Appendix 8

This appendix consists of prepared statements describing and providing the support for the four broad stock-structure hypotheses (Appendices 8a, 8b and 8c), concerns raised by members regarding each of these stock-structure hypotheses (Appendices 8d, 8e and 8f) and responses to these concerns (Appendices 8g and 8h). Appendix 8i by Smith and Polacheck summarises comments on determining plausibility and relative plausibility.

Appendix 8a

DESCRIPTION AND SUPPORT FOR BASELINES A AND B

M. Goto and L.A. Pastene

Description

Baseline A is a 3-stock scenario ('J', 'O' and 'W') with the 'W' stock found only in sub-area 9W, and then only sporadically (occurrence of 'W' stock has been found in three out of five years of surveys in sub-area 9W). This interpretation, based on hypothesis testing, has been developed from analyses of genetic and other data presented over a relatively long period.

Baseline B is a 2-stock scenario and reflects a limited case of Baseline A with no W stock whales present in sub-areas 8, 9 or 12. It is based on similar data and analyses to Baseline A.

The Baseline A scenario was proposed based on the results of genetic (mtDNA) data that showed the sporadic appearance of 'W' stock in sub-area 9W. This scenario is based mainly on the results of genetic (hypothesis testing of mtDNA) and non-genetic analyses discussed during the JARPN review meeting, which overall provide no evidence for additional structure in sub-areas 7, 8 and 9 (IWC, 2001). Evidence for sporadic occurrence of 'W' stock in sub-area 9W derives from an analysis of mtDNA, which showed some degree of heterogeneity in that sector in some years, though microsatellites did not show such sub-structure (IWC, 2001).

Basis of support

AMOVA analysis using Fst statistics and chi-square test detected some mtDNA heterogeneity within sub-area 9. When samples in sub-area 9W in 1995, 2000 and 2001 were excluded from the analysis these significant differences disappeared. Therefore the heterogeneity in the putative 'W' stock is due to animals sampled in sub-area 9W. These results are supported by previous genetic studies (Cui *et al.*, 2002).

The same result was also obtained from more thorough analysis conducted incorporating geographical (longitudinal boundaries), temporal (early and late periods in the migration season) and biological (sexual components) considerations (SC/55/IST2). This study was initially conducted to argue against Baseline scenario C. Genetic heterogeneity was only found in comparisons among male mature samples. In order to examine the source of the genetic heterogeneity, pair-wise comparison was conducted. SC/55/IST2 again confirmed that the genetic heterogeneity was attributable to the samples collected from sub-area 9 west, late in the season.

The Baseline B scenario was proposed based mainly on the results of genetic and non-genetic analyses discussed during the JARPN review meeting, which overall provided no evidence for additional structure in sub-areas 7, 8 and 9 (IWC, 2001). The possible existence of 'W' stock was excluded in Baseline B because the evidence of 'W' stock was detected only in some of the collection years and because analysis of non-genetic markers, such as morphometric (Hakamada and Fujise, 2000), pollutant burden (Fujise *et al.*, 2000), parasite load (Kuramochi *et al.*, 2000) and biological parameters (Zenitani *et al.*, 2000; 2002) all showed no evidence of heterogeneity among samples.

