Report of the Workshop on North Pacific Common Minke Whale Implementation Simulation Trials

Report of the Workshop on North Pacific Common Minke Whale (Balaenoptera acutorostrata) Implementation Simulation Trials

Members: Donovan (Chair), Allison, Butterworth, Goto, Kawahara, Kim, Martien, Miyashita, Ohsumi, Pastene, Polacheck, Punt, Smith, Taylor, Tomita (I), Wade.

1. CONVENOR'S OPENING REMARKS

The Workshop took place from 19-22 January 2002, at the National Marine Mammal Laboratory in Seattle, USA. Butterworth welcomed the participants and reminded the meeting that the Terms of Reference established by the Scientific Committee (SC) for the Workshop were:

- Review results of further analyses of genetic data for sub-areas 7, 8 and 9 to decide what trial modifications may be necessary in consequence, and re-estimation of mixing proportion between 'J' and 'O' stocks in sub-areas 7 and 11.
- (2) Specify final trials in the light of discussions at the 2001 SC meeting and the results of trials run intersessionally, and decide upon which combinations of *Small Area* definitions and RMP variants to run the final trials.
- (3) Initiate discussion on approaches to advise on the relative plausibility of trials and their application in this instance, to facilitate discussion of this matter at the 2002 SC meeting.
- (4) Specify Terms of Reference for continued work under the intersessional e-mail group until the 2002 meeting.

He also highlighted the comment from the last Scientific Committee meeting that the Committee had agreed at its 2001 meeting that the results of the *Implementation Simulation Trials* would be examined at the 2002 meeting with the goal of recommending to the Commission one variant of the RMP irrespective of any further data forthcoming in the interim – this will constitute the end of the *Implementation* (IWC, 2002a, p.100).

2. ELECTION OF CHAIR

Donovan was elected Chair.

3. APPOINTMENT OF RAPPORTEURS

Butterworth and Punt acted as rapporteurs with assistance from the Chair.

4. ADOPTION OF AGENDA

The adopted agenda is given as Annex A.

5. REVIEW OF DOCUMENTS

The list of documents is given as Annex B. It was **agreed** that these documents should also be made available to the sub-committee on the RMP at the 2002 SC meeting.

6. GENERAL ISSUES

6.1 Conditioning

Conditioning is the process of selecting the values for the parameters of the operating model so that this model is consistent with the existing data for the species/*Region* under consideration. Each simulation involves: (1) generating a pseudo-dataset based on the information on abundance and mixing of stocks in sub-areas; and (2) estimating the parameter values for the operating model which provide the best fit to the maximum-likelihood value for the objective function.

SC/J02/NP1 outlined a set of diagnostic statistics that could be used to assist in the evaluation of whether the operating model fits the pseudo-datasets adequately and whether the resultant model fits appear realistic. The diagnostic statistics include: histograms of standardised residuals; bivariate plots of these residuals; the time trajectories of 1+ population size with the dataset used for *conditioning* superimposed; the time series of annual catches by stock; the observed and model-predicted mean lengths of the catch; the time-trajectories for the proportion of each stock in each sub-area; and the observed and model-predicted catches of males. Lowering the age-at-recruitment from 4 to 1 was shown in SC/J02/NP1 to lead to better fits to the mean length information.

In considering the value of comparing observed versus predicted mean lengths in the catch as a diagnostic for conditioning, the Workshop **agreed** that this was problematic because of: (1) the general shape of minke whale growth curves; (2) the fact that growth in North Pacific common minke whales remains poorly understood; and (3) the fact that changes in mean length of captured whales over time may be a consequence of operational changes.

It was suggested that basing diagnostic statistics on the fraction mature may be more robust, although maturity information for the catches is not available before the 1970s. Butterworth noted that an inability to mimic the mean length information was not necessarily a concern for the selection of a variant of the RMP because many previous analyses using the Baleen II model suggested that population sizes and trends were insensitive to most specifications regarding mortality and growth. Polacheck noted that changes in mean length could provide information on seasonal movement patterns.

The abundance estimate for sub-area 7^1 in 1990 has been assumed to be a minimum value (of 1,741) when *conditioning* the trials. The operating model population size in that sub-area is therefore constrained not to be less than this estimate. This constraint played a role in determining the values for the operating model parameters for several of the trials because the operating model 1+ population size in sub-area 7 in 1990 frequently equalled the pre-specified minimum value. The abundance estimate for sub-area 7 in 1991 is taken to be unbiased. However, given its CV, some of the abundance estimates generated from this estimate are less than the pre-specified minimum. The Workshop noted that no account was currently taken of the uncertainty associated with the minimum abundance estimate because previous attempts to do this led to a large number of cases in which the generated abundance estimate for 1991 was less than the minimum abundance estimate for 1990². Wade suggested that consideration should be given to defining the minimum population size constraints based on a lower confidence limit for the abundance estimates considered to be minima (see Item 8.5).

The Workshop noted that the trials specified last year (IWC, 2002b) do not explicitly allow for 'additional variance', except through the impact of stochasticity on the catch mixing matrices for the 'J' and 'W' stocks. The evidence for additional variance in the data is the lack of temporal consistency in the abundance estimates for sub-area 9 (see Table 1). There are several possible explanations for the differences in abundance estimates among years other than changes in abundance: for example, variability in the timing of the migration or variability in the spatial distribution of the animals. One reason for the extra-sampling variation for the abundance estimates used previously when conditioning the trials may relate to differences in the assumptions underlying the calculation of the abundance estimates (e.g. the range of Beaufort states considered).

The Workshop requested that two trials be conducted during the meeting to examine issues of conditioning.

¹ See Fig.1 for sub-areas and Table 1 for abundance estimates.

 2 It was later agreed that the 1990 estimate for sub-area 7 was not suitable for use in the trials – see Item 8.5 and Annex C.

- (1) A trial in which there is a single mixing matrix only for the 'W' stock and the operating model is fitted only to the abundance estimates that were not derived from JARPN (see Table 1). Annex C overviews reasons for the use (or otherwise) of the full set of abundance estimates.
- (2) A trial based on the abundance estimates used in trial 1 plus abundance estimates from the JARPN surveys (see Table 1). The two catch-mixing matrices for the 'W' stock for this trial were randomly selected each year within a simulation from two alternative matrices: one in which all 'W' stock animals are found west of 170° E and another in which a fraction ϕ of these animals is found in this area.

Annex D provides diagnostic plots (histograms of standardised residuals and time-trajectories of population size with the abundance estimates used for conditioning superimposed) for the two trials. The number of simulations on which the plots in Annex D are based is 18 (trial 1) and 30 (trial 2). The 30 simulations for trial 2 are the best 30 in terms of the value of the objective function of the 80 simulations conditioned. The standardised residuals for the abundance estimates for trial 1 are satisfactorily normal while those for trial 2 are not. Even though trial 2 includes stochastic catch mixing matrices for the 'W' stock, the fits to the abundance estimates for sub-areas 8 and 9 are poor. Furthermore, there is evidence from the trajectories of population size of numerical problems when fitting the operating model.

Based on the results in Annex D, the Workshop **agreed** that the final set of trials would be based on the specifications that underlie trial 1 (i.e. no stochastic catch-mixing matrices for the 'W' stock and use of only a subset of the abundance estimates when conditioning). It also **agreed** that an additional factor would be considered in trials to quantify the impact of additional variation i.e. to assume that there is additional variance reflected by a CV of 40%.

6.2 Data availability

During its discussions, the Workshop recognised the importance of data collected by national research programmes (which are not necessarily freely available to all

_	The abundar	nce data use	ed in the two	trials (1 a	nd 2) run durin	g the Wor	kshop.			
Sub- area	Timing	Areal coverage	Abundance	CV	Used in Trial 1&/or 2?	Survey Type	Estimate also used by CLA ²			
Data also used in previous trial specifications										
6	Aug-Sep 1992	56.8	893 ¹	0.67	1 / 2	D	No			
7	Aug-Sep 1991	66.5	2,202	0.383	1 / 2	D	Yes			
8	Aug-Sep 1990	62.2	1,057	0.706	1 / 2	D	Yes			
9	Aug-Sep 1990	35.1	8,264	0.396	1 / 2	D	Yes			
9	Jun-Jul 1994	35.0	4,673	0.441	2	J	No			
9	Jun-Jul 1995	45.1	2,145	0.315	2	J	No			
10	Aug-Sep 1992	30	707 ¹	0.57	1 / 2	D	No			
11	Aug-Sep 1990	100.0	2,120	0.449	1 / 2	D	Yes			
12SW	Aug-Sep 1990	100.0	5,244	0.320	1 / 2	D	Yes			
12NE	Aug-Sep 1990	100.0	10,397	0.171*	1 / 2	D	Yes			
12NE	Aug-Sep 1992	89.4	11,544	0.157*	1 / 2	D	Yes			
New dat	ta									
8	July-Aug 1996	31.3	1,385	0.31	2	J	No			
8	May-June 1998	81.6	843	0.541	2	J	No			
11	Aug 1996	32.3	608	0.266	2	J	No			
11	July 1999	32.3	881	0.338	2	J	No			

J: JARPN survey; D: Dedicated survey; * Provisional values, to be recalculated after the meeting. ¹Used as a minimum estimate; ²i.e. Estimate acceptable for calculating catch limits if the Commission decides to implement the RMP.

Table 1

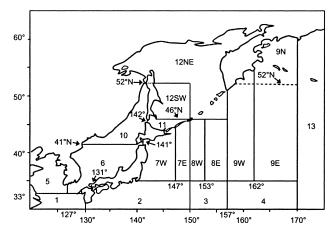


Fig. 1. Map showing the North Pacific region, including the areas and sub-areas relevant to *Implementation Simulation Trials* (see Item 7).

members of the Committee) for the development of the trial process (e.g. the genetics data considered in SC/J02/NP13). It noted that the question of data availability is a complex and sensitive one. A balance must be struck between the needs of the Committee and the rights of the scientists who have invested considerable time and effort in collecting the data. In the past, the Committee spent some time on this general issue when discussing the Guidelines for Surveys and those for Data Collection under the RMP. Although some conflicting views were expressed over this issue, the Workshop agreed that it had neither the time to address the matter thoroughly at the present meeting nor the authority to determine new guidelines. It recognised the great importance of the issue to the working of the Committee in the context of both the development of Implementation Simulation Trials and the discussions of the relative plausibility of any such trials. The Workshop strongly recommends that the question of data availability/access for the Implementation process be considered by the Committee at the 2002 SC meeting.

7. REVIEW OF FURTHER GENETIC ANALYSES RESULTS

Before discussing this item, the Chair reminded the participants that the primary aim of the Workshop was to finalise the Implementation Simulation Trials (IWC, 2002a, p.106). In the context of discussions under this item, therefore, he expected to concentrate on whether any of the stock hypotheses put forward were implausible and should not be considered in the Trials. Severe time pressure meant that the question of the relative plausibility of the various hypotheses could not be discussed in detail at the Workshop (i.e. in advance of running the trials). He noted that the Workshop report therefore only briefly explains the methods used and the hypotheses developed; the short discussion sections do not represent a detailed critique of these. He expected participants to submit papers to the 2002 SC meeting that performed this function and explained in detail their rationale for weighting the various hypotheses put forward.

7.1 Re-estimation of J-O mixing

This is discussed under Item 8.1

7.2 Methods

Prior to the Workshop, a collaborative meeting had been held in Tokyo between Pastene, Goto, Kanda, Taylor and Martien to discuss available genetic techniques and analyses, and to apply some of these further. These discussions are given in SC/J02/NP13. The Workshop thanked these individuals for their efforts, which assisted in the development of much of the material reported upon in the following sections.

7.2.1 Hypothesis testing

Hypothesis testing is one of the more traditional ways to look at issues of stock identity and it has been the subject of much discussion in the Committee in the past (e.g. IWC, 2001a; b).

SC/J02/NP10 presented results of hypothesis testing based upon a null hypothesis of panmixia, making use of mtDNA data from JARPN I and II (1994-2001). Possible 'J' stock animals are excluded from the comparisons, based upon an 'extreme' genetic criterion. The number of samples by sub-area is (total sample/number of samples after excluding suspected J stock animals): sub-area 7 = 213/173; sub-area 8 = 112/96; sub-area 9 = 233/192 and sub-area 11 = 80/50. A large number of comparisons were performed, leading to the conclusion that the only source of heterogeneity established to the north and east of Japan (sub-areas 7, 8 and 9) could be attributed to whales sampled in the western part of sub-area 9 in 1995, 2000 and 2001 (although sample sizes were low in the last two years). The paper concluded that the results support a one-stock scenario in the sub-areas concerned, except for the possibility of sporadic appearance of another stock in sub-area 9W.

SC/J02/NP11 reported the results of similar hypothesis testing based upon microsatellite data (seven loci) from these sub-areas, again using data from JARPN and JARPN II from 1994-2001 and excluding possible 'J' stock animals. The number of samples by sub-area after the exclusion of suspected J stock animals is as follows: sub-area 7 = 173; sub-area 8 = 96; sub-area 9 = 192 and sub-area 11 = 50. No evidence of heterogeneity was found, except for inter-annual heterogeneity in sub-area 9 which might indicate sporadic intrusion of a further stock into that region.

The Workshop thanked the authors of these two papers for the substantial effort that had been applied to analyse the samples and the data.

7.2.1.1 SHORT DISCUSSION

In discussion, it was reiterated that for a number of reasons (including small sample sizes), failure to detect significant differences in such tests does not necessarily mean an absence of structure.

The approach used to exclude 'J' animals was considered. Some suggested that this might be too conservative (i.e. it would also exclude some non-'J' stock animals). It was suggested that tests should be reported without such exclusions with the resultant larger sample sizes possibly revealing greater discriminatory power.

Some questions over the authors' conclusions regarding temporal variability of structure in sub-area 9W were raised. It was noted that these rested strongly on the inclusion of data from JARPN in 1997, when samples had been collected much earlier in the season.

During the Workshop, AIC-based evaluations of different stock structure models to explain the frequency of haplotype 9 in various sub-areas were carried out. These suggested strong support for a frequency in sub-area 9W that differed from that in sub-areas 7, 8 and 9E. Evidence for inter-annual variability in 9W was, however, relatively weak. The Workshop **recommends** that these analyses be extended to consider all haplotypes, and to investigate the possibility of temporal variation in sub-areas 7 and 8. It also **recommends**: (1) a general examination of the effect of inclusion of data from past commercial operations in the analyses; and (2) the use of alternative methods for exclusion of 'J' stock animals (e.g. using an 'assignment' method, or using more than simply genetic data).

7.2.2 Bayes and empirical Bayes approaches

SC/J02/NP4 outlined an approach based on Bayesian estimation for comparing single with multiple stock hypotheses. The use of Bayesian methods is arguably preferable to traditional methods because, unlike methods based on hypothesis testing, such methods have the potential to discriminate whether non-rejection of the null hypothesis of a single stock is indeed a reflection of only one stock being present or rather of the low power associated with small sample size. The likelihood of the data in SC/J02/NP4 is assumed to be multinomial and the multivariate prior for the probability of an individual having a particular haplotype is assumed to be of the Dirichlet- β form. The values for the parameters of this prior are either determined using an Empirical Bayes approach or assumed to be distributed according to a log-normal hyper-prior (the 'Full Bayes' approach). The Empirical and Full Bayes methods are examined using simulation. The performance of the Empirical Bayes method is found to be much worse than that of the Full Bayes method. The latter performs adequately if applied to data for two stocks that differ substantially in haplotype frequency, or when sample sizes are large.

