466 x 2 alleles, which corresponded to the twice the observed number of individuals in the populations OW, OE and W respectively. The migration rate was set between OW and W to zero. The migration rate per generation (m) between OW and OE and between OE and W was allowed to vary between 0.001 and 0.05 by increments of 0.001. Thus, 50 migration rates in total were tested and for each migration rate, 1000 independent simulations were performed.

MS outputs the segregating sites, coded as zeros (ancestral state) and 1 (derived state) for each simulated chromosome. In order to simulate microsatellites, we post processed MS output with MS2MS, a perl script that converts MS output into microsatellites. Finally, Genepop was used to estimate the F_{ST} between each pair of islands.

Results

Fig. 1A shows the frequency histograms for estimated levels of genetic differentiation for a range of dispersal rates between putative stocks OW and OE. The range of migration rates that is consistent with the estimated Fst value (=0.0007; indicated by the red line) is quite large. The observed F_{ST} falls within the 95% confidence interval obtained with the simulations using (per generation) migration rates between 0.033 and 0.05. The migration rate that best fit the observed F_{ST} is m=0.049 per generation. Note, however, that the results are rather inconclusive due to the very low level of genetic differentiation.

Conclusions

As mentioned before, this analysis was carried out only to comply with the terms of the contract. These results should not be considered as reliable because (1) the stock structure assumed by the simulations is unlikely to be correct and (2) even if the assumed structure is correct, the low genetic differentiation does not allow us to provide reliable estimates of migration rates between putative stocks OE and OW.