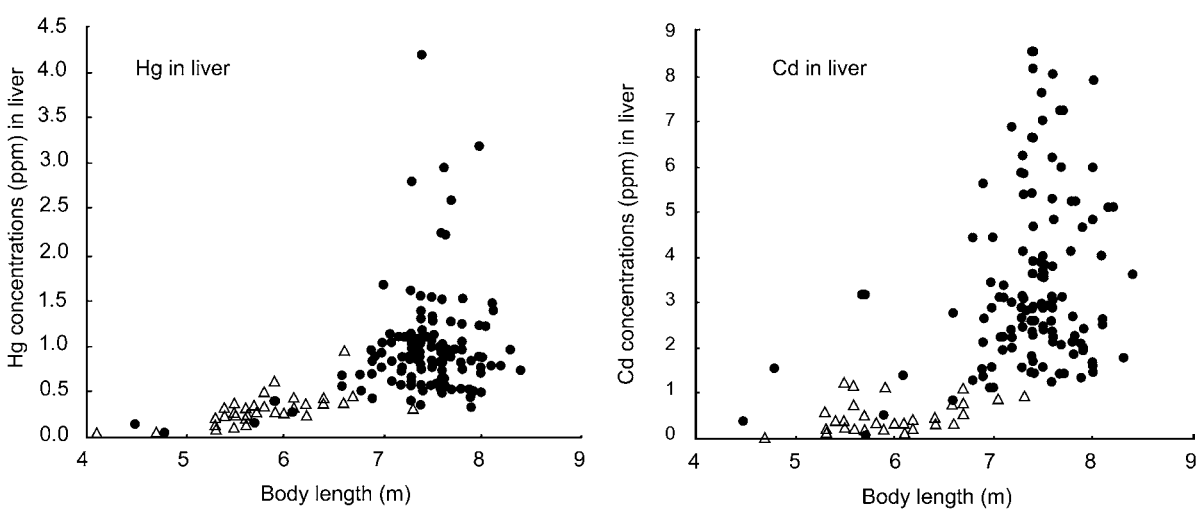

Fig. 1.Relationship between concentration (ppm) of hepatic Hg and Cd and body length (m). Key: Δ = sub-area 7; ● = sub-area 9.