7.2.2.1 SHORT DISCUSSION

The Workshop **agreed** that the approach had promise and thanked the authors for their work. However, some concerns were expressed. For example, it appeared unclear how account was being taken of whatever genetic effect size was pertinent to distinction between stocks. It was suggested that this must be effected through the forms of prior distributions specified. The Workshop **agreed** that additional work was required to better clarify the relationship. Taylor noted that this technique requires *a priori* stratification of the data which may have a strong effect on the results.

Application of the approach to mtDNA data for North Pacific common minke whales yielded results broadly consistent with those from hypothesis testing. Some considered that although further development and review of the approach was needed, this was indicative of some support for the hypothesis test results. Others, however, believed that such a view was premature, and that a wider set of comparisons than those reported in SC/J02/NP4 would need to be considered before reaching such a conclusion.

7.2.3 Boundary rank techniques

The boundary rank method is a relatively new approach, developed to generate hypothetical population structures (originally for non-migratory species such as the harbour porpoise and harbour seal). A brief overview of the method is given in Martien and Taylor (SC/J02/NP3). A detailed description is given in Martien and Taylor (2001). The authors' summary of the method is provided as Annex E to this report.

7.2.3.1 SHORT DISCUSSION

The authors were commended for the substantial efforts they had expended and there was an extensive and wide-ranging discussion of these papers and the underlying methodology.

One point raised was that the approach distinguished areas of different haplotype frequencies, rather than biological stocks *per se*. In response, it was pointed out that this applies to all the genetics methods considered. Furthermore, in answer to the assertion that differences detected could reflect overlap between two stocks, rather than a 'hard' boundary with no interchange, it was argued that dispersal rates would be over-estimated in such circumstances, thus compensating (at least in part) for such incorrect inference.

There were a number of comments on the sensitivity of the approach to the initial clusters chosen. The analysis presented to the Workshop had separated clusters of samples spatially, but without consideration of differences in the months or years in which the samples had been taken. However, it was noted that there was little inter-annual overlap in sample positions. The authors advised the Workshop of their desire to examine further the sensitivity of their results to alternative clustering choices. They stated that the short time for which the data were available to them for analysis in Japan (SC/J02/NP13) did not allow them to fully explore the effects of different initial clusters as they would have wished.

Other concerns raised included the sensitivity of boundaries indicated by the method to the specification of connectivity matrices, double use of the data to both formulate and then effectively test hypotheses and the need for expert review of a new technique before using it as a management tool (e.g. by publication in an appropriate scientific journal). These concerns were not shared by all and in particular, some noted their view that the review of a method within the Committee was often more rigorous than the review process in some scientific journals.

The authors concluded that their results provided evidence for two stock boundaries: one in the vicinity of the existing sub-area 8-9 boundary and the other at either 147°E or 153°E, i.e. not only evidence for the classically postulated 'W' stock in sub-area 9, but also for two stocks rather than one in sub-areas 7 and 8. This pattern of results was evident for a number of alternative clustering choices.

Reservations raised about these conclusions (more particularly that of two stocks in sub-areas 7 and 8) generally mirrored concerns raised above about the methodology (at least as applied and interpreted in this instance).

7.3 Stock structure proposals

In discussion, three baseline scenarios were put forward to account for patterns observed in the results from the genetic analyses. Certain features are common across these scenarios, but they also differ in several important respects. It is stressed that inclusion of these scenarios does **not** imply agreement among the Workshop participants that all were equally plausible (or even plausible at all).

It should be noted that Annex G (see Item 7.3.3 below) was written after the meeting. It represents a report of the discussions of a small group (convened by Smith) established by the Chair during the meeting. Smith reported verbally on the deliberations of the small group at the Workshop and their discussions were used in the formulation of *Baseline-D* (below). Participation in that small group meant merely that the individual provided at least technical or biological advice/information – it does not necessarily imply agreement by all participants in the small group that

(a) *Baseline-D* is the most plausible (or even likely); and (b) that other scenarios presented are not plausible. The detailed Annex is included because it documents the basis for a new scenario, not previously discussed by the Scientific Committee and not presented in an authored document to the Workshop.

7.3.1 Baseline-A and Baseline-B

This is a 3-stock scenario ('J', 'O', 'W') with the 'W' stock found only in sub-area 9, and then only sporadically. This interpretation is argued on the basis of the results of hypothesis tests, and particularly that these had provided no significant results (other than those which the scenario reflects) for tests for heterogeneity in sub-areas 7, 8 and 9.

One major concern of those who had reservations to this scenario was that sample sizes may have been too small for such tests to distinguish further stock structure (and see the other comments on the hypothesis testing approach discussed under Item 7.2). As a sensitivity test making some allowance for this concern, a trial is to be conducted that includes some 'W' stock animals in sub-area 8.

Baseline-B (2-stocks) reflects a limiting case of this scenario with no 'W' stock whales present in sub-areas 8, 9 or 12.

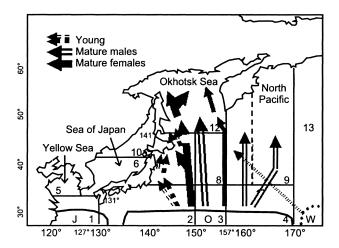


Fig. 2. Illustration of the Baseline-A stock scenario. This is based on a three stocks hypothesis, J, O and W, with the W stock occurring only sporadically in the western part of sub-area 9. This interpretation is based on the results of hypothesis testing heterogeneity in sub-area 7, 8 and 9, except some degree of genetic heterogeneity in the western part of sub-area 9 in three years (although the sample sizes for two years are low). The assumed locations of the unknown breeding grounds for these three stocks are shown. These are not definitive. The possible feeding migration routes of the different sexual classes of the O stock are shown. These are based on the investigation by Hatanaka and Miyashita (1997).

7.3.2 Baseline-C

In this scenario, there are 4 stocks overall, with three (' O_W ', ' O_E ' and 'W') to the east of Japan. This is motivated by the divisions suggested by the boundary rank method (see Annex E and SC/J02/NP5). The preferred hypothesis is one of no mixing between the stocks, with boundaries at 147°E and 157°E. Variants of this hypothesis first place the ' O_W ','' O_E ' boundary at 153°E, then allow ' O_W ' and ' O_E ' mixing between 147°E and 153°E, further allow intrusion of the ' O_E ' stock into sub-area 9E, and finally allow for some mixing of the ' O_W ' and ' O_E ' stocks throughout sub-areas 7 and 8. Fig. 3 (a-d) illustrate these different hypotheses.

Those who had reservations concerning the above scenario based these largely on the concerns expressed above about the boundary rank method, and, in particular, whether the haplotype frequency differences this may detect are a sufficient basis to postulate 'hard' inter-stock boundaries. Some members commented that the results were not supported by the hypothesis testing approach. Others believed that in fact the results of the boundary rank method were broadly in agreement with those from hypothesis testing with a strong boundary near the 8-9 line and a weaker boundary near the 7-8 line.

The low proportion of juveniles in sub-area 8 (see SC/J02/NP12) was argued as a basis for rejecting the possibility of a separate ' O_E ' stock. In response, counter opinions were offered that these results did not suggest differences in the juvenile proportions in sub-areas 7, 8 and 9 (7W excepted). The Workshop **recommends** that a statistical analysis be conducted to test whether or not these juvenile proportions did differ.

7.3.3 Baseline-D

Those suggesting this scenario presented it as representing one plausible hypothesis based on a synthesis of the implications of the results of the various methods discussed in Item 7.2 and other biological information available (see Annex G). It has 'O' and 'W' stocks to the east of Japan mixing across the area from 147°E to 162°E. The basis of this interpretation is the argument that the genetic data suggest a change in haplotype frequencies as one moves east from Japan, and that this could result from two stocks mixing in proportions that differ by longitude. 'O' stock animals dominate in the west, but become increasingly less prevalent as one moves further east; the reverse is true for 'W' stock whales. This hypothesis is illustrated conceptually in Fig. 4.

Those who had reservations concerning this hypothesis based these largely on the assertion that the genetic data provide insufficient indication of the haplotype frequency change across sub-areas 7 and 8 that this scenario suggests. Some members also noted that there is an apparent contradiction with the results of hypothesis testing in so much as they believed that those results showed that sub-area 9 is genetically closely related to sub-areas 7 and 8.

7.3.4 Distinguishing among the scenarios

The Workshop discussed the possibility of using the JARPN data on sex and size composition of catches by sub-area and time to assist conditioning the trials, and possibly to distinguish between the scenarios above. Concerns were raised about this suggestion, including the fact that there was in any case insufficient time to implement it before the 2002 Scientific Committee meeting. It was suggested, however, that such data might assist in determining the relative plausibilities of the different stock structure scenarios (see Item 11).

8. PROGRESS ON OTHER TRIAL-RELATED ISSUES

8.1 Mixing of the 'J' and 'O' stocks

The fraction of 'J'/'O'/'W' stock animals (of a given sex and age) in a sub-area is determined from the catch mixing matrix. The entries in this matrix consist of pre-specified constants (usually 0, 1, 2 or 4 to reflect qualitative assumptions regarding migration and presence/absence of animals by stock, sex and age) and estimated parameters (the parameters are sometimes multiplied by pre-specified constants to force differences in abundance at different times). The entries for each sex, age and month are normalised within the computer code to determine the

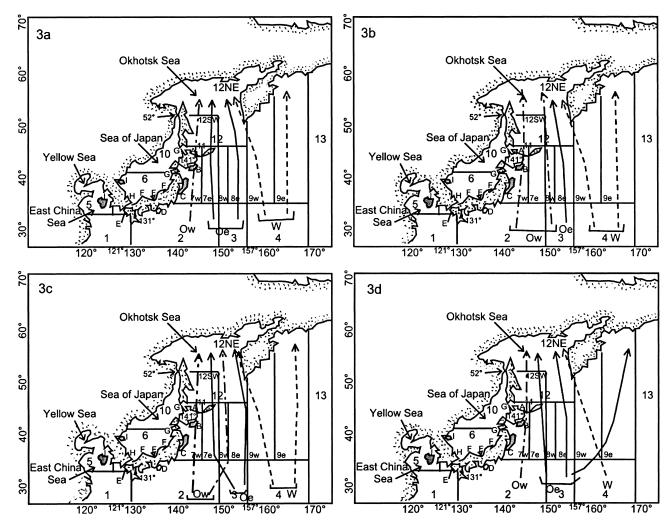


Fig. 3(a-d). Illustration of the proposed Baseline-C and variant hypotheses based on the results of the boundary rank method (see text).

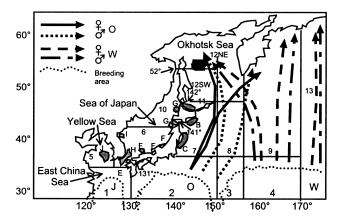


Fig. 4. Illustration of the proposed Baseline-D scenario (see text and Annex G).

fraction of the stock in each sub-area in a particular month. The values for the parameters of the catch-mixing matrix are determined during the conditioning process, primarily based on fitting to data on the fraction of (1+) animals in a sub-area that consist of 'J' stock animals (referred to as the 'J'-'O' mixing proportions although, in some trials, these data actually refer to the fraction of 'J' relative to 'O' and 'W' stock animals).

'J' stock animals are known to be found to the north and east as well as to the west of Japan. The information on the fraction of 'J' stock animals in sub-areas 7 and 11 in the trials has been based in the past on analyses of the genetics data for these sub-areas. Last year, the Scientific Committee recommended that the 'J'-'O' mixing proportions be based on a mixed-stock analysis of updated mtDNA data (IWC, 2002a). SC/J02/NP9 therefore provided estimates of the 'J'-'O' mixing proportions for sub-areas 2, 7 and 11 using mtDNA data and the method of Kishino et al. (1994). The information on bycatch in the Sea of Japan was used to define the baseline proportions for the 'J' stock. Mixing proportions were determined for sub-areas 7 and 11 for each month and sex where the data were sufficient to permit estimation. The Workshop thanked the authors of SC/J02/NP9 for their hard work.

The Workshop noted that the standard deviations for the 'J'-'O' mixing proportion estimates for some combinations of sub-area, month and sex were very large. Direct use of the information in SC/J02/NP9 in the trial specifications would therefore result in some simulations in which the 'J'-'O' mixing proportion was very high for certain combinations of sub-area, month and sex, although the point estimate of the corresponding 'J'-'O' mixing proportion is virtually zero. The reason for the high standard deviations for cases in which the point estimate was essentially zero was probably

the consequence of the application of an analytical approach to computing standard errors when the point estimate was equal to its lower bound. The Workshop therefore **agreed** to base the 'J'-'O' mixing proportions on an alternative Bayesian approach (Annex F).

Tables 2a and 2b list the revised 'J'-'O' mixing proportions based on the Bayesian approach. Sensitivity is explored in Table 2b to the choice of the baseline samples for the 'J' stock (bycatch samples or the combination of these samples and the commercial samples from Korea). The Workshop **agreed** that, given the insensitivity of the results to the choice of baseline, the 'J'-'O' mixing proportions for use in the trials would be those based on the bycatch samples only. This choice represented the base-case specification agreed at the 2001 Scientific Committee meeting. Sensitivity to the choice of the baseline sample for the 'O' stock was also examined by estimating mixing proportions using the data for sub-area 8 only, rather than including sub-area 9 as well; this was found to be minor.

The extent of mixing between the 'J' and 'O' stocks in the operating model depends on the specifications for the 'J'-'O' mixing proportions based on the genetics data (the data fitted during the conditioning process) and the structure of the mixing matrix. The Workshop therefore considered whether and how the information in Table 2 should be included in the trials, and the associated underlying trial structure, given the small sample sizes for some combinations of sub-area, month and sex and the hypotheses/information on movement patterns of common minke whales in sub-areas 2, 7 and 11.

The Workshop **agreed** that a single estimable parameter would be included in the catch mixing matrices to determine the proportion of 'J' stock animals in sub-area 2 during April and May. This parameter will be used *inter alia* to determine the split of the bycatch in sub-area 2 between the 'J' and 'O' stocks.

The posterior modal estimates of the 'J'-'O' mixing proportions for sub-area 7 are essentially zero for several of the month-sex combinations, although the corresponding mean values are larger than zero due to the relatively small sample sizes and the fact that the posterior distribution is restricted to the interval [0-1]. No hypotheses based on biological considerations are available to describe the mixing of 'J' stock animals in sub-area 7. The Workshop **agreed** therefore that the data used to condition the simulations would be based on a mixed stock analysis of the data for sub-area 7, in which all samples are pooled (over both month and sex). It also **agreed** that the population dynamics model would include a single parameter in the catch-mixing matrix to allow a low level of 'J' stock mixing in sub-area 7.

Migration patterns into and through sub-area 11 differ by stock and sex. The 'J' stock females are hypothesised to arrive in sub-area 11 before the 'O' stock females, and to migrate north into sub-area 12 before returning to sub-area 11 and migrating south. The estimates of 'J'-'O' mixing rates based on genetics are consistent with this hypothesis. In contrast, between-stock differences in the migration pattern of males are poorly understood. Migration of 'O' stock animals into sub-area 11 in April is probably restricted due to ice coverage in the east of this sub-area.

Based on biological considerations, the Workshop **agreed** that: (1) separate 'J'-'O' mixing proportions would be generated for each month from April to August for females; and (2) different parameters would be included in the catch mixing matrices for each month for females to ensure an adequate fit to the data. There are very few data for sub-area

11 for September. However, it is expected that there would be fewer females in sub-area 11 in September than in August as more should be further south by then. The Workshop **agreed** therefore that a reasonable way to model this was to force the parameter in the catch-mixing matrix for females in sub-area 11 in September to be half of that in August. It also **agreed** that, given the difficulty that 'O' stock animals should have entering sub-area 11 in April, the parameter in the catch-mixing matrix for males in April would be equal to that for females (noting that the total number of females in sub-area 11 in April exceeds that of males).