References

Fig. 1A. Frequency histograms for estimated levels of genetic differentiation for a range of dispersal rates between 'OW' and 'OE' with the bin containing the observed F_{ST} value noted with the vertical red line. The absence of the red line indicates that none of the migration rates included in the histogram are consistent with the F_{ST} value observed.
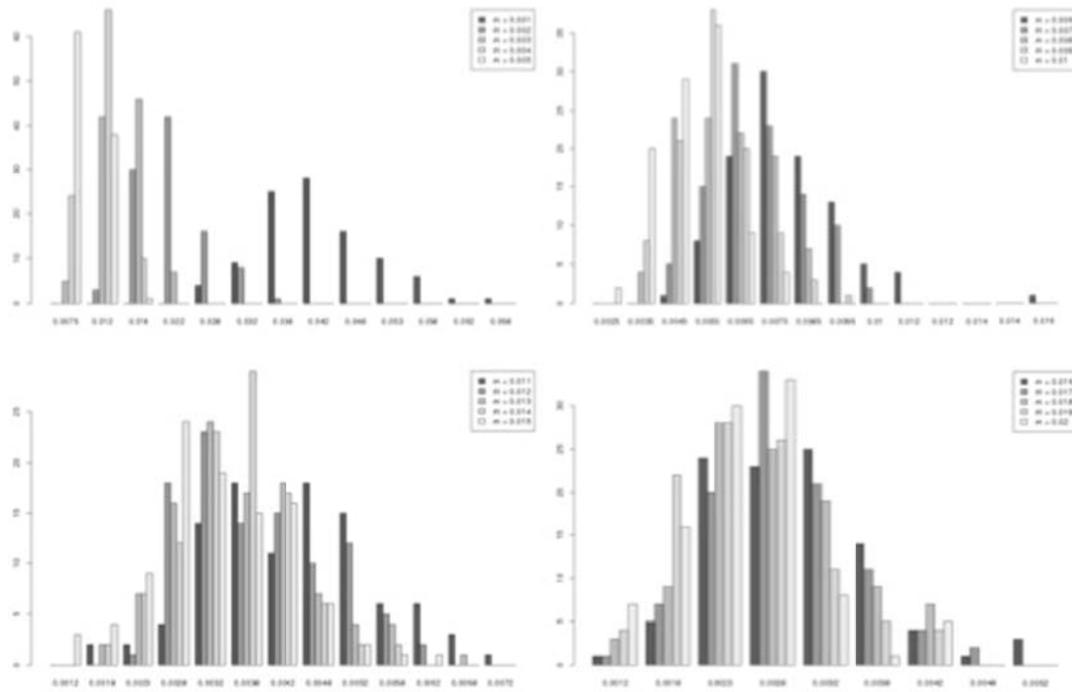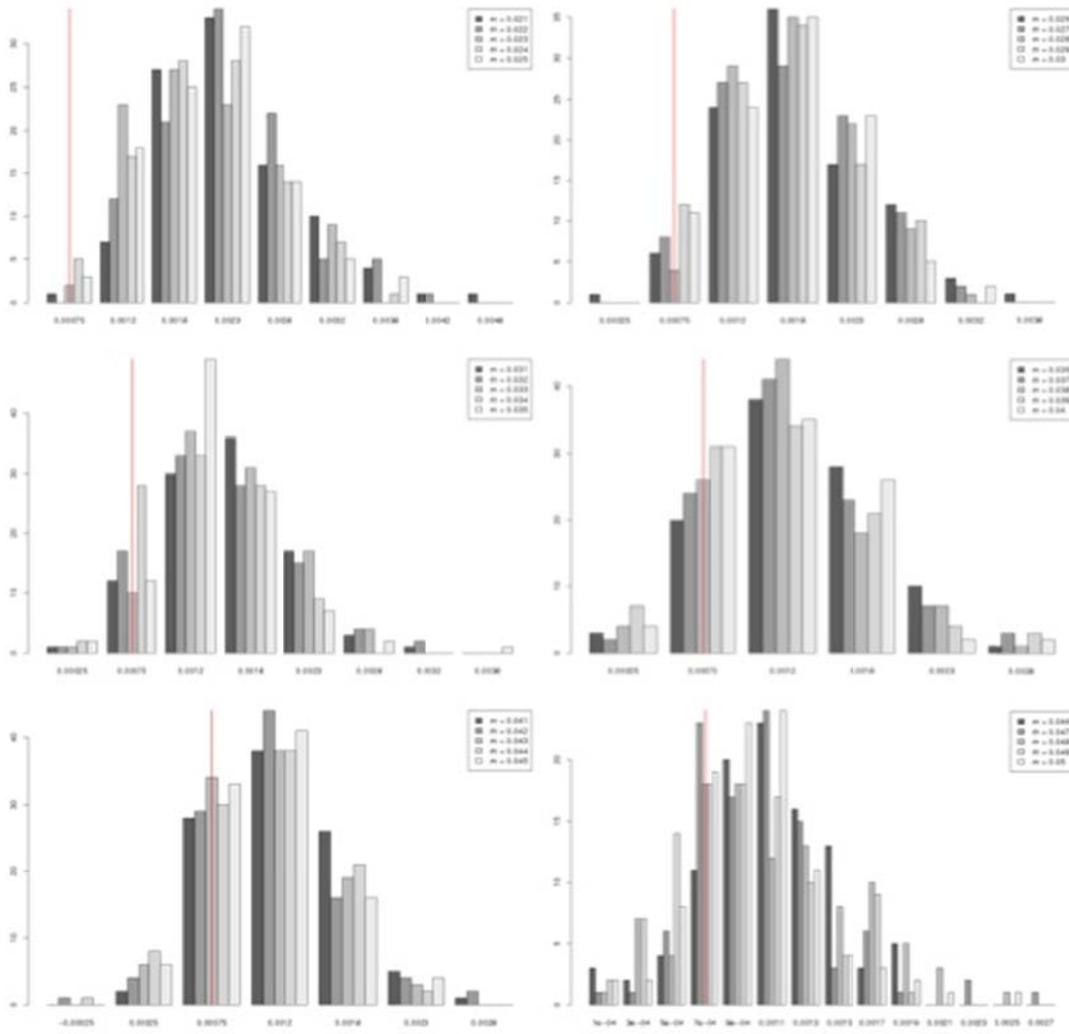
Annex N
Some new genetic analyses to evaluate relative plausibility of stock-structure hypotheses

WAPLES, HOELZEL AND GAGGIOTTI

The following analyses, which could be conducted using existing genetics data, would provide useful information regarding relative plausibility of the competing stock-structure hypotheses. It should be possible to conduct most or all of the analyses prior to the First Annual Meeting. It might be possible to perform some of the analyses sooner to help inform the conditioning. The proposed analyses are of three major types (Note: this is not intended to be an exhaustive list; additional analyses of other types might also be useful).