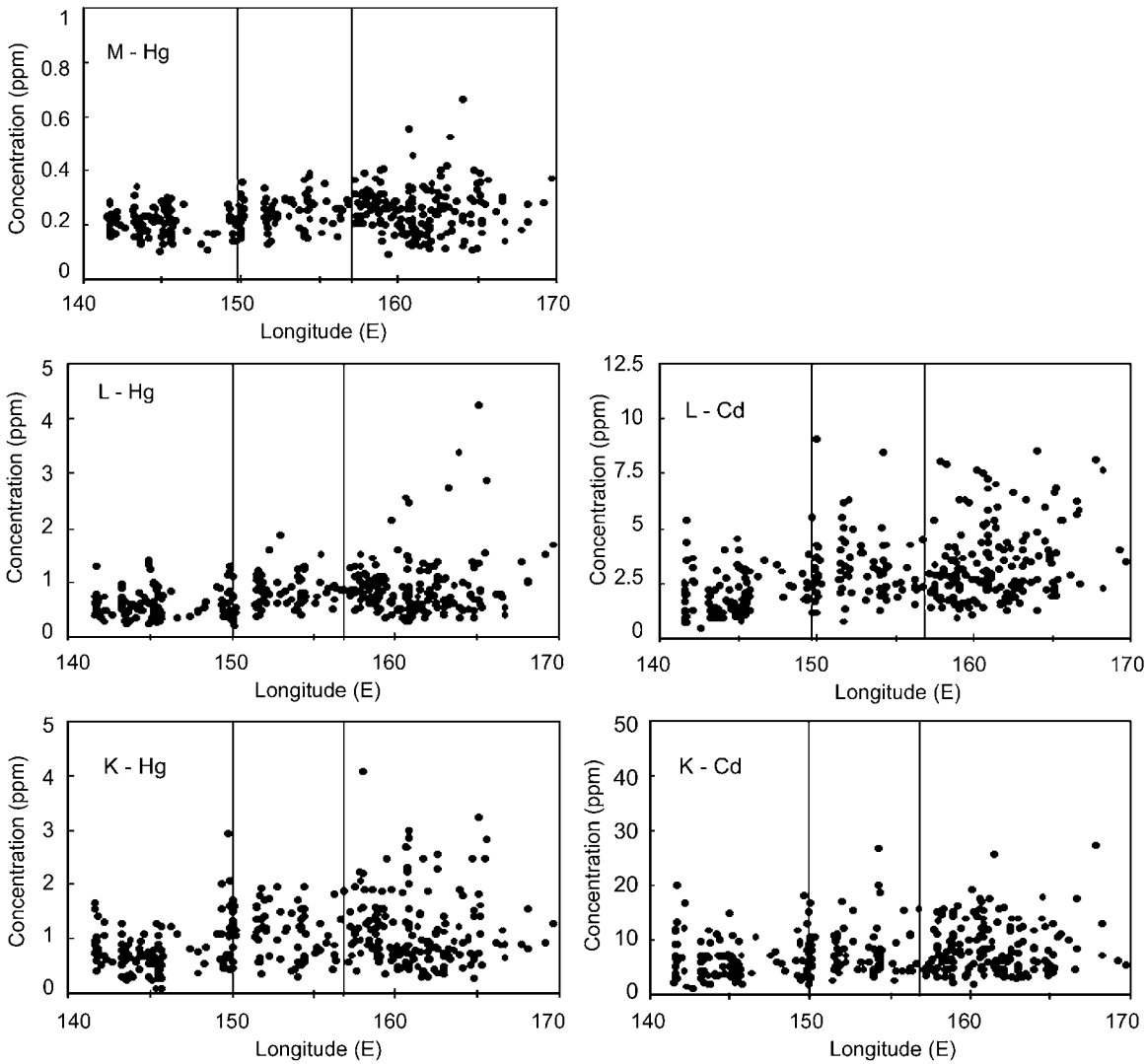

Fig. 2. Longitudinal variation of mercury and cadmium in muscle, liver and kidney in common minke whales (mature individuals), used in Yasunaga *et al.* (2002).

Therefore these results are consistent with the hypothesis of a single stock in these sub-areas.

Life history patterns also support Baselines A and B. Based on body size and sex ratio of commercial catches and seasonal change of whaling grounds, the migration pattern of 'O' stock was estimated (Hatanaka and Miyashita, 1997). This showed remarkable segregation by sex and reproductive status. Immature animals migrate mainly to the coastal area of sub-area 7, mature males distribute widely in offshore areas and mature females migrate further north to the Okhotsk Sea for feeding. Baselines A and B therefore appropriately describe the migration pattern of minke whales ('O' stock) which is firmly supported by genetic analyses and studies on various biological markers.

The first attempt to look at the question of stock structure of North Pacific minke whales using pollutant load was at the working group meeting held in 1996 (IWC, 1997). Fujise (1996) showed the geographical variations of mercury and cadmium between sub-areas 7 and 9. Although relatively higher concentrations of Cd and Hg were found in whales from sub-area 9, such apparent differences could be explained by the length-related (possibly age-related) accumulation characteristics of these pollutants (Fig. 1). Using the data in Yasunaga *et al.* (2002), the longitudinal variations of mercury and cadmium concentrations in muscle, liver and kidney were examined. Fig. 2 shows that the concentration appears to gradually increase eastwards. The accumulation level of pollutants is usually related to age and length of the whale as well as to their prey species. If the significantly different levels of pollutants are observed between different sub-areas, it might suggest different aggregations for stock structure and/or different feeding habitats. These results should therefore be carefully considered. In the case of Fig. 2, we concluded that no significant differences exist between sub-areas 7 and 9.

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Appendix 8b

DESCRIPTION AND SUPPORT FOR BASELINE C

Barbara L. Taylor and Karen K. Martien

Description

In addition to a single J-stock (a feature common to all Baseline hypotheses), Baseline C has three stocks to the east of Japan: 'Ow', 'Oe' and 'W' (Fig. 1). This is the only baseline stock structure hypothesis that represents a coastal stock ('Ow') in the area of anticipated future catches. The base case trial (numbered C-0) has boundaries at 147 and 157°E. These boundaries represent approximations of divisions between demographically 'independent' stocks. Thus, they represent the best average separation of the abundances into stocks to the east of Japan. As with all other Baselines, the boundaries are representations for the purposes of the models used in the *Implementation* and does not require that individual whales never cross the line. Dispersal (permanent change of a whale from one stock to another stock) occurs between the three stocks at rates estimated from the genetic data. Other plausible variants of this hypothesis are represented by the Baseline C sensitivity trials.