The sample sizes for males in sub-area 11 in May and June are small. The Workshop agreed therefore that the data for these months would be pooled and a parameter common to both months included in the catch-mixing matrix. The mixing proportion for males in July is roughly half that for females, so it was **agreed** that the parameter in the catch mixing matrix for males in July would be fixed to be half of that for females. Separate parameters should be estimated for males and females in the catch-mixing matrix for August. There are two ways to approach specification of the 'J'-'O' mixing proportion for males in September: (1) this should exceed that for August as the male mixing proportions show an increasing trend with month; or (2) this should be less than that for August as the females are leaving and the males should accompany them to some extent. In the absence of data, the Workshop **agreed** that the parameter in the mixing matrix for males in September should equal that for August.

The previous trials were based on the assumption that the mixing proportions were normally distributed when generating the data used for conditioning. However, the posterior distributions for the mixing proportions from the Bayesian approach are better approximated by a beta distribution. The Workshop **agreed** that future trials be based on the assumption that the 'J'-'O' mixing proportions used during conditioning are generated from beta distributions fitted to the posterior distributions from the Bayesian approach of Annex F.

Some of the mixing proportions are based on data from several years. It was **agreed** that the model estimates to which these proportions are fitted during conditioning would be sample size-weighted year-specified proportions.

8.2 Temporal variability in sub-area 9

In the model conditioning process, a simple approach of random choice each year between two alternative mixing matrices specifying different spatial distributions for the 'W' stock was attempted to reconcile the rather different estimates of abundance for sub-area 9 from dedicated surveys around 1990 and from JARPN in 1994 and 1995. The computations possible within the meeting indicated that this was not successful: they might succeed with fits for very many data replicates and a high rejection rate for poor fits, but this would place an impractical time burden on the conditioning exercise. It was accordingly **agreed** not to model temporal variability in sub-area 9 but rather to use only the 1990 abundance estimate in the conditioning process. Although this means discarding the 1994 and 1995 JARPN estimates, they are probably not comparable with that for 1990 because of the different survey methodology in JARPN. It was agreed that additional variance should be taken into account when generating simulated abundance estimates for future surveys for the RMP testing process (such additional variance is not added to the sampling variance of estimates input to the RMP itself).

Table 2

'J'-'O' mixing proportion estimates for sub-areas 2, 7 and 11. The baseline sample for the 'J' stock is either (a) the bycatch sample from the Sea of Japan or (b) bycatch sample from the Sea of Japan combined with the historical commercial data off Korea. The rows indicated by asterisks will form the basis for the 'J'-'O' mixing proportions used when conditioning the trials.

Sub-										
area	Month	Sex	Years	Ν	Mean	SD	CV	Mode	Beta-α	Beta-β
(a) 'J	stock baseli	ne = by	catch sample from	the Se	ea of Jana	an				
(u) 0 2*	All	Both	1996-2000	12	0.705	0.120	0.170	0.743	9.4367	3.9409
11*	April	F M	1984-87	50 2	0.623	0.069 0.199	0.111 0.267	0.629 0.999	29.8428	18.0575 0.9844
11 11*	April	F	1984-87 1984-87	2 39	0.743 0.081	0.199	0.287		2.8503 2.5963	0.9844 29.4271
11	May May	M	1984-86	9	0.081	0.047	0.980	0.055 0.001	0.9963	9.6786
11*	June	F	1984-80	15	0.093	0.101	0.912	0.187	3.6056	12.4940
11	June	M	1984-87	8	0.224	0.093	0.430	0.187	0.9955	8.6701
11*	July	F	1984-87, 1999	20	0.443	0.106	0.239	0.439	9.3355	11.7201
11*	July	M	1986, 1999	26	0.201	0.079	0.392	0.175	5.0063	19.9174
11*	August	F	1986-87, 1996	16	0.087	0.071	0.815	0.009	1.2894	13.5903
11*	August	M	1986-87, 1996	19	0.363	0.109	0.300	0.349	6.6987	11.7522
11*	May-June	M	1984-87	17	0.054	0.051	0.948	0.001	0.9978	17.4243
7	-	F	1984-87	19	0.049	0.047	0.953	0.001	0.9983	19.4338
7	April April	M	1983-87	19	0.049	0.047	0.933	0.001	1.2518	19.4338
7	May	F	1983-87, 1998	13	0.133	0.000	0.637	0.001	1.9999	12.9997
7	May	M	1983-87, 1998	62	0.133	0.085	0.037	0.077	1.5957	37.4264
7	June	F	1983-86, 1998	15	0.041	0.074	0.808	0.013	1.3026	13.0068
7	June	M	1983-86, 1997-99	52	0.034	0.029	0.867	0.001	1.2529	35.6562
, 7	July	F	1986, 1996	12	0.077	0.071	0.925	0.001	1.0006	11.9659
, 7	July	M	1984-87	14	0.063	0.059	0.939	0.001	1.0001	15.0010
7	August	F	1986, 1996	3	0.215	0.175	0.811	0.001	0.9768	3.5628
7	August	М	1986, 1996	17	0.057	0.053	0.945	0.001	0.9992	16.6735
7	September	F	1986-87, 1996	6	0.125	0.110	0.882	0.001	1.0000	7.0001
7	September	Μ	1986-87, 1996	28	0.129	0.063	0.494	0.099	3.4454	23.3471
7*	All	Both	1983-87, 1996-99	260	0.028	0.012	0.441	0.023	4.9600	173.5495
(b) 'J	' stock baseli		ycatch sample from		ea of Jap				al sample off	Korea
2	All	Both	1996-2000	12	0.709	0.119	0.168	0.745	9.6347	3.9616
11	April	F	1984-87	52	0.636	0.067	0.106	0.641	31.9878	18.3254
11	April	M	1984-87	2	0.746	0.197	0.264	0.999	2.9007	0.9894
11	May	F	1984-87	39	0.081	0.047	0.579	0.055	2.6590	30.3484
11	May	М	1984-86	9	0.093	0.084	0.913	0.001	0.9973	9.7825
11	June	F	1984-87	15	0.227	0.101	0.443	0.191	3.7155	12.6171
11	June	Μ	1984-87	8	0.102	0.092	0.904	0.001	0.9966	8.7758
11	July	F	1984-87, 1999	20	0.442	0.106	0.240	0.437	9.2539	11.6961
11	July	Μ	1986, 1999	26	0.194	0.077	0.395	0.167	4.9693	20.6590
11	August	F	1986-87, 1996	16	0.092	0.072	0.778	0.029	1.4083	13.8745
11	August	Μ	1986-87, 1996	20	0.398	0.106	0.266	0.389	8.0720	12.1854
11	May-June	М	1984-87	17	0.054	0.051	0.948	0.001	0.9985	17.6170
7	April	F	1984-87	19	0.048	0.046	0.953	0.001	0.9989	19.6242
7	April	Μ	1983-87	19	0.077	0.062	0.800	0.019	1.3656	16.3954
7	May	F	1983-87, 1998	13	0.133	0.085	0.637	0.077	1.9999	12.9997
7	May	Μ	1983-87, 1998	62	0.050	0.033	0.664	0.031	2.1034	39.7826
7	June	F	1983-86, 1999	15	0.097	0.075	0.771	0.033	1.4236	13.2108
7	June	M	1983-86, 1997-99	52	0.037	0.030	0.812	0.005	1.4243	36.7464
7	July	F	1986, 1996	12	0.075	0.070	0.928	0.001	0.9979	12.2555
7	July	M	1984-87	14	0.063	0.059	0.939	0.001	1.0001	15.0010
7 7	August	F M	1986, 1996 1986, 1996	3 17	0.210	0.171 0.052	0.814 0.947	0.001 0.001	0.9815 0.9980	3.6878
7	August September	M F	1986, 1996	6	0.055 0.125	0.052	0.947 0.882	0.001	0.9980	17.0781 7.0001
7	September	г М	1986-87, 1996	28	0.123	0.063	0.882	0.001	3.5652	23.9313
7	All	Both	· · ·	260	0.130	0.003	0.483	0.027	5.9135	177.4300
'	4311	Dom	1,05 07, 1,00-99	200	0.052	0.015	0.405	0.027	5.7155	177.1500

8.3 Incidental catches

The Workshop reviewed the Committee's decision last year (IWC, 2002a, p.101), regarding scenarios for incidental catches off Japan (25 or 75 each year) in the light of the new information provided by the Japanese scientists that, following revision of Japanese reporting laws regarding such catches, a total of 54 common minke whales had been reported incidentally caught during the latter half of 2001. The Workshop consequently **agreed** that option (iv) put forward last year (IWC, 2002a, p.101) should be pursued, i.e.

the baseline levels of 25 and 75 remain as they are, but additional explorative results be obtained for levels of 50 and of 100 whales for one trial in order to test the extent to which interpolation/extrapolation can be achieved reliably.

8.4 Modified method for conditioning

The approach suggested last year (IWC, 2002c, p.143) to deal with temporal variability in sub-area 9 had proved unsatisfactory, and the simpler approach described in Item 8.2 above also failed. Given the consequential decision not to

use the 1994 and 1995 JARPN abundance estimates in the conditioning process, the need for a modification of the original method fell away³.

Procedures to check the adequacy of the conditioning achieved for trials are detailed in Item 12.1 below.

8.5 Abundance estimates

Annex C reviews the results of sighting surveys in the western North Pacific and their acceptability for use in conditioning the trials. The Workshop **agreed** with the recommendations in Annex C, except that the JARPN estimates for sub-area 9 in 1994 and 1995 would not be used in this manner for reasons detailed in Item 8.1 above. It was also **agreed** that if abundance estimates were used as 'minimum' rather than as 'best' estimates for conditioning purposes (often because only a small portion of a sub-area was covered by the survey), the lower bound imposed on the model population should be the estimate in question less one standard error.

Although analysis of the dedicated survey of sub-area 12 in 2000 required further refinement, and so could not be used in the conditioning process, it was agreed that RMP tests would assume that an acceptable estimate from that survey would become available in due course.

Given the decision to split each of sub-areas 7, 8 and 9 into two for stock structure representation purposes (by lines at 147°E, 153°E and 162°E respectively), estimates of abundance are required which are split on this basis. It was **agreed** that the splits for sub-areas 8 and 9 would be *pro rata* by area, but that more care would be needed for sub-area 7 to make allowance for greater densities closer to the coast of Japan. An e-mail group under Miyashita, and including Butterworth and Taylor, would finalise these estimates (see Item 12.1 below). Punt and Allison were requested to finalise other aspects of the trials (such as mixing matrix revisions) necessitated by this splitting of these sub-areas.

Miyashita undertook to report further to the 2002 Scientific Committee meeting on aspects related to the estimation of abundance from the various sighting surveys associated with JARPN and JARPN II.

8.6 Harvesting plans

It is necessary to specify harvesting plans (areas and seasons in which harvesting is proposed to occur or not to occur) in order to fully specify a management option and hence conduct the *Implementation Simulation Trials*. The *Implementation* recommended by the Scientific Committee will be based on one of the management options evaluated (and see Item 10.2). If the actual harvesting plan differs from the management options evaluated, additional trials (in an *Implementation Review*) will have to be conducted.

Kawahara advised that Japan planned future small-type whaling in sub-areas 7 and 11, and pelagic whaling in sub-areas 8, 9 and 12. However, there would be no operations in sub-area 11 in April and July to reduce possible catches of 'J' stock whales.

To investigate whether more stringent spatial closures to further reduce catches of 'J' stock whales would provide any substantial additional benefit, the Workshop **agreed** that as a sensitivity test, the consequences of complete closure of sub-area 11 in all months, together with sub-area 12SW in June, should also be investigated.

8.7 Other

The Workshop considered whether it was necessary to specify that the sex ratio in sub-area 12NE was 50:50 based on data collected by the *Miwa Maru* in the north of this sub-area. Ohsumi explained that imbalance in this ratio was motivated by analogy with the Antarctic, where female whales dominated closer to the ice-edge. The Workshop therefore **agreed** that it would not change the current specification that the density of females exceeds that of males in the Okhotsk Sea.

The Workshop **reconfirmed** decisions reflected in IWC (2002c) regarding 'J' stock depletion, bycatches off Korea and trials with higher *MSYR*. These are reflected in the final trials specified, as listed in Item 10.1 below. The Workshop noted the response given to Hatanaka last year (see IWC, 2002a, p.101) regarding use of *MSYR* values pertinent to the 1+ component of the population, to the effect that such trials could be run during 2002 Scientific Committee meeting if required. Punt and Allison will make the necessary preparations to the able to deal with such a request.

9. RESULTS OF TRIALS CONDUCTED SINCE THE 2001 SC MEETING

The results of the two trials conducted during the Workshop are discussed under Item 6.1.

10. FINAL TRIALS AND RUNNING THEREOF

10.1 Specification of final trials

The Workshop developed a final set of *Implementation Simulation Trials* (see Annex H) in the light of its discussion regarding stock structure hypotheses that are consistent with the available information. In developing these trials, the Workshop noted that account needed to been taken of:

- the time required to: (i) finalise the specifications of the trials; (ii) code them; and (iii) run them;
- (2) whether the trials are likely to be informative regarding the performance of RMP variants; and
- (3) the need for the trials to be appropriately balanced in terms of the factors considered.

The stock structure hypotheses can be divided into three classes:

- those based on the results of hypothesis testing, which primarily imply the possibility of some 'W' stock animals in sub-area 9 but no additional stock structure to the east of Japan (henceforth referred to as '3 stocks with 2 in sub-area 9');
- (2) those based on the results of the boundary rank method, which suggest that there are three stocks (' O_W ', ' O_E ' and 'W') in addition to the 'J' stock to the east of Japan (henceforth referred to as '4 stocks'); and
- (3) those based on two stocks to the east of Japan (excluding the 'J' stock), which allow mixing of these stocks across most of sub-areas 7-9 during April-September (henceforth referred to as '3 stocks with mixing gradient').

The Workshop **agreed** that all the key factors (e.g. hypotheses regarding the current status of the 'J' stock) to be considered in the trials should be combined with one

 $^{^3}$ This does not necessarily mean that substantial inter-annual variability does not exist; rather there are no data to determine its extent.

'baseline trial' from each of three classes. It should be noted, however, that the Workshop did not select these three trials on the basis of plausibility, even within each class. The three 'baseline' trials and their key features are:

- Baseline-A: 'W' stock in sub-area 9 each year with 60% probability. In a year when the 'W' stock is in sub-area 9, 50% of the animals in sub-area 9W are from the 'W' stock. The fraction of 1+ non-J stock animals in sub-area 12 in August-September in a pristine state that are from the 'W' stock is determined from the relative abundance of such animals in sub-areas 7, 8 and 9 at that time.
- (2) Baseline-C: 4 stock model of which three non-J stocks (' O_W ', ' O_E ' and 'W') occur to east of Japan. The divisions between the ' O_W ' and ' O_E ' and 'W' stocks occur at 147°E and 157°E respectively. These boundaries are 'hard' (no mixing across them). The fraction of 1+ non-'J' stock animals in sub-area 12 in August-September in a pristine state that are from the 'W' stock is determined from the relative abundance of such animals in sub-areas 7, 8 and 9 at that time.
- (3) Baseline-D: 2 stocks ('O' and 'W') to the east of Japan which mix across the area 147°E to 162°E. The highest densities of 'O' stock animals occur in sub-area 7W and decline to the east, while the highest densities of 'W' stock animals occur in sub-area 9E and decline to the west. Two thirds of the 'W' stock moves into sub-area 12 while all of the 'O' stock does this.