A. Can evidence for spatial and/or temporal genetic heterogeneity, esp in area 7, be explained by different mixture fractions of the same two core stocks (O and J), or is it necessary to postulate an additional stock (JE)? Proposed lead: Waples

1. Estimating mixture fractions and compatibility with two-stock model
    * Develop matrices of allele frequency estimates for 'pure' O and J stocks (from areas 8+9 and 6, respectively)
    * For each spatial/temporal stratum, use existing genetic stock identification (GSI) software to estimate mixture fractions of O and J stock. Compare these to estimates based on likely O and J individuals from STRUCTURE analyses.
    * For each statum, statistically evaluate the hypothesis that gene pools besides O and J are present
2. Evidence of mixture based on departures from single-locus (Hardy-Weinberg) and two-locus (linkage) equilibrium (aka, evidence for a Wahlund effect)
    * For each stratum, quantify magnitude of heterozygote deficit (indicated by positive F_{IS}) and magnitude of linkage disequilibrium (LD). Check whether magnitude of F_{IS} and LD are positively correlated with estimated mixture fractions (as expected with population mixtures).
    * For each locus, calculate magnitude of allele frequency difference between O and J stocks.
    * For each stratum, compute F_{IS} for each locus and compute LD for each pair of loci. If departures from equilibrium are due to a mixture of populations, they should be highest at loci for which there are large frequency differences between O and J stocks.

B. Additions to the PCA analyses presented at Agadir and Pusan.   Proposed lead: Gaggiotti
Several related types of analyses might be informative

(1) Carry out a PCA of simulated data for a randomly mating population to verify that PC1 and PC2 patterns observed for real data are not random. This is simply a control to verify that results presented in Pusan are indeed suggestive of a distinct genetic cluster. However, it will not necessarily provide strong support to hypothesis III unless the results of the analysis suggested below are not observed.

(2) Carry out PCAs for coastal samples where we now exclude O individuals. If doing so also generates a cluster in the Northwest, then we can conclude that it represents a mixture of J and O and not a distinct population. This result would make hypothesis III less likely and would provide support for hypothesis II. However, if no clear structuring is revealed then hypothesis II would be supported in the sense that it would strengthen the case for the existence of a Ow stock.

(3) It would be very useful to carry out all these analyses and update previous ones by also including all the bycatch data from area 7.

(4) A test of the existence of stocks JE and JW using samples from areas 2 and 6 and the same PCA technique.

(5) It may also be useful to carry out PCAs for specific periods of the year representing the times during which the putative migrant stocks are present and compare them with analyses for the period of time in which they are supposed to be absent.

C. Possible evolutionary pathways for the generation of stock structure as proposed in the three hypotheses.
Proposed lead: Hoelzel