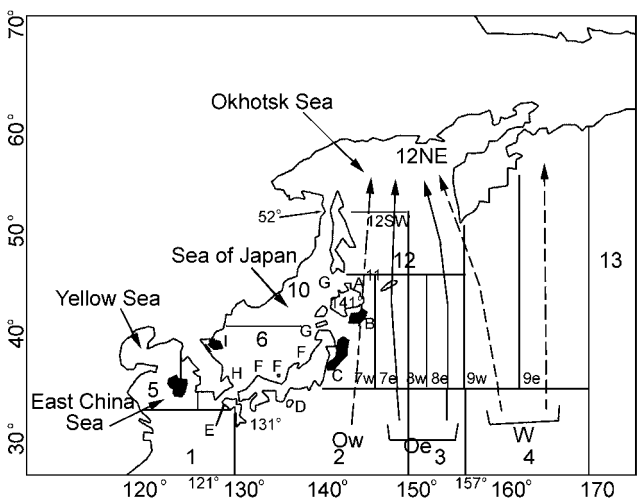

Fig. 1. Map depicting Baseline C stock structure hypothesis (IWC, 2003, p.460).

Basis Of Support

Introduction

Baseline C is supported by:

(1) Analysis by a genetic method designed and performance tested for placing stock boundaries.
(2) Statistical significance using the boundary placement method for three stocks.
(3) Statistical significance using standard hypothesis tests.
(4) Low dispersal estimates across stock boundaries.
(5) Does not rely on arbitrary stratification of the data either before or after testing hypotheses.
(6) Avoids the pitfalls of hypothesis testing that have been published and acknowledged by the Stock Definition group.
(7) Compatible with data on distribution and contaminants.

Genetics

Genetic data are the primary tool for estimating stock structure in minke whales because photo-identification and satellite tagging are not currently feasible methods. However, we expect to have poor ability to unequivocally delineate stocks for minke whales for several reasons. First, we have no data from the breeding grounds where stocks are 'pure' and instead have data primarily from adult males in mid-latitudes where many are on migration. Any spatial mixing of stocks will greatly reduce the chances of detecting structure using genetic data. Second, differentiation between populations strongly depends on abundance; genetic differences between abundant stocks (> 1,000) will be very small even for low levels of dispersal between stocks. The

tiny amount of expected genetic differences will greatly reduce the power to detect the existence of different stocks.

Our ability to detect stock structure is also dependent on whether genetic data come from mitochondrial DNA (mtDNA inherited only through the mother) or nuclear DNA (nuDNA inherited from both parents). Many theoretical publications (Avise, 1995) and empirical examples (e.g. Fitzsimmons *et al.*, 1997; Brown Gladden *et al.*, 1999; Andersen and Born, 2000; Escorza-Treviño and Dizon, 2000; Chivers *et al.*, 2002) have shown that mtDNA is preferred for questions like stock structure. This is particularly important if the objective is sustainable coastal whaling. If calves learn their migratory pattern and feeding grounds from their mothers (e.g. right, blue, gray and humpback whales), then this biological pattern is captured by mtDNA, but not nuDNA. Basing management on structure within nuDNA could lead (and would clearly lead in the case of North Atlantic humpback whales) to unsustainable coastal whaling. We do not know these important behavioural patterns for minke whales.

Baseline C originates from a Boundary Rank (BR) analysis (Martien and Taylor, 2001). This method was used because hypothesis testing performs poorly for questions of population structure. Martien and Taylor (2003) demonstrated that hypothesis testing usually underestimates the number of stocks. In addition, hypothesis tests require that samples first be divided subjectively into hypothesised stocks. This step is very difficult to accomplish for species like North Pacific minke whales, where there are no distributional breaks to suggest how the data should be stratified. The decision of how to define hypothesised stocks can strongly affect results of the analysis.