The Workshop **agreed** that all of the 'J' stock animals in sub-areas 12SW+12NE would occur in sub-area 12SW while all of the 'W' stock animals in sub-areas 12SW+12NE would occur in sub-area 12NE. The specification regarding the proportion of 'J' stock animals in sub-area 12SW is based on the analyses of the flipper colour information which indicates a high proportion of 'J' stock animals in that sub-area in June (see Table 2). Previous trials that did not split sub-area 12 into smaller sub-areas, instead reduced this estimate of 'J'-'O' mixing by multiplying it by 0.32 so that it applied to the whole of sub-area 12 (IWC, 1997, p.215).

10.1.1 Changes to previous trials

The Workshop developed the full set of trials by first examining the trials developed last year (IWC, 2002c, p.146; and reproduced here as Table 3). It **agreed** that a number of these could be dropped because the factor on which the trial was based was now a specific part of one of the new stock structure proposals. The trials dropped, and the associated reasons, are as follows.

(1) TRIALS 118 AND 119

These trials specify that no 'J' animals are found in sub-area 12NE while no 'W' stock animals are found in sub-area 12SW. These assumptions are now part of the specifications for all of the trials. The previous 'base-case' assumption that the ratio of the 'J', 'W' and 'O' stocks in 12SW and 12NE is the same has been dropped primarily in the light of the information on the fraction of 'J' stock animals in sub-area 12SW based on the flipper colour information and hypotheses for how 'W' stock animals migrate from sub-areas 9 to 12.

(2) TRIALS 122, 123, 124 AND 125

These trials relate to stochastic mixing of 'W' stock animals from sub-area 9 into the sub-areas to the east of this. These trials have been dropped because they were designed to allow for additional variance in sub-area 9. However, the conditioning analyses conducted during the meeting (see Item 6.1) suggest that the stochastic mixing approach underlying these trials did not resolve the problem it was designed to address. Furthermore, the abundance estimates for 1994 and 1995 which suggest additional variance in sub-area 9 and which would form the basis for the estimation of the parameters that define stochastic mixing have been omitted from the conditioning process (see Item 6.1).

(3) TRIALS 105, 105A, 112, 112A, 113, 113A, 120 AND 121

These trials modify the specifications for the fraction of 'O' and 'W' whales in sub-areas 8 and 12 to examine sensitivity to the base-case assumptions. The stock structure hypotheses proposed during the meeting provide revised specifications for this fraction as well as revised sensitivity tests.

(4) TRIAL 117

This trial was developed to assess the implications of the sensitivity to the data used to form the baseline for the 'J' stock when computing the 'J'-'O' mixing proportions for sub-areas 7 and 11 by basing a trial on the 'J'/'O' mixing proportions estimated from the new bycatch samples combined with the earlier commercial samples off Korea. However, the results in Table 2 indicate that the 'J'-'O' mixing proportions are insensitive to the choice of baseline for the 'J' stock. All of the trials will be conducted using the 'J'-'O' mixing proportions in Table 2a (i.e. using only the bycatch samples as the baseline for the 'J' stock).

In addition, the Workshop **agreed** to add a new factor to those considered in the trials based on the assumption that the CV supplied to the RMP is negatively biased because there is additional variance with CV of 40%. This factor is required because the catch mixing matrix for the 'W' stock is not stochastic (see Item 6.1), so there is no additional variance associated with the abundance estimates for the sub-areas to the east of Japan due to stochastic mixing of stocks.

10.1.2 Conclusions

The full set of revised trials is given as Table 4. These therefore consist of the base-case trials, the trial variants specified last year, as well as some new variants that examine sensitivity to the now revised stock structure hypotheses and larger incidental catches off Japan. It should be noted that some of the factors that underlie the trials specified last year cannot be combined with some of the stock structure proposals. For example, *Baseline-D* does not include dispersal so the factors 'lower/higher dispersal' cannot be combined with this baseline trial.

The bulk of trials are conducted for $MSYR_{mat} = 1\%$ because it is known that trials in which $MSYR_{mat} = 1\%$ are more informative regarding the risk-related performance of variants of the RMP than trials that involve $MSYR_{mat} = 4\%$.

The full set of trials is based on longitudinal boundaries at 147°E, 150°E, 153°E, 157°E and 162°E although all of the trials merge at least one of the longitudinal sectors defined by these boundaries when defining sub-areas. The Workshop **agreed** that if a trial is specified in terms of a sub-area that is a combination of two of these longitudinal sectors, the relative fraction of each stock in each sector will be the same although the total abundance in each sector may differ as the operating model will be fitted to the information on abundance from surveys for every one of these sectors.

The Workshop **agreed** that it was necessary to check that the conditioning exercise had been successfully achieved. It **recommends** that Allison develop the facility to provide the

Table 3

.

The set of <i>Implementation Simulation Trials</i> for North Pacific common minke whales specified by the 2001 Scientific Committee meeting. All trials to
be run using both the J1 and J2 incidental catch options. (P=proportional; C=constant). For details see Allison (2002) and IWC (2002c).

Trial no. NPM-	No. of stocks	<i>MSYR</i> Stock J		<i>MSYR</i> Stock W	status in 2000	area 12	of Ĵ in 7&11	in sub- area 12	O/W in 7,8&9 (see item 3)	Korea catch data (see 6)	Description
Base-ca	ises										
101	3	1 (A/B)	1 (F)	1 (K1)	30% K	30	i)	i)	i): No W in 8	Р	Base-case
102	2	1 (A/B)	1 (G1)	-	30% K	-	i)	i)	-	Р	2 stock variant
103	3	4 (A/B)	4 (F)	4 (K1)	30% K	30	i)	i)	i): No W in 8	Р	NPM-101 + <i>MSYR</i> =4%
104	2	4 (A/B)	4 (G1)	-	30% K	-	i)	i)	-	Р	NPM-102 + <i>MSYR</i> =4%
Other											
105	3	1 (A/B)	1 (G)	1 (K1)	30% K	30	i)	i)	iv): 80% O in 9	Р	101 + some O in sub-area 9 (80%)
105a	3	4 (A/B)		4 (K1)	30% K	30	i)	i)	iv): 80% O in 9	Р	101 + some O in sub-area 9 (80%)
106	3	1 (A/B)	1 (F)	1 (K1)	30% K	30	i)	i)	i): No W in 8	Р	101 + lower dispersal rate
106a	3	4 (A/B)	4 (F)	4 (K1)	30% K	30	i)	i)	i): No W in 8	Р	101 + lower dispersal rate
107	3	1 (A/B)	1 (F)	1 (K1)	30% K	30	i)	i)	i): No W in 8	Р	101 + higher dispersal rate
108	3	1 (A/B)	1 (F)	1 (K1)	15% K	30	i)	i)	i): No W in 8	Р	101 + 15% J stock depletion
109	3	1 (A/B)		1 (K1)	50% K	30	i)	i)	i): No W in 8	Р	101 + 50% J stock depletion
109a	3	1 (A/B)	1 (F)	1 (K1)	70% K	30	i)	i)	i): No W in 8	Р	101 + 70% J stock depletion
109b	3	4 (A/B)	4 (F)	4 (K1)	70% K	30	i)	i)	i): No W in 8	Р	103 + 70% J stock depletion
110	3	1 (A/B)	1 (F)	1 (K1)	30% K	30	i)	i)	i): No W in 8	Р	101 + 20% J in 12SW (or max. achievable)
111	3	1 (A/B)	1 (F)	1 (K1)	15% K	30	i)	i)	i): No W in 8	Р	101 + 15% J stock depletion + 20% J in sub- area 12SW+12NE
112	3	1 (A/B)	1 (F)	1 (K1)	30% K	100	i)	i)	i): No W in 8	Р	101 + no W stock in sub-area 12
112a	3	1 (A/B)	1 (F)	1 (K1)	30% K	80	i)	i)	i): No W in 8	Р	101 + 80% O in sub-area 12(SW+NE)
113	3	1 (A/B)		1 (K1)	30% K	10	i)	i)	i): No W in 8	Р	101 + 10% O in sub-area 12(SW+NE)
113a	3	4 (A/B)	4 (F)	4 (K1)	30% K	10	i)	i)	i): No W in 8	Р	101 + 10% O in sub-area 12(SW+NE)
114	3	1 (A/B)	1 (F/H)	1 (K1)	30% K	30	i)	i)	i): No W in 8	Р	101 + some O animals in sub-area 10
115	3	1 (A/B)	1 (F)	1 (K1)	30% K	30	i)	i)	i): No W in 8	Р	101 + g(0) = 0.5 (see item F.h)
116	3	1 (A/B)	1 (F)	1 (K1)	30% K	30	i)	i)	i): No W in 8	Р	101 + misreport Japan incidental catch
117	3	1 (A/B)	1 (F)	1 (K1)	30% K	30	ii)	i)	i): No W in 8	Р	101 + different J proportions in 7 & 11
118	3	1 (A/B)		1 (K1)	30% K	30	i)	ii)	i): No W in 8	Р	101 + no J in 12NE
119	3	1 (A/B)	1 (F)	1 (K1)	30% K	30	i)	iii)	i): No W in 8	Р	101 + no J in 12NE + no W in 12SW
120	3	1 (A/B)	1 (F)	1 (K1)	30% K	30	i)	i)	ii): 1:1 O:W in 8	Р	101 + 1:1 O:W in 8
121	3	1 (A/B)	1 (F)	1 (K1)	30% K	30	i)	i)	iii): No O in 8	Р	101 + no O in 8
122	3	1 (A/B)	1 (F)	1 (K2)	30% K	30	i)	i)	i): No W in 8	Р	101 +different temporal variability (between 9 & 14)
123	2	1 (A/B)	1 (G2)	-	30% K	-	i)	i)	-	Р	102 + different temporal variability (between 9 & 14)
124	3	1 (A/B)	1 (F)	1 (K)	30% K	30	i)	i)	i): No W in 8	Р	101 + no temporal variability
125	2	1 (A/B)	· · ·	- ()	30% K	-	i)	i)	-	Р	102 + no temporal variability
126	3	1 (A/B)	· · ·	1 (K1)	30% K	30	i)	i)	i): No W in 8	C	Different Korean catch data model

plots displayed in Annex D as well as plots that show the time-trajectories of the fraction of each stock in each sub-area for those month/sub-area combinations for which information is available on the 'J'-'O' mixing rate. A small group consisting of Butterworth, Kawahara, Polacheck, Punt and Wade was established to work intersessionally with Allison to examine the details of some of the initial conditioning attempts and to develop summary statistics for conditioning.

10.2 Small Areas /RMP variants to be considered

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 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:

- Small Areas equal sub-areas. For this option, the Small Areas for which catch limits would be set are 7W, 7E, 8W, 8E, 9W, 9E, 11, 12SW and 12NE.
- (2) 7+8, 9, 11 and 12 are *Small Areas* and catches are taken from sub-areas 7W, 9W, 11 and 12SW.

- (3) 7+8+11+12 and 9 are *Small Areas* and catches are taken from sub-areas 11 and 9W.
- (4) 7W, 7E+8+12, 9 and 11 are *Small Areas* and catches are taken from sub-areas 7W, 9W, 11 and 12SW.
- (5) 7+8+11+12 and 9 are combination areas and catches are cascaded to the sub-areas within each combination area.
- (6) as (3) except that the catches from the 7+8+11+12 *Small Area* are taken from sub-areas 7W and 11 using catch cascading across those two sub-areas.

Following the advice of Kawahara (see Item 8.6), catch limits will not be set for sub-area 11 in April or July in any of the trials. The Workshop noted that the fraction of 'J' stock animals was not insubstantial in sub-area 12SW in June and in sub-area 11 in all months. Therefore, it **agreed** to conduct two additional RMP variants based on variants (1) and (5). These will be based on the assumption that catches are zero in sub-area 11 in all months and in sub-area 12SW in June.

In cases where a *Small Area* consists of more than one sub-area, the general approach followed above (as in the past) is to assume the extreme that all catches are taken from the sub-area that would lead to the worst performance in terms of risk-related statistics.

Table 4

The revised list of *Implementation Simulation Trials* for the North Pacific common minke whales. All trials will be run using both the J1 and J2 incidental catch options. The detailed version of this table included in Annex H also lists the mixing matrices.

Tri no NF		No. of stocks	MSYR	'J' stock status in 2000	Description	Old trial equivalent
Ba	se	Lines				
А		3	1%+4%	30% K	Base-case 3 stocks with 2 in sub-area 9	NPM-105 ¹
В		2	1% + 4%	30% K	2 stock variant	NPM-102
С		4	1%+4%	30% K	Base-case 4 stocks with hard boundary at 147°	
D		3	1%+4%	30% K	Base-case with mixing gradient {all moving left} (=Annex G)	
Se	nsitiv	ity trials	6			
	А	С	D			
1	1%+4	₩ 1%+4	.%	30% K	+ lower dispersal rate	NPM-106
2	1%			30% K	+ higher dispersal rate	NPM-107
3	1%			15% K	+ 15% 'J' stock depletion	NPM-108
4	1%			50% K	+ 50% 'J' stock depletion	NPM-109
5	1%+4		% 1%+4%	70% K	+70% 'J' stock depletion	NPM-109a
6	1%		1%	30% K	+ 20% 'J' in 12SW (or max. achievable)	NPM-110
7	1%		1%	15% K	+ 15% 'J' stock depletion + 20% 'J' in 12SW (or max achievable)	NPM-111
8	1%	1%		30% K	Some whales from 9 go east of Kamchatka (162° line)	NPM-112
9	1%	1%		30% K	+ some 'O' animals in sub-area 10 ('O _w ' in 4 stock hypothesis)	NPM-114
1	1%		1%	30% K	+g(0) = 0.5 (see item F.f of Annex H	NPM-115
0 1	1%	1%	1%	30% K	+ mis-report Japan incidental catch	NPM-116
1	1%	1%	1%	30% K	Different Korean bycatch data model	NPM-126
2 1 3	1%	1%	1%	30% K	Different Japanese incidental catch level (50 and 100)	
5 1 4	1%			30% K	Sensitivity to A: some W in 8	
1 5		1%		30% K	More 'O _E ' in 12 SW	
1 6		1%		30% K	Less 'O _E ' in 12 SW	
1 7		1%		30% K	4 stocks with hard boundary at 153°	
1 8		1%		30% K	4 stocks with mixing	
1 9		1%		30% K	4 stocks with intrusion	
2 0		1%+4	·%	30% K	4 stocks ' O_E ' mixing. (intrusion with mixing)	
2 1			1%	30% K	3 stocks with mixing gradient {all moving right}	
2 2			1%	30% K	3 stocks with stochastic mixing	
2 3	1%	1%	1%	30% K	40% additional variance in CV supplied to <i>CLA</i> (see item 10.1)	
2 4	1%	1%	1%	30% K	Sub-area 11 closed in all months + sub-area 12SW closed in June (see item 10.2)	

¹ Note: this is not completely equivalent as it includes a temporal variant.

The Workshop noted that the 'partial cascading' of RMP variant (6) was not in accord with the definition of catch cascading included in the specifications of the RMP because the catch limit is cascaded between two sub-areas rather than among all of the sub-areas in the combination area. The Workshop recalled that this variant arose during discussions among the members of the intersessional Steering Group between the 2000 and 2001 meetings of the Scientific Committee; it was developed because of the fact that it is unrealistic to assume that all of the catches from the 7+8+11+12 *Small Area* would be taken from sub-area 11 only. Rather it implements the specification that the catches from this *Small Area* would be distributed between sub-areas 7W and 11, the two sub-areas in which coastal whaling has occurred in the past.