The objective is to consider putative populations in the context of possible evolutionary scenarios. Differential support for models may help with the interpretation of relative plausibility. The models are all (with the exception of the first model) based on the assumption that the O-type population is ancestral, and that environmental change has driven the generation of population divisions over time. For example, the two models under 'H2' could be based on vicariance (e.g. during the period when ice disrupted habitat availability during a glacial epoch), while later divisions proposed in 'H3' may be related to changes in habitat during subsequent warming periods. The relative likelihood of the models would be tested using approximate Bayesian computational methods (a simulation-based approach to fitting models to observed data – could be run in DIYABC). The scenarios modeled in 'H3' are alternative to the possibility that proposed regional populations in area 2 (JE) and area 7 (OW) were founded by hybridization between stocks O and J.
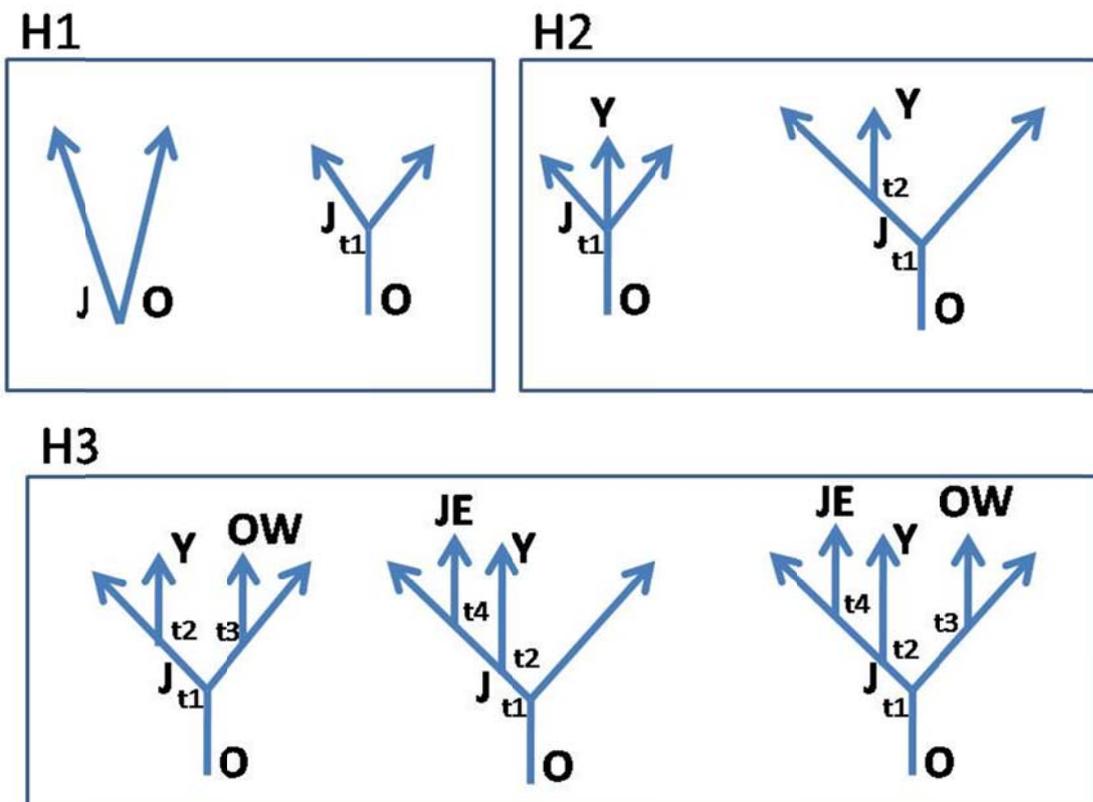
t1 – t4 represent splitting times between lineages and would be estimated as part of the analysis

Annex O
Proposal to estimate migration rates

SHORT TITLE
Estimates of migration rates among putative stocks of North Pacific common minke whales using population genetics data

RELEVANT AGENDA ITEM (NO. AND TITLE)
Evaluation of dispersal rates between stocks using genetic data (Item 7 of the First Intersessional Workshop for the Western North Pacific common minke whales).

BRIEF DESCRIPTION OF PROJECT AND WHY IT IS NECESSARY TO YOUR SUB-COMMITTEE
Estimates of dispersal are required for undertaking a full *Implementation Review* for the WNP minke whales and to examine effects of catches on stocks. Three alternative stock-structure hypotheses with varying numbers of putative stocks have been proposed. Hypothesis III includes five stocks referred to Y, JW, JE, OW, and OE, two of which (Y and JW) occur in the Sea of Japan, and three of which (JE, OW, and OE) are found to the east of Japan. The *Implementation Simulation Trials* includes scenarios with different levels of dispersal between stocks JE and JO as well as between stocks OW and OE, but there is currently no basis to assign plausibility ranks to these scenarios. The First Intercessional Workshop held in Busan concluded that it was very important to obtain these estimates or at least a range of values that could be used to carry out sensitivity analyses.

Data will be provided through the IWC Data Availability Group. The datasets should include multilocus genotypic data and geographic coordinates for each individual, together with information about how to identify individuals which under hypothesis III are definitely assigned to stock.

Data will be analysed using the programs IMa2 (Hey 2010), which assumes an isolation with migration model, and BIMr (Faubet and Gaggiotti 2008), which assumes a non-equilibrium island model. These methods are computationally intensive and require several preliminary runs in order to assure convergence of the MCMC chains, but they are deemed to be the most appropriate for the estimation of migration rates. We will obtain estimates of migration rates between putative stocks under hypothesis III and we will provide credibility intervals that could be used for sensitivity analyses.

References

TIMETABLE
A total of four full months will be required to carry out these analyses. All efforts will be made for submitting a report presenting all the results before the next annual meeting in Tromsø provided that data files and precise instructions on how to assign individuals into putative stocks are provided by 15 January 2011.

RESEARCHERS' NAME
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ESTIMATED TOTAL COST WITH BREAKDOWN AS NEEDED (E.G. SALARY, EQUIPMENT)
Salary   8,000 Euros