Further, hypothesis test results are often misinterpreted as providing evidence for a specific boundary placement. In fact, a statistically significant result from a hypothesis test indicates that there is structure but provides no evidence confirming boundary placement. In contrast, the BR method was specifically designed and performance tested to place boundaries accurately for management purposes.

Baseline C is supported by several statistical analyses. The BR permutation test was designed to determine whether the results of the BR analysis were consistent with the hypothesis of a single population East of Japan. The BR permutation test has been shown to be unbiased (Martien and Taylor, 2002), meaning that it does not define more stocks than are actually present. The Stock Definition Working Group agreed that the BR permutation test was a useful tool for evaluating stock structure hypotheses. This test provides strong statistical support ($p < 0.049$) for the stock structure represented by Baseline C, especially in light of statistical power analysis that revealed low power to detect structure using this test ($p = 0.626$).

The genetic data were also used to estimate dispersal rates between the three stocks represented by Baseline C. Annual dispersal rate estimates across all boundaries were less than 0.5% per year (SC/55/IST8). Finally, all pairwise hypothesis tests of stocks represented in Baseline C are statistically significant ($\alpha = 0.05$ using a χ^2 permutation test).

Distribution

The distributional data show a high density of minke whales near the Japanese coast and sharp drop in the density to a constant low density in all of the offshore areas. The high density area revealed by the distributional data corresponds closely to the range of the 'O_w' stock hypothesised in Baseline C.

Age/sex segregation

Baseline C assumes that each stock ('O_w', 'O_e' and W) migrates from southern breeding areas to northern feeding areas segregated by age and sex and that habitat constraints