In discussing this item, it was noted that the approach above is substantially different to that envisaged when the RMP was developed. This is because the RMP was originally developed for baleen whales hunted on their feeding grounds rather than during migration. The Workshop **draws this** to the Committee's attention and **recommends** that it thoroughly reviews the concept of 'partial cascading' and, if deemed appropriate, develops any necessary additions to the explanatory notes to the RMP.

10.3 Methods to examine results including specification of statistics and plots

The Workshop recognised the importance of developing simple and clear approaches to summarise the results of trials to the Scientific Committee (and Commission), but

٦	Га	h	le	5

Work plan and timetable.

(1) Finalise the abundance estimates for subdivisions of sub-areas 7, 8 and 9 (Miyashita (Chair), Butterworth and Taylor)	7 February
(2) Finalise adaptations of existing mixing matrices to cater for the subdivisions of sub-areas 7, 8 and 9 (Allison and Punt)	7 February
(3) Check conditioning on an initial set of trials (Allison [Chair], Butterworth, Kawahara, Polacheck, Punt, Wade)	late February
(4) Specify dispersal rates for the 4 stock trials (Taylor and Martien)	end February
(5) Completion of the specification of the trials based '3 stocks with mixing gradient' hypothesis (Smith [Chair], Polacheck, Punt, Ohsumi,	mid March
Kim)	
(6) Develop format for reporting of results of trials (Smith [Chair], Allison, Butterworth, Kawahara, Taylor)	mid April
(7) Conduct preparatory work to handle a request to conduct trials with MSYR defined in terms of the 1+ component of the population	mid April
(Allison and Punt)	-
(8) Run final trials specified. For practical reasons, these will be coded and run in the order '3 stocks with 2 in sub-area 9', '4 stocks' and	late April
the '3 stocks with mixing gradient' (Allison)	

unfortunately had insufficient time available to discuss this matter in any detail. It therefore **established** an intersessional correspondence group (led by Smith and including Allison, Butterworth, Kawahara and Taylor) to try and develop such approaches prior to the 2002 Scientific Committee meeting. They would attempt to format simple summaries from the more comprehensive tabulation of results previously prepared by Allison (2002) on the basis of Scientific Committee requests for statistics to be reported. The utility of graphical approaches to facilitate comparison of results for different trials or for different RMP variants was emphasised, for example by use of the software developed by Zeh for this purpose in the AWMP sub-committee.

11. RELATIVE PLAUSIBILITY OF TRIALS

Although there was insufficient time to discuss this item, the Chair reiterated his remarks made under Item 7. In particular, he stressed the need for members to develop papers for the 2002 SC meeting addressing this issue, particularly but not exclusively with respect to the various stock structure hypotheses put forward at this meeting. This should also be the mechanism whereby anyone who had to leave the meeting early can comment on the conclusions reached after their departure.

12. WORK REQUIRED PRIOR TO NEXT SC MEETING

12.1 Schedule

The Schedule of work timetabled before the next Scientific Committee meting is given in Table 5.

The Workshop recognised that the above work plan was extremely ambitious and that it may not be possible to complete it within the expected timeframe, given the other computing requirements of the Scientific Committee, particularly with respect to the AWMP.

12.2 Terms of Reference for the intersessional group to facilitate conduct of this work

It was **agreed** that that the intersessional group established at the 2001 SC meeting should continue to facilitate the conduct of the work identified by the Workshop as required prior to the 2002 SC meeting.

13. ADOPTION OF REPORT

The meeting finished at 11.55pm on its final day without having time to consider a draft report. The Chair thanked the participants for their forbearance and noted his concern that insufficient time had been allocated to cover the extensive agenda. He noted that all members had participated fully in the discussion of complex scientific issues that were important to the satisfactory completion of the *Implementation Trials* process. He expressed a general concern that the process of undertaking the *Implementation* exercise required further serious consideration by the Committee outside the pressure of having to complete such an exercise. The Workshop **strongly recommends** that the Scientific Committee thoroughly addresses the question of determining the most appropriate procedure for scheduling and conducting any future RMP *Implementation (Reviews)*, in addition to the discussions held at last year's meeting.

The report was adopted after conclusion of the meeting by means of e-mail correspondence.

14. CLOSURE

The participants thanked: the Chair for his effective and patient handling of this difficult and highly technical meeting; the rapporteurs; and the meeting hosts, the US National Marine Mammal Laboratory, especially Paul Wade.

REFERENCES

- Allison, C. 2002. Report of the Scientific Committee. Annex D. Report of the Sub-Committee on the Revised Management Procedure. Appendix 10. The detailed results for trial NPM101-J1. J. Cetacean Res. Manage. (Suppl.) 4:123-5.
- Hatanaka, H. and Miyashita, T. 1997. On the feeding migration of Okhotsk Sea-West Pacific stock minke whales, estimates based on length composition data. *Rep. int. Whal. Commn* 47:557-64.
- International Whaling Commission. 1997. Report of the Scientific Committee, Annex J. Report of the Working Group on North Pacific minke whale trials, Appendix 3. Estimates of mixing between J and O stocks. *Rep. int. Whal. Commn* 47:214-5.
- International Whaling Commission. 2001a. Report of the Scientific Committee. Annex I. Report of the Working Group on Stock Definition. J. Cetacean Res. Manage. (Suppl.) 3:229-38.
- International Whaling Commission. 2001b. Report of the Workshop to Review the Japanese Whale Research Programme under Special Permit for North Pacific Minke Whales (JARPN), Tokyo, 7-10 February 2000. J. Cetacean Res. Manage. (Suppl.) 3:375-413.
- International Whaling Commission. 2002a. Report of the Scientific Committee. Annex D. Report of the Sub-Committee on the Revised Management Procedure. J. Cetacean Res. Manage. (Suppl.) 4:93-147.
- International Whaling Commission. 2002b. Report of the Scientific Committee. Annex D. Report of the Sub-Committee on the Revised Management Procedure. Appendix 12. Specifications of the North Pacific minke whaling trials. J. Cetacean Res. Manage. (Suppl.) 4:127-38.
- International Whaling Commission. 2002c. Report of the Scientific Committee. Annex D. Report of the Sub-Committee on the Revised Management Procedure. Appendix 15. North Pacific minke whale trials Working Group: details of trial modifications. J. Cetacean Res. Manage. (Suppl.) 4:140-7.
- Kishino, H., Kitada, S. and Hiramatsu, K. 1994. Sampling scheme for the estimation of the stock composition in the mixed population based on genetic data. *Nippon Suisan Gakkaishi* 60(3):359-64. [In Japanese].
- Martien, K.K. and Taylor, B.L. 2001. A new method of generating hypothesized population structures for continuously distributed species using genetic data. Paper SC/53/SD7 presented to the IWC Scientific Committee, July 2001, London (unpublished). [Paper available from the Office of this Journal].

Annex A

Agenda

- 1. Convenor's opening remarks
- 2. Election of Chair
- 3. Appointment of Rapporteurs
- 4. Adoption of agenda
- 5. Review of documents and (within-meeting) computing capabilities
- 6. General issues
 - 6.1 Conditioning
 - 6.2 Data availability
- 7. Review of further genetic analyses results
 - 7.1 Re-estimation of J-O mixing
 - 7.2 Methodologies
 - 7.2.1 Hypothesis testing
 - 7.2.2 Bayes and empirical Bayes approaches
 - 7.2.3 Boundary rank techniques
 - 7.3 Stock structure proposals
- 8. Progress on other trial-related issues
 - 8.1 Mixing of the 'J' and 'O' stocks
 - 8.2 Temporal variability in sub-area 9

- 8.3 Incidental catches
- 8.4 Modified method for conditioning
- 8.5 Abundance estimates
- 8.6 Harvesting plans
- 8.7 Other
- 9. Results of trials conducted since the 2001 SC meeting
- 10. Final trials and running thereof
 - 10.1 Specification of final trials
 - 10.2 Small Areas/RMP variants to be considered
 - 10.3 Methods to examine results including specification of statistics and plots
- 11. Relative plausibility of trials
- 12. Work required prior to SC meeting 12.1 Schedule
 - 12.2 Terms of Reference for the intersessional group to facilitate conduct of this work
- 13. Adoption of report
- 14. Closure

Annex B

List of Documents

SC/J02/NP

- 1. PUNT, A.E. On diagnostic statistics to evaluate *conditioning* of *Implementation Simulation Trials*
- 2. TAYLOR, B.L. and MARTIEN, K. Interpretation of Boundary Rank results for North Pacific minke whales.
- 3. MARTIEN, K. and TAYLOR, B.L. Estimating the degree of support for population structure hypotheses generated by Boundary Rank.
- 4. CUI, G., PUNT, A.E., PASTENE, L.A. and GOTO, M. Bayes and Empirical Bayes approaches to addressing stock structure questions using mtDNA data, with an illustrative application to the North Pacific minke whales.
- 5. TAYLOR, B.L. and MARTIEN, K. Proposed trial specifications for four stock scenarios.
- 6. TAYLOR, B.L. and MARTIEN, K. What measures of genetic similarity should be used to delineate stocks?
- 7. PASTENE, L.A., GOTO, M. and KANDA, N. Proposal on an update to the defaults on stock structure in item 3 of Appendix 15 of Annex D (RMP Sub-Committee Report).

- PASTENE, L.A., GOTO, M. and KANDA, N. Scientific background supporting the stock scenarios proposed by Pastene, Goto and Kanda in SC/J02/NP7.
- GOTO, M. and PASTENE, L.A. Re-estimations of the mixing proportion of O and J stocks in sub-areas 2, 11 and 7 following the guidelines offered in Appendix 15 of Annex D (RMP Sub-Committee Report).
- GOTO, M., KANDA, N. and PASTENE, L.A. Further mtDNA analysis on North Pacific minke whales including JARPN and JARPN II samples from 1994 to 2001.
- 11. KANDA, N., GOTO, M. and PASTENE, L.A. Further microsatellite analysis on North Pacific minke whales including JARPN and JARPN II samples from 1994 to 2001.
- 12. ZENITANI, R., FUJISE, Y., KAWAHARA, S. and KATO, H. Examination of the distribution and reproductive status of western North Pacific minke whales collected in sub-areas 7, 8 and 9 during JARPN and JARPN II from 1994 to 2001.
- 13. Report of the 'Small Drafting Group'.

Annex C

Report of the Small Working Group on Abundance Estimates for Use in Conditioning the *Implementation Simulation Trials*

The small Working Group (Wade, Polacheck, Miyashita, Butterworth) reviewed the abundance data available to the Workshop. The purpose of this was to: (1) document the full source and reference for each estimate; (2) determine whether and what kind of extrapolation might have been made to any of the estimates; and (3) re-examine each estimate's suitability for inclusion in the conditioning of the *Implementation Simulation Trials*.

1. DATA USED IN THE 2001 TRIALS

The data used for *Trials* agreed at the last Scientific Committee meeting are shown in Table 1.

1.1 General points

Initially, there was uncertainty about how the values of areal coverage were made, how they were used, and whether extrapolations of the abundance estimates were made. It was confirmed that areal coverage was calculated as the size of the study area divided by the size of the sub-area. Review of IWC reports revealed that a consistent process was used to make abundance estimates for a given sub-area consistent with each other. An abundance estimate was available for all sub-areas in 1990. Therefore, abundance estimates from

other years were scaled to the 1990 abundance by the ratio of areal coverages. Specifically, an abundance estimate from a different year was divided by the ratio of its areal coverage to the areal coverage in 1990. The abundance estimates that appeared in this table have had this areal coverage correction already performed.

1.2 Specific points

Sub-area 6. 1992. Acceptable for use in conditioning.

Covers only the eastern part of sub-area 6 (southern Sea of Japan), therefore it is properly treated as a minimum estimate.

Sub-area 7. 1990. Not acceptable for use in conditioning.

The same data are used again in making the 1991 estimate (which pools 1990, 91, 92). Only goes down to 39°N, whereas sub-area 7 goes down to 35°N, which explains why it was treated as a minimum. Exact source of estimate also needs to be further documented (see discussion of other 1990 estimates).

Sub-area 7. 1991. Acceptable for use in conditioning, needs documentation.

OK, but source needs to be further documented. The estimate of 2,202 comes from pooling data from 1990, 1991 and 1992. The 1990 survey only went to 39°N. The 1991 and 1992 surveys only went to 145°E, whereas sub-area 7 goes to

Table 1
The abundance data upon which the trials specified by the 2001 Scientific Committee are based

Sub-area	Timing	Areal coverage	Abundance	CV	Туре	Use by CLA? ²
6	Aug-Sep 1992	56.8	893 ¹	0.67	D	No
7	Aug-Sep 1990	54.8	1,741	0.655	D	No
7	Aug-Sep 1991	66.5	2,202	0.383	D	Yes
8	Aug-Sep 1990	62.2	1,057	0.706	D	Yes
9	Aug-Sep 1990	35.1	8,264	0.396	D	Yes
9	Jun-Jul 1994	35.0	4,673	0.441	J	No
9	Jun-Jul 1995	45.1	2,145	0.315	J	No
10	Aug-Sep 1992	30	707^{1}	0.57	D	No
11	Aug-Sep 1990	100.0	2,120	0.449	D	Yes
12	Aug-Sep 1990	100.0	15,641	0.363	D	Yes
12	Aug-Sep 1992	91.2	11,948	0.46	D	Yes
12SW	Aug-Sep 1990	100.0	5,244	0.320	D	Yes
12SW	Aug-Sep 1992	100.0	404	0.432	D	No
12NE	Aug-Sep 1990	100.0	10,397	0.171*	D	Yes
12NE	Aug-Sep 1992	89.4	11,544	0.157*	D	Yes

J: JARPN survey; D: Dedicated survey; *Provisional values, to be recalculated after the meeting. ¹Used as a minimum estimate; ²i.e. Estimate acceptable to calculating catch limits if the Commission decides to implement the RMP.

150°E. Therefore, coverage of the entire sub-area is only achieved by combining the surveys. It is believed that the estimate of 2,202 was calculated at an SC meeting by Buckland (and possibly colleagues). It is verbally described as an inverse-variance weighted average of abundance estimates from the area surveyed in common by the three surveys, with other areas added to that estimate.

Sub-area 8. 1990. Acceptable for use in conditioning, needs documentation.

Source needs to be further documented (derivation of Buckland et al., 1992). The estimate of 1,057 comes from Buckland et al. (1992). Buckland made estimates for the Sea of Okhotsk and for the NW Pacific, areas that correspond mostly (but not entirely) to sub-areas 11+12 and sub-areas 7+8+9, respectively. The Buckland *et al.* estimates therefore needed to be adjusted to correspond to those areas. First, the Sea of Okhotsk estimate needed to be split between sub-areas 11 and 12. The NW Pacific estimate needed to be divided between sub-areas 7, 8 and 9. Additionally, part of it is allocated to sub-area 12 to account for the SE corner of sub-area 12 that extends SE of the Kurils. It is believed that this division was done just by using areas. Buckland *et al.* (1992) state that their estimate using Beaufort states 0-4 is to be preferred, which is 25,049 (7,909 SE, 0.316 CV). However, the sum of the 1990 estimates in Table 1 for areas 7, 8, 9, 11 and 12 is 28,823. If the allocation to sub-areas had been done solely by using areas, the sum should have been conserved. These numbers first appeared in 1993.

Sub-area 9. 1990. Acceptable for use in conditioning, needs documentation.

Source needs to be further documented (derivation of Buckland *et al.*, 1992), and small discrepancy in sum of numbers needs to be investigated.

Sub-area 9. 1994. Acceptable for use in conditioning, needs documentation.