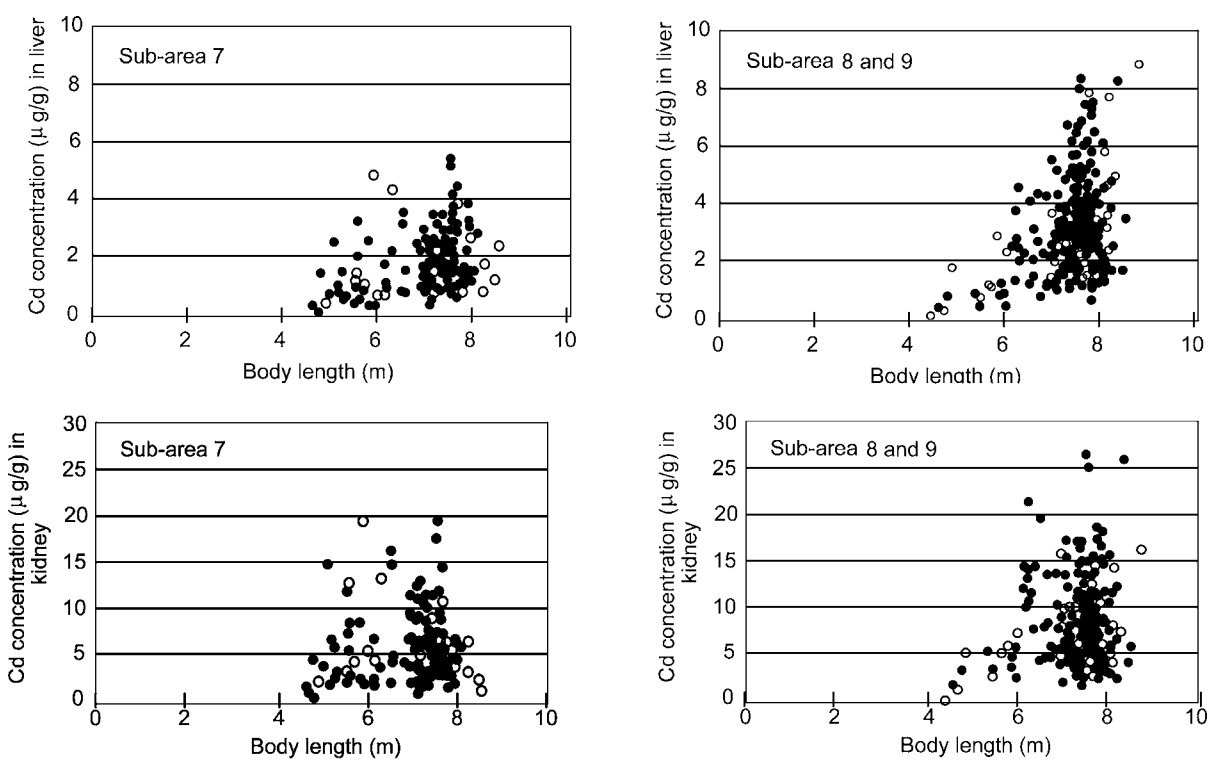

Fig. 2. An example of contaminant data shown by age and for coastal offshore strata (from Fig. 3 of Yasunaga *et al.*, 2002).

within the North Pacific make the migrations similar across the North Pacific by latitude. One would expect, therefore, to observe roughly the same age/sex proportions by latitude for the same month. No statistical differences were found in the proportion of males or in the ratio of immature to mature males across the three mid-latitude sub-areas (SC/55/IST9) based on data from Zenitani *et al.* (2000, Table 7) and Zenitani *et al.* (2002).

Contaminant data

There were striking differences between both Cd and Hg levels in an early comparison of males from sub-areas 7 ($n = 23$) and 9 ($n = 109$) (Fujise, 1996), however interpretation was compromised because most sub-area 7 whales were immature and most in 9 were mature. However, these preliminary results are consistent with more recent data. Recent comparisons by age (Yasunaga *et al.*, 2002) reveal higher levels of contaminants in offshore animals (Fig. 2). No statistical analyses were done to compare the spatial strata using the more recent data.

Summary

The RMP *Implementation* to be chosen should be robust with respect to uncertainty about stock structure. The more complex stock structure depicted in Baseline C has strong statistical support based on a method designed to place boundaries for management purposes. Dispersal estimates across these boundaries are at a rate that is trivial to the population dynamics. Traditional hypothesis tests performed on these strata are all statistically significant. The boundary of the coastal stock went undetected, as expected, using traditional hypothesis tests that use boundaries placed in an arbitrary manner. Although stock structure in coastal waters, which are the intended focus of future catches, may be even more complex than that depicted in Baseline C, it currently most plausibly captures this complexity with comparison to other baselines. RMP variants that ignore the possibility of a coastal stock run a high risk of serious over-exploitation, even in the short-term.

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Appendix 8c

DESCRIPTION AND SUPPORT FOR BASELINE D

Tom Polacheck and Tim Smith

Description

The Baseline D stock structure hypothesis was developed during the North Pacific Minke Whale *IST* Workshop held in January 2002 (IWC, 2003) based on new information that had become available from Japanese research whaling operations as well as past information that had been considered by the Scientific Committee. The hypothesis involves three minke whale stocks with differential degrees of mixing on migratory and feeding grounds. This hypothesis constitutes one plausible hypothesis that we consider to be consistent with the data and information that has been presented on stock structure of the minke whales in

the western Pacific. We note that we do not consider this hypothesis as the only plausible hypothesis that is consistent with the available data.

The hypothesis

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

(1) 'J' is primarily in the Sea of Japan:

- (a) Migrating seasonally into Japanese Pacific coastal waters and into the southwestern Okhotsk Sea.
- (b) Migrating out of the Sea of Japan:
  - (i) as early as April;
  - (ii) with high relative abundance just north of Japan;
  - (iii) with high relative abundance in the southwest Sea of Okhotsk; and
  - (iv) occurring in Pacific waters near the northern Japanese Islands from April through September year-round in low abundance relative to other minke whales in Pacific waters.
- (c) Additional structure within the breeding ground is possible.