Source is Miyashita and Fujise (1997), but needs to be further documented. Estimate is based on JARPN SSV (sighting/sampling vessel surveys) data only (there is no dedicated vessel survey data). Numbers in Miyashita and Fujise (1997) do not correspond directly to estimate here of 4,673. Areal coverage of survey is reported as 35.0 in Table 1, but source of this number is unclear. The text from the 1997 report states that this estimate was areal coverage extrapolated to match areal coverage in 1990 (35.1). Given that this was SSV data, the maps in Miyashita and Fujise (1997) showing tracklines were examined to see whether they had provided approximately equal coverage probability throughout the study area. Although not randomly sampled, coverage did occur throughout the study area, and for the purposes of conditioning, it was felt that these estimates could remain.

Sub-area 9. 1995. Acceptable for use in conditioning, needs documentation.

Source is Miyashita and Fujise (1997), but needs to be further documented, and small discrepancy in sum of numbers needs to be investigated (see comments in preceding paragraph).

Sub-area 10. 1992. Acceptable for use in conditioning, needs documentation.

Covers only the eastern part of sub-area 6 (northern Sea of Japan), therefore it is properly treated as a minimum estimate.

Sub-area 11. 1990. Acceptable for use in conditioning, needs documentation.

Source needs to be further documented (derivation of Buckland *et al.*, 1992), and small discrepancy in sum of numbers needs to be investigated.

Sub-area 12. 1990. Acceptable for use in conditioning, needs documentation.

Source needs to be further documented (derivation of Buckland *et al.*, 1992), and small discrepancy in sum of numbers needs to be investigated.

Sub-area 12. 1992. Acceptable for use in conditioning.

The areal coverage was 91.2, compared to 100.0 in 1990. This was due to SE corner of sub-area 12 that is SE of Kurils. Estimate of 10,897 (Miyashita and Shimada, 1994) was divided by 91.2/100.0 to get estimate of 11,948.

Sub-area 12SW and 12NE. 1990 and 1992. Acceptable for use in conditioning, need new CV calculations.

The total estimates for sub-area 12 (15,641 and 11948, respectively) were divided into the SW and NE sub-divisions, using the observed n/L in these areas (this assumes constant effective search width and school size across sub-area). Miyashita reported that this was done using a table of calculated n/L by one-degree squares. This necessitated calculating CVs based on one-degree squares as the sampling unit. This differs from the total sub-area 12 estimates, which calculated CVs using daily effort as the sampling unit. It was noted that the one-degree sampling unit calculations led to much lower estimates of the variance compared to using a daily effort sampling unit. It would not be possible to make daily effort variance calculations at the Workshop. Therefore, it was recommended that the variances for the pieces be approximated by allocating the variance for the total estimate calculated from daily effort to the sub-areas 12SW and 12NE estimates using the amount of effort in each sub-area, and using the usual assumption about sample size and expected CV. Even better would be to recalculate the variances using daily effort within the SW and NE sub-areas, which Miyashita indicated could be done, but this was not seen as being necessary.

2. NEW ESTIMATES PRESENTED AT THIS MEETING

A number of new abundance estimates were kindly provided by Japanese scientists to the Workshop. These are summarised in Table 2.

2.1 General points

All of the new estimates were based on JARPN/JARPN II data except for dedicated vessel surveys in 2000 in sub-areas 11 and 12. Areal coverages are provided in the table, but it was confirmed that these had not yet been used. In other words, none of the estimates in the table had been adjusted yet by areal coverage. If they are going to be used in conditioning, the estimates would need to be adjusted to the areal coverage achieved in 1990.

2.2 Specific points

Sub-areas 7 (1999-2000), 8 (1996, 1998), 11 (1996, 1999). Not acceptable for use in conditioning

New estimates in Table 2 for JARPN/JARPN II data from 1996-2000 include both SSV data and dedicated vessel data. Miyashita provided maps of on-effort tracklines for these surveys, but they were pooled across years and stratified by month. This made it impossible to evaluate whether the surveys provided approximately equal coverage probability of a sub-area in a given year. Therefore, the group recommended against using these estimates in the conditioning.

		Additional abu	ndance estimate	s.		
Sub-area	Timing	Areal coverage	Abundance	CV	Source	Use by CLA?
7	June 1999	13.1	1,663	0.528	J	No
7	May-June 2000	62.6	2,332	2.405	J	No
8	July-Aug 1996	31.3	1,385	0.31	J	No
8	May-June 1998	81.6	843	0.541	J	No
11	Aug 1996	32.3	608	0.266	J	No
11	July 1999	32.3	881	0.338	J	No
11	Aug-Sep 2000	100.0	1,456	0.565	D	Yes
12	Aug-Sep 2000	71.1	12,625	0.317	D	No
12SW	Aug-Sep 2000	100.0	3.259	0.574	D	No
12NE	Aug-Sep 2000	63.8	9.366	0.377	D	No

Table 2 Additional abundance estimate

J: JARPN; D: Dedicated survey.

Sub-area 11. 2000. Acceptable for use in conditioning. This estimate is reported for the first time in SC/J02/NP4, and was based on dedicated vessel surveys in 1999 and 2000 pooled. These were naked-eye surveys, done in passing mode, using an independent observer. Miyashita noted that the estimates used: (1) 0-3 Beaufort data; and (2) non-duplicate independent observer sightings in the analysis. Although no details of the analysis were available beyond this, the tracklines in the maps indicate roughly equal coverage probability. On this basis, the group agreed that this estimate was acceptable for use in the conditioning. There was 100% areal coverage, so no adjustment of this estimate was necessary, as the 1990 sub-area 11 estimate also had 100% coverage.

Sub-area 12. 2000. Not acceptable for use in conditioning.

This estimate is reported for the first time in SC/J02/NP4, and was based on dedicated vessel surveys in 1999 and 2000 pooled (see further comments under sub-area 11). Examination of the survey tracklines indicated a lack of approximately equal coverage probability, as very little effort was accomplished in the eastern half of the survey area, due to unfortunate problems with bad weather in 1999 and a mechanical breakdown of a vessel in 2000. However, the estimate was calculated in a pooled fashion, and therefore encounter rates in the western half of the survey area were essentially extrapolated to virtually unsurveyed areas in the eastern half of the survey. The group agreed that a post-stratification into at least two strata (east and west) would be necessary before an estimate from these data would be acceptable.

Sub-area 12SW. 2000. Not acceptable for use in conditioning.

This estimate is reported for the first time in SC/J02/NP4, and was based on dedicated vessel surveys in 1999 and 2000 pooled (see further comments under sub-area 11). Although this survey had 100% survey coverage of this sub-area, examination of the survey tracklines indicated a lack of approximately equal coverage probability. Even though this sub-area was in the SW corner of the study area, this area still had very little effort in the eastern half of the survey area.

REFERENCES

- Buckland, S.T., Cattanach, K.L. and Miyashita, T. 1992. Minke whale abundance in the northwest Pacific and the Okhotsk Sea, estimated from 1989 and 1990 sighting surveys. *Rep. int. Whal. Commn* 42:387-92.
- Miyashita, T. and Fujise, Y. 1997. Abundance estimate of the western North Pacific minke whale in sub-area 9 with notes on the results of dedicated surveys. *Rep. int. Whal. Commn* 47:543-51.
- Miyashita, T. and Shimada, H. 1994. Minke whale abundance in the Okhotsk Sea, the Sea of Japan and off the Pacific coast of Northern Japan estimated from sighting data. Paper SC/46/NP6 presented to the IWC Scientific Committee, May 1994 (unpublished). 9pp. [Paper available from the Office of this Journal].

Annex D

Diagnostic Plots for the Two Trials

Cherry Allison and Andre Punt

Figs. 1-3 on following pages

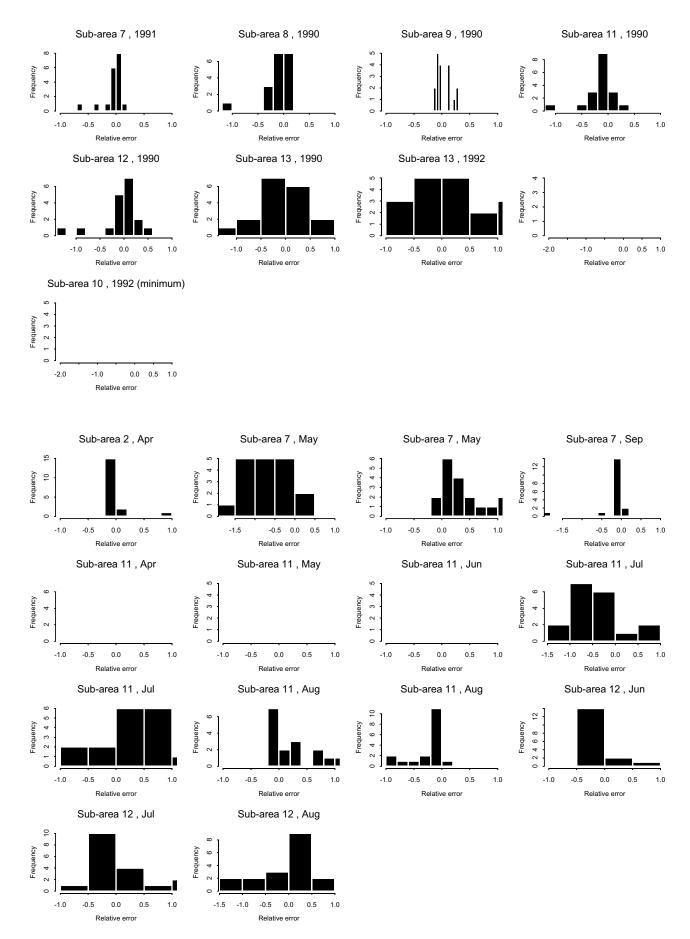


Fig. 1(a). Standardised residuals for the trial 1.

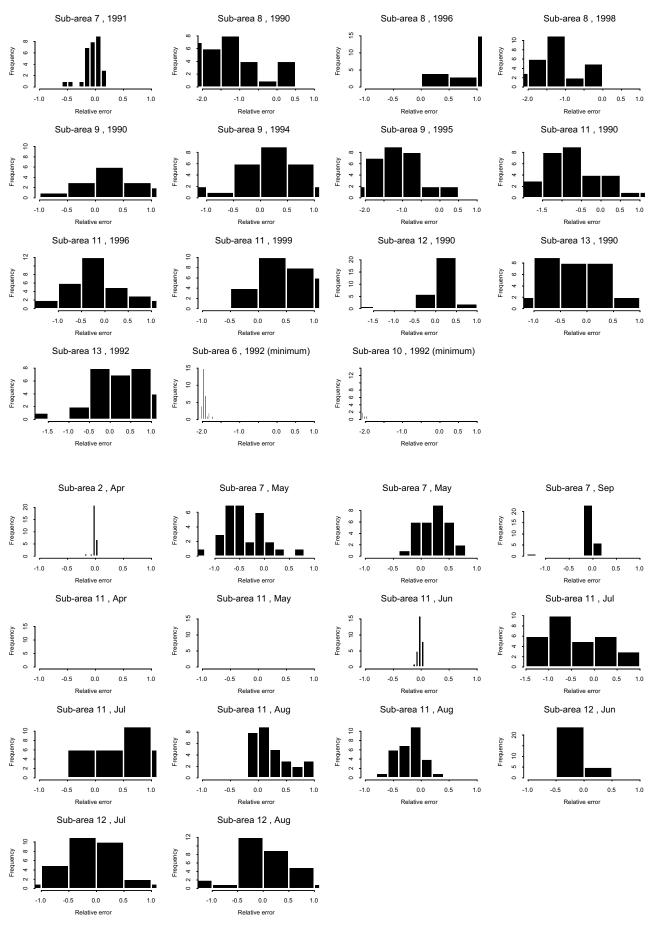


Fig. 1(b). Standardised residuals for trial 2.

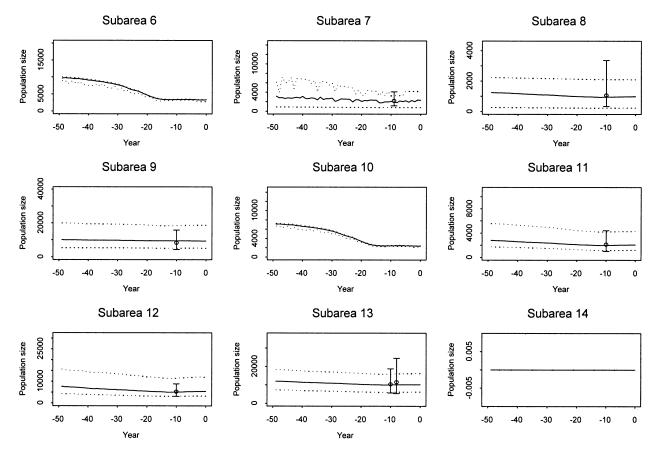


Fig. 2(a). Time-trajectories (medians and 90% intervals) of 1+ population size in August for trial 1. The abundance estimates used when conditioning the simulations are shown by the estimate plus / minus one standard deviation.

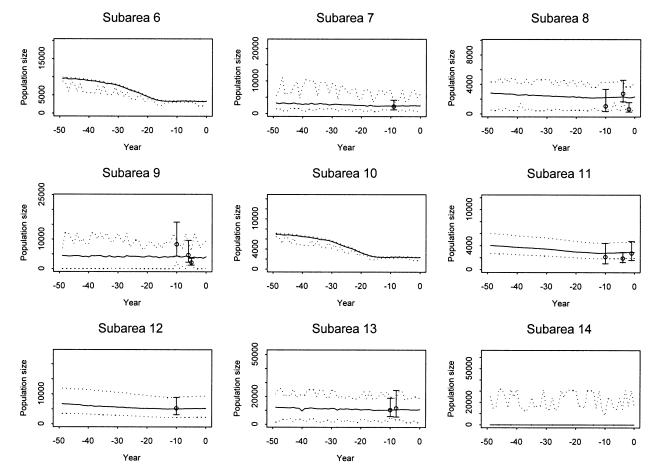
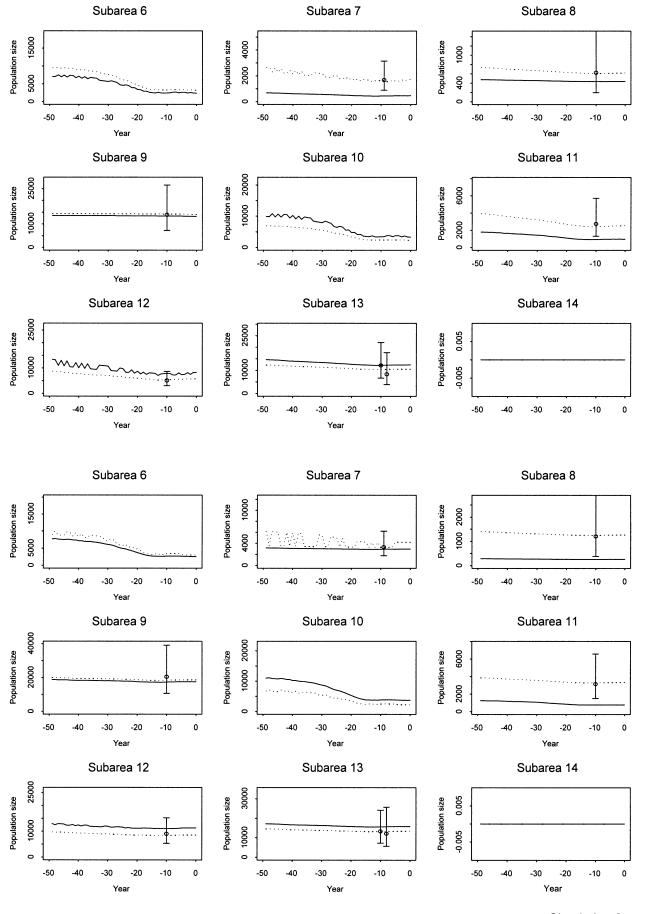
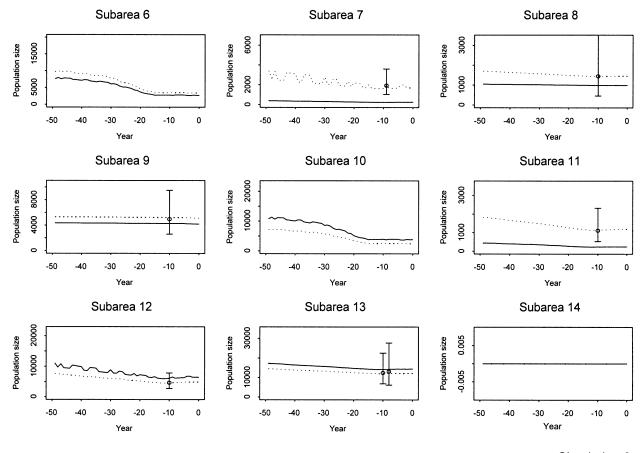


Fig. 2(b). Time-trajectories (medians and 90% intervals) of 1+ population size in August for trial 2. The abundance estimates used when conditioning the simulations are shown by the estimate plus/minus one standard deviation



Simulation 2

Fig. 3(a). Time-trajectories (May – solid line; August – dotted line) for simulations 1-3 of trial 1. The solid dots denote the abundance estimates used for fitting the selected simulations plus/minus one standard deviation.



Simulation 3

Fig. 3(a) cont.

8000

4000

0

20000

10000

25000

-50

Population size 10000 -50

Population size

-50

-40

-40

-40

Population size

Subarea 6

-10

-10

-20

-20

-30

-30

Year

Subarea 6

-20

Year Subarea 12 0

0

0

-10

15000

5000

0

8000

4000

0

15000 Population size

5000 0

-50

-40

-50

Population size

-50

-40

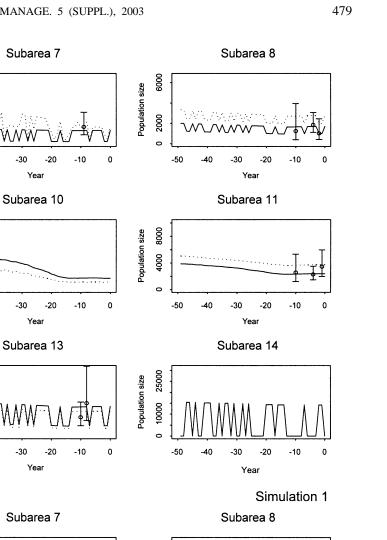
-40

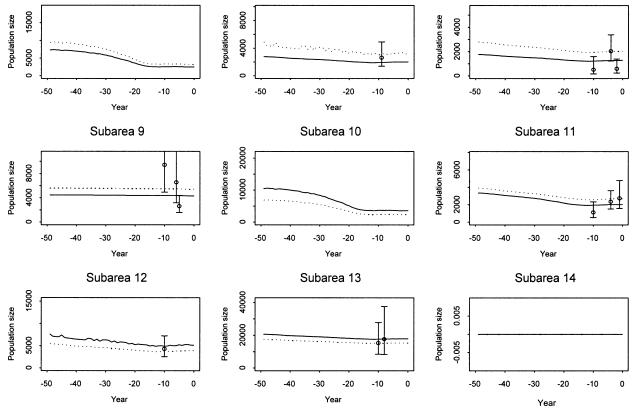
-30

Year

Subarea 9

Population size





Simulation 2

Fig. 3(b). Time-trajectories (May - solid line; August - dotted line) for simulations 1-3 of trial 2. The solid dots denote the abundance estimates used for fitting the selected simulations plus/minus one standard deviation.

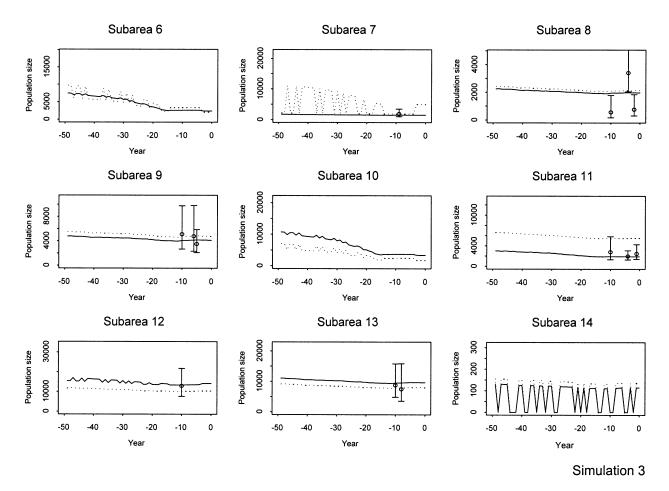


Fig. 3(b) cont.

Annex E The Boundary Rank Method

B.L Taylor and K. Martien

The boundary rank method was developed to generate hypothesised population structures that could then be evaluated through parameter estimation by estimating dispersal rates across putative boundaries. A brief overview of the method is given in SC/J02/NP3. A detailed description is in Martien and Taylor (2001). The method begins with the samples already grouped into initial units based on geographical proximity. The units are connected to conform to a hypothesised type of population structure (such as isolation-by-distance) using a connectivity matrix. The genetic similarity of all connected units is calculated and the most similar units are then clustered together to form a new, larger unit. The measure of genetic similarity used by the analysis is the *p*-value from a χ^2 permutation test. However, no inference regarding statistical significance is made from these *p*-values. They are simply used as a measure of similarity. The clustering continues, at each step removing the boundary separating the two most similar connected units, until only a single boundary remains. The order in which boundaries are removed and the level of genetic similarity between the units being clustered at each step is recorded. This results in a ranking of the boundaries, with the lowest-ranked boundary being the first one removed, and the highest-ranked boundary being the last boundary removed.

The connectivity matrix constrains the geographical form that stocks defined by the boundary rank method can take. In Bayesian terms, it represents the prior on what we believe is plausible regarding the behavior and movement patterns of the whales (SC/J02/NP2). For this reason, it is important that the connectivity matrix conform to some biologically plausible hypothesis, such as isolation-by-distance or an 'intrusion hypothesis' in which 'W' stock is being caught on migration in the vicinity of sub-area 9W, in the middle of a much more broadly distributed 'O' stock. When the connectivity matrix does not correspond to any biologically plausible hypothesis regarding minke whale population structure, the results will have no biologically meaningful interpretation.

The definition of initial strata for use in the boundary rank method requires careful consideration of the number of samples within each initial stratum. The sample size within the initial strata relative to their haplotypic diversity can have a dramatic impact on any genetic analysis of population structure. When sample size is low relative to haplotypic diversity, the degree of genetic similarity between units (as measured by any frequency based statistic) tends to be biased upward. Since the method combines initial units with the highest genetic similarity, if some units have low sample sizes relative to their diversity, the initial clusterings may be driven more by sample size than by actual biology. In other words, units with small sample sizes will be combined simply because they have small sample sizes, not because they really are similar. These early clusterings can strongly influence subsequent clusterings and lead to an incorrect result. The diagnostics help us to determine whether the result for a given set of initial units is likely to be strongly influenced by small sample size. The diagnostics list the sample size within each initial unit along with three different measures of haplotypic diversity. The 'prop. Unique' and 'n-#haps' (columns 3 and 5 in the tables at the top of each diagnostic sheet) are both measures of sample size relative to haplotypic diversity. When these two measures are low, the results of any frequency-based genetic analysis, including the boundary rank method, are likely to be strongly influenced by low sample size and are likely not to reflect the true structure of the population.

The measure of genetic similarity between adjacent units is the *p*-value from a χ^2 permutation test. However, because of the many pairwise comparisons performed by the boundary rank method, it is not appropriate to use the genetic similarity values to evaluate the statistical significance of the boundaries identified by the method. Therefore, a permutation test that can be used to evaluate the strength of boundaries was developed (SC/J02/NP3). This permutation test is used to determine how often the boundary rank method would have detected boundaries with genetic similarity values as low as or lower than those observed if the samples actually came from a single panmictic population. The logic behind the test is that if there is truly only a single population then the strata are completely arbitrary and individuals can be assigned to the different strata randomly. Therefore, we permute the data by randomly assigning individuals to initial units and run boundary rank on the permuted data. This permutation is repeated 500 times and the results obtained from the permuted datasets compared to those observed for the actual data. To ensure that this method is not biased, it was applied to a dataset generated by a computer simulation in which it was known that there was only a single panmictic population. Thus, the null hypothesis of panmixia was correct. When α (the threshold for declaring a *p*-value to be statistically significant) was set to 0.05, the permutation test falsely rejected the null hypothesis at a rate of 0.058, indicating no bias (SC/J02/NP3).

REFERENCE

Martien, K.K. and Taylor, B.L. 2001. A new method of generating hypothesized population structures for continuously distributed species using genetic data. Paper SC/53/SD7 presented to the IWC Scientific Committee, July 2001, London (unpublished). [Paper available from the Office of this Journal].

Annex F

A Bayesian Approach to Estimating 'J'-'O' Mixing Proportions

Andre E. Punt

The estimate of the fraction of 'J' stock animals of a given sex, in a given sub-area during a given month, p, is determined from a Bayesian analysis in which the data are assumed to be multinomially distributed and the prior for pis U[0,1].

The likelihood function is:

$$L \propto \prod_{i} \left(\hat{q}_{i} \right)^{N_{i}}$$
(1)

where

- N_i is the number of animals for the given sub-area, sex and month with haplotype *i*
- \hat{q}_i is the model-estimate for the proportion of animals of the given sub-area, sex and month with haplotype *i*:

$$\hat{q}_i = p \; q_i^J + (1 - p) q_i^o \tag{2}$$

 q_i^I is the relative frequency of hapolype *i* in the baseline sample for the 'J' stock; and

 q_i^o is the relative frequency of hapolype *i* in the baseline sample for the 'O' stock.

The posterior probability assigned to a given value of p is proportional to the likelihood under the assumption of a uniform prior on p. This posterior distribution is summarised by its mean, mode, standard deviation and coefficient of variation. The entire distribution is summarised by a beta(α , β) distribution. Such a distribution could form the basis for the generation of the mixing proportions for the trials. Note that, in some cases, the mixed sample contains haplotypes that are not represented in either of the baseline samples. The data for such haplotypes are ignored.

Annex G

A Three-Breeding-Group Migratory Hypothesis for Common Minke Whales in the Western North Pacific¹

Tim D. Smith

INTRODUCTION

The Implementation Simulation Trial (IST) structure that formed the basis for the trials presented to the Scientific Committee in July 2001 did not cover the full range of uncertainties, primarily because new data from JARPN and from recent bycatches off Korea and Japan suggested uncertainties not previously included in the ranges of hypotheses considered. The Committee established a Steering Group to, *inter alia*, 'specify final trials in the light of discussions at the 2001 SC meeting and the results of trials run intersessionally'. During the present Workshop, results of more extensive hypothesis testing and some new spatially based analyses were reviewed.

Those statistical results along with the biological knowledge of this species based on scientific studies of the earlier commercial whaling operations were reviewed in detail. This Annex outlines a hypothesis that three minke whale breeding groups with differential degrees of mixing on migratory and feeding grounds occur in this area – called *Baseline-D* under Item 7.3 of the main report. This hypothesis is consistent with all the available data, and plausible in its biological basis. Further, it is useful in suggesting possible additional observations that might be made to test it. However, it is not the only hypothesis that is consistent with the existing data and uncertainties.

HYPOTHESIS

There are three breeding groups of minke whales in the western North Pacific.

(1) One group (J) occurs primarily in the Sea of Japan (East Sea)

A. Migrating seasonally from unknown southern breeding areas into the Sea of Japan (East Sea) from the south.

- B. Migrating out of the Sea of Japan (East Sea):
- (a) as early as April;
- (b) with high relative abundance just north of Japan;

¹ This Annex was written after the meeting. It represents a report of the discussions of a small group (Smith (Chair), Kim, Punt, Ohsumi and Polacheck) established by the Chair during the meeting and initially written by Smith. Smith reported verbally on the deliberations of the small group at the Workshop and their discussions were used in the formulation of *Baseline-D* (Item 7.3), predominantly by Smith and Polacheck. Participation in this group means that the individual provided at least technical or biological advice/information – it does not necessarily imply agreement by all members of the group that (a) *Baseline-D* is the most plausible (or even likely); and (b) that other scenarios presented are not plausible.

- (c) with high relative abundance in the southwest Sea of Okhotsk;
- (d) occurring in Pacific waters near the northern Japanese Islands from April through September in low relative abundance.

C. Additional structure within this breeding group is possible.

(2) A second group (O) is restricted to Pacific waters along and offshore of the coast of Japan

A. Migrating from unknown southern breeding areas north, parallel to the coast of Japan.

- B. Migrating into northern feeding areas to:
- (a) the Okhotsk Sea;
- (b) east of the Kamchatka Peninsula.
- C. Distributed seaward from the coast of Japan:
- (a) in decreasing abundance with distance;
- (b) differentially by sex and age, with males travelling further offshore;
- (c) with females and younger animals migrating earlier and closer to shore;
- (d) occurring in greater proportion to the Okhotsk Sea;
- (e) with no (or limited) intrusion west into the Sea of Japan.

(3) A third group (W) occurs offshore of the coast of Japan

A. Migrating north from unknown southern breeding areas in the region offshore of the Bonin-Japan Trench.

- B. Migrating into northern feeding areas:
- (a) east of the Kamchatka Peninsula;
- (b) in the Okhotsk Sea.

C. Distributed from offshore areas towards the coast of Japan:

- (a) in decreasing abundance with closeness to the shore;
- (b) with females migrating earlier and in greater proportion to the feeding areas.

(4) The spatial overlap between the W, O and J groups differs

- A. The J and O groups have limited and seasonal overlap:
- (a) greatest in the SW Okhotsk Sea (sub-areas 11 and 12SW);

(b) less around the Japan Islands.

- B. The O and W groups have broad overlap:
- (a) during migration and on the feeding grounds;
- (b) not overlapping west of the Bonin-Japan Trench.

C. The overlap of O and W varies in the feeding grounds with environmental conditions, with both groups being more abundant in the east or in the west in different years.

D. The hypothesis is not specific about the nature of the breeding stock dynamics and would not preclude some overlap corresponding to a spatial gradient structure, some temporary exchange of animals among the O and W breeding grounds or low levels of permanent dispersal of animals.

BASIS OF HYPOTHESIS IN DATA

That minke whales in the western North Pacific are distributed in at least three groups that breed separately is indicated by differences in genetic frequencies. One difference is between whales sampled from the Sea of Japan (East Sea), and seasonally on the Pacific side of Japan, and those sampled from near Japan on the Pacific side. These data are best explained by two breeding groups that overlap at the edges of their distributions seasonally. Morphological differences have been identified that are consistent with these genetic data, and that extend these conclusions into the feeding grounds.

The second difference is in genetic frequencies among animals sampled from near shore and from further offshore in the Pacific. Various spatial and seasonal partitions of the samples have revealed significant differences. Further, agglomerative methods of combining various small pre-defined groupings of the samples have suggested spatial differences in frequencies that are broadly consistent, with one partition around 147°E, and the other around 157°E.

Although neither the multiple hypothesis testing nor the agglomerative clustering methods suggest spatial boundaries between the O and W groups, the genetic frequency differences clearly imply the existence of separate breeding groups. Further, the differences between early and last season samples in the south and the north of the furthest offshore area sampled suggest substantial and possibly variable mixing between the two groups.

Differences in seasonal timing and sex ratios in the earlier commercial catch and in the Japanese research whaling samples are consistent with differential seasonal migration by sex and age. Migrating calves and females are more frequent in samples taken along the coast of Japan than in more offshore waters.

This model is based primarily on the peak season commercial whaling data. However, it should be noted relative to the hypothesised J group migration that some whales have been taken in pre-April season and during winter in areas around Japan and Korea, suggesting that not all J group minke whales are on the hypothesised breeding ground in the winter months. These data need to be examined in greater detail to validate this portion of the hypothesis.

IMPLEMENTING THE THREE GROUP MIGRATORY HYPOTHESIS

We assume that the three groups of minke whales (W, O and J) breed in southern areas during winter months. In the absence of information on the geographic extent of minke whale breeding grounds in any ocean, we assume that these areas are located such that the main locus of spring migrations are into the Sea of Japan (East Sea) for the J group

and along the coast of Japan for the O group. While the locus of migration for the W group does not have to be within the sampled area, substantial numbers of animals relative to O group abundance must occur in that area. Given the lack of information on minke whale breeding areas, the hypothesis is not meant to preclude possible overlaps between the O and W stock breeding areas (e.g. some form of clineal structure). Also, the hypothesis is not meant to exclude the possibility of some temporary exchange or low of dispersal of animals among the O and W breeding grounds. However, in the implementation developed here, no specific allowance is made for such exchanges.

The basic simulation structure that has been previously developed provides an adequate basis for implementing this hypothesis, and below we identify the changes in that model that would be required to accommodate this hypothesis.

The general migratory patterns for the O and W groups postulated in this hypothesis are shown diagrammatically in fig. 4 of the Workshop report. Their movements from the putative southern breeding areas (depicted by bold wavy lines) are depicted with lines with arrow heads, showing differential patters for the two breeding groups by sex. The bolder solid and dashed lines depict O and W females migrating east of the Kamchatka Peninsula and into the Okhotsk Sea. The finer solid and dashed lines depict O and W males migration, with the change in the lines to include dots denoting that some males do not migrate as far north as do the females.

The proportion of O group animals is assumed to decrease with distance from the coast of Japan, with especially the males spreading east seasonally (and hence latitudinally). We implement this pattern into an analytic framework by assuming that while the abundance of whales varies spatially by season, the proportion of the O and W groups does not. We assume that the migration of the O animals is related to the Bonin-Japan-Kuril Trench (approximated by a line from 140°E, 30°N to 147°E, 47°N, extended north of 47°N along 147°E). To the east of this line, the proportion of O animals decreases exponentially with distance from the line. The proportion of O animals at 155°E is assumed to decline linearly with decreasing latitude from a fixed value at 47°N (p_{47}) to a value of 0.01 at 30°N. The corresponding exponential rates for each latitude are computed to achieve that specified proportion at 155°E (Appendix 1).

We allow the proportion O animals at 155°E and 47°N, p_{47} , to range from 0.60 to 0.20 (Figs 1a-c). The amount of spreading eastward decreases as p_{47} decreases. We account for the differences in migration of males and females by assuming different values of p_{47} , with that for females being always lower than that for males. The proportion of W animals in each sub-area is computed the complement of the proportion of O group whales in that area. This latter is computed to account for the differential migration and longitudinal spreading of the sexes by computing the sex specific abundance weighted average of the modelled proportions. The sex distribution of the W animals on the feeding grounds is assumed to be the same as for the O group animals.

Plausible seasonal distributions of O group males, females and juveniles are shown in Table 1 in terms of proportions of the total of each group located in each of three regions by month over the summer migratory period. Thus males, females and juveniles are assumed to be equally abundant in sub-areas '2' and '3' before April and after September. Females and juveniles are assumed to become less abundant more rapidly than males in sub-areas 2 and 3, and to show up first in the 7-9 sub-areas and then in the 12 sub-area and the

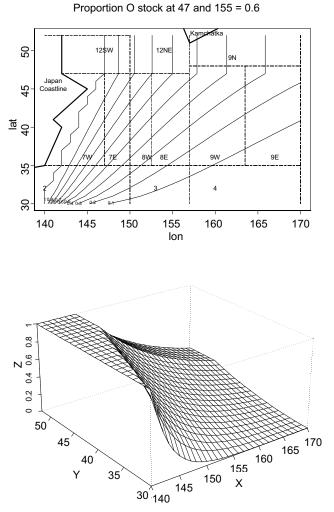


Fig. 1a. Model of proportion of 'O' group minke whales over space on migration route with $p_{47} = 0.60$.

northern portion of sub-area 9 (9N). Females maintain their numerical advantage in the feeding grounds and males occur in greater numbers in sub-areas 7-9 throughout the season. The values in Table 1 are scaled by introducing three estimable parameters multiplying the relative abundance for males, females and juveniles in the 7-9 sub-areas (Table 2).

Abundance of whales in the sub-areas 7-9 is allocated among the sub-areas 7W, 7E, 8W, 8E, 9W and 9E by integrating the equation defining the spatial distribution across each sub-area and using the results to pro-rate total abundance to each of the smaller areas. Similarly, the abundance in 12 and 9N is allocated among sub-areas 12SW, 12NE and 9N in a similar manner. Thus, the spatial distribution function would be numerically integrated for a sufficiently fine spatial grid for each sub-area 7W to 9E and 12 and 9N. Table 2 would then be expanded to a full catch-mixing matrix using the relative abundance in 7W to 9E, while the relative abundance in 12SW and 12NE and 9N would define the differential between those latter areas. In this, W breeding group animals would not occur in 12SW while the split of O breeding group animals would be estimated. This allows the allocation to be computed once the value for p_{47} is specified, rather than as part of the conditioning process.

We assume two scenarios relative to the distribution by sex and breeding group. In the first, the Okhotsk Sea is assumed to be the more desirable and hence the parameter p_{47} is 0.20 for females and 0.40 for males. This is referred to

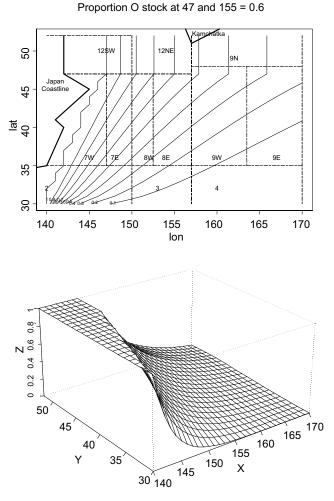


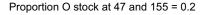
Fig. 1b. Model of proportion of 'O' group minke whales over space on migration route with $p_{47} = 0.40$.

as 'leaning west' toward the assumed better habitat. The second is where that area is less desirable, and p_{47} taking on the values 0.40 for females and 0.60 for males i.e. 'leaning east'. These two scenarios are combined in three ways. The first is to assume that the habitat is consistently better in the west ('leaning west') and second that it is better in the east ('leaning east'). The third is that the habitat quality varies stochastically with probability one half from year to year, and the animals respond to this without lag.

This specification of how to implement this hypothesis is tentative given its spatial complexity, and more flexibility is likely needed than allowed for here. One area is in the assumption that the proportion of O and W groups does not vary seasonally. Another is in how to treat lack of fit to abundance data, either as something to be reparameterised for or as additional variance. Further, the assumption about habitat quality differences should imply greater numbers of whales in the better habitat, and parameterisations must ensure for example that when the habitat is better in the west, O group animals drawn into the Okhotsk Sea do not 'displace' W group animals to the east.

CONCLUSIONS

The three breeding group hypothesis suggested here is consistent with the available data, and the implementation suggested is plausible biologically. We suggest that the performance of the RMP should be tested assuming a three breeding group migratory model to ensure the RMP's



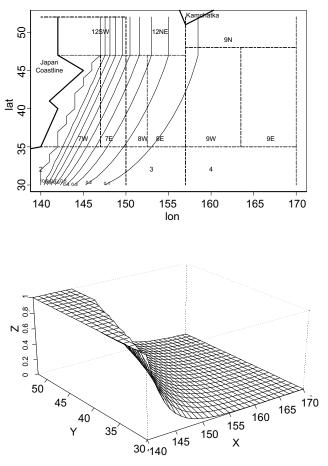


Fig. 1c. Model of proportion of 'O' group minke whales over space on migration route with $p_{47} = 0.20$.

Table 1

Relative abundance of O group whales by area and month for mature males (M) and females (F), and for juveniles (age <5, J). The row entries sum to 1.0 for males, females and juveniles, separately.

2 & 3				7-9		12 & 9N			
Month	М	F	J	М	F	J	М	F	J
Pre	1.0	1.0	1.0	0.0	0.0	0.0	0.0	0.0	0.0
Apr	0.8	0.7	0.7	0.2	0.1	0.2	0.0	0.2	0.1
May	0.5	0.1	0.3	0.3	0.3	0.4	0.2	0.6	0.3
Jun	0.0	0.0	0.0	0.7	0.2	0.4	0.3	0.8	0.6
Jul	0.0	0.0	0.0	0.7	0.2	0.2	0.3	0.8	0.8
Aug	0.0	0.0	0.0	0.8	0.3	0.3	0.2	0.7	0.7
Sep	0.1	0.1	0.1	0.8	0.3	0.4	0.1	0.6	0.5
Post	1.0	1.0	1.0	0.0	0.0	0.0	0.0	0.0	0.0

performance when it is applied to whales on the migratory route. It should be noted that the hypothesis developed here is not necessarily the only plausible hypothesis that is consistent with the available data.

Our model could be tested further by additional observations both in the areas that have been sampled previously and in areas further north. For example, observations on relative abundance of minke whales in the Okhotsk Sea and east of the Kamchatka Peninsula would allow the feeding area spatial distribution to be validated. Similarly, additional observations on genetic frequencies

Table 2a

Generic catch mixing matrices for the 'O' stock. Distribution pattern are provided for mature males (age 10 and older), mature female (age 10 and older), and juveniles (age 4 and younger). The catch mixing matrices for animals aged 5-9 are determined by linear interpolation.

	2-3			7-9			12 & 9N		
Month	М	F	J	М	F	J	М	F	J
Pre	1.0	1.0	1.0	-	-	-	-	-	-
Apr	0.8	0.7	0.7	$0.2\gamma_1$	$0.1\gamma_1$	$0.2\gamma_1$	-	$0.2\gamma_2$	$0.1\gamma_2$
May	0.5	0.1	0.3	$0.3\gamma_1$	$0.3\gamma_1$	$0.4\gamma_1$	$0.2\gamma_2$	$0.6\gamma_2$	$0.3\gamma_2$
Jun	-	-	-	$0.7\gamma_1$	$0.2\gamma_1$	$0.4\gamma_1$	$0.3\gamma_2$	$0.8\gamma_2$	$0.6\gamma_2$
Jul	-	-	-	$0.7\gamma_1$	$0.2\gamma_1$	$0.2\gamma_1$	$0.3\gamma_2$	$0.8\gamma_2$	$0.8\gamma_2$
Aug	-	-	-	$0.8\gamma_1$	$0.3\dot{\gamma}_1$	$0.3\gamma_1$	$0.2\gamma_2$	$0.7\gamma_2$	$0.7\gamma_2$
Sep	0.1	0.1	0.1	•	$0.3\gamma_1$	•	$0.1\gamma_{2}$	$0.6\gamma_2$	$0.5\gamma_2$
Post	1.0	1.0	1.0	-	-	-	-	-	-

Table 2b

Generic catch mixing matrices for the 'W' stock. Distribution pattern are provided for mature males (age 10 and older), mature female (age 10 and older), and juveniles (age 4 and younger). The catch mixing matrices for animals aged 5-9 are determined by linear interpolation.

Month	2-3			7-9			12 & 9N		
	М	F	J	М	F	J	М	F	J
Pre	1.0	1.0	1.0	-	-	-	-	-	-
Apr	0.8	0.7	0.7	0.2γ3	0.1γ ₃	0.2 ₃	-	$0.2\gamma_4$	0.1γ ₄
May	0.5	0.1	0.3	0.3γ3	$0.3\gamma_3$	$0.4\gamma_3$	$0.2\gamma_4$	$0.6\gamma_4$	$0.3\gamma_4$
Jun	-	-	-	0.7γ3	0.2γ3	0.4γ ₃	$0.3\gamma_4$	$0.8\gamma_4$	0.6γ4
Jul	-	-	-	0.7γ ₃	0.2γ ₃	$0.2\gamma_3$	$0.3\gamma_4$	$0.8\dot{\gamma}_4$	0.8γ4
Aug	-	-	-	0.8γ3	$0.3\gamma_3$	$0.3\gamma_3$	$0.2\gamma_4$	$0.7\gamma_4$	$0.7\gamma_4$
Sep	0.1	0.1	0.1	0.8γ3	$0.3\gamma_3$	$0.4\gamma_3$	$0.1\gamma_{4}$	$0.6\gamma_4$	0.5γ4
Post	1.0	1.0	1.0	-	-	-	-	-	-

throughout the 7-9 sub-areas may possibly help to further clarify the degree of mixing between the two suggested breeding groups.

Observations on winter distribution patterns, and on movements when leaving the feeding areas, such as might be obtained from multi-month satellite tagging data would help clarify the location and possible discreteness of breeding areas. Similarly, multi-monthly satellite tagging of individuals across the longitudinal range early in the year would provide important information on the extent to movement and mixing of animals across the feeding grounds.

This migration model would be consistent with the possibility their being only three breeding groups in across the entire Pacific, and the low frequency of calves in offshore waters being explained by calves migrating near the coasts of Japan on the west and North America on the east. Observations about minke whales in other areas of the Pacific could help resolve these questions. However, the available data are also consistent with a number of other hypotheses about the unsampled area that are less extreme, including additional breeding groups. However, given the potential for low levels of exchange of individuals between the two breeding grounds combined with temporal variability in the annual migration, the power of further genetic sampling to determine the level of mixing may be low.

Appendix 1 MODEL FOR THE SPATIAL DISTRIBUTION OF THE O GROUP

The proportion of O group animals (p_o) varies with latitude and longitude seasonally according to the following equations, where functions are shown in bold. The function \forall (lat) determines the value of the exponential parameter that will ensure the proportion of O animals at longitude 155°E is as specified by the function $p_{155}(lat)$. This latter function specifies a linear reduction in the proportion of O group animals from the parameter value p_{47} (0.20, 0.40, 0.60) at 47° N to 0.01 at 30°N. The function \forall (lat) also depends on the longitude of the Bonin-Japan-Kuril Trench, which approximated by a line from 140°E, 30°N to 147°E, 47°N, and extending north of 47°N along 147°E. This longitude is specified by the function $lon_{tr}(lat)$.

 $p_o(\text{lat, lon}) = \min(1, \exp((\text{lat}) * (\text{lon} - lon_t(\text{lat}))))$ where:

 $\forall (lat) = \log (p_{155}(lat)/(155 \cdot lon_{tr}(lat)))$ $p_{47} \qquad \text{if } lat > 47^{\circ} \text{ N}$ $p_{155}(lat) = 0 \qquad \text{if } lat < 30^{\circ} \text{ N2}$

$$p_{155}(1at) = 0$$
 in fact < 50 N2
0.01+((p₄₇-0.01)/(47-30))*(1at-30) otherwise

 $lon_{tr}(lat) = 30+(47-30)/(147-140)*(lat-30)$

Annex H

Final Specifications of the North Pacific Minke Whaling Trials

[See Scientific Committee Report, Annex D, Appendix 10 this volume, pp. 133-149]