(2) 'O' is restricted to Pacific waters along and spreading offshore of the coast of Japan:

- (a) Migrating from unknown southern breeding areas parallel to the coast of Japan.
- (b) Migrating into northern feeding areas to:
  - (i) the Okhotsk Sea; and
  - (ii) east of the Kamchatka Peninsula.
- (c) Distributed seaward from the coast of Japan:
  - (i) in decreasing abundance with distance;
  - (ii) differentially by sex and age, with males travelling further offshore;
  - (iii) with females and younger animals migrating earlier and closer to shore; and
  - (iv) in greater proportion to the Okhotsk Sea.

(3) 'W' 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:
  - (i) east of the Kamchatka Peninsula;
  - (ii) in the Okhotsk Sea.
- (c) Distributed from offshore areas towards the coast of Japan:
  - (i) in decreasing abundance with closeness to the shore;
  - (ii) differentially by sex;
  - (iii) with females migrating earlier and in greater proportion to the feeding area.

(4) Spatial overlap between:

- (a) The 'J' and 'O' groups have limited and seasonal overlap:
  - (i) greatest in the SW Okhotsk Sea (sub-areas 11 and 12SW);
  - (ii) less around the Japan Islands.
- (b) The 'O' and 'W' groups have broad overlap:
  - (i) during migration and on the feeding grounds;
  - (ii) 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 between the O and W breeding grounds or low levels of permanent dispersal of animals.

Basis of support

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 (and seasonally on the Pacific side of Japan) and those sampled from near Japan on the Pacific side. These data strongly suggest at least two breeding groups that overlap in their distributions seasonally at the edges of their distributions. Morphological differences have been identified that are consistent with these genetic data, and that extend these conclusions into the feeding grounds.

The genetic data also indicate substantial heterogeneity in genetic frequencies among animals sampled from nearshore and from further offshore in the Pacific. Various spatial and seasonal partitions of the samples have revealed significant differences. Further, clustering methods (i.e. boundary rank) of combining various small pre-defined groupings of the samples have suggested spatial differences in frequencies that are broadly consistent, with longitudinal structuring.

Although neither the multiple hypothesis testing nor the clustering methods can be used to determine clear spatial boundaries between the 'O' and 'W' groups, the differences clearly imply the existence of three breeding groups and also suggest that there is overlap in their distribution. Further, the differences such as between early and last season samples in the south and the north of the furthest offshore area suggest substantial and possibly variable mixing between the two groups both within and between years.

Differences in sex ratios in both the earlier commercial catch and in the Japanese research whaling samples are consistent with the differential season and spatial migration by sex. Timing of commercial catches, in consideration of catching effort, are consistent with the seasonal timings suggested. Migrating calves are more frequent in samples taken along the coast of Japan than in more offshore waters, consistent with females migrating closer to the coast.

In summary, differences in genetic frequencies have been demonstrated on a variety of spatial scales in the area from near the Japan coastline as far offshore as sub-area 9, the furthest east sampled. These differences leave a wide range of interpretations in terms of spatial mixing because there is not sufficient power in the genetic and other data to allow specific geographic areas and boundaries to be identified. One plausible and consistent interpretation of this uncertainty is that there are two breeding groups intermixing broadly, but variably, with the abundance of 'W' animals decreasing to the east. Such a hypothesis is also consistent with broad but variable stock overlaps and mixing indicated by the genetic data from Japan research whaling studies in the Antarctic. We would note that there are other possible two-stock hypotheses for minke whales in the Western Pacific which involve substantial broad and variable mixing that would be consistent with the data. In this context,

discussions of the plausibility of the Baseline D scenario needs to consider that this hypothesis is the only base case that involves substantial mixing of 'O' and 'W' stocks in the western Pacific. As such, Baseline D should be considered to represent these ranges of hypotheses within the *IST* trials.

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Appendix 8d

PROBLEMS WITH THE BASELINE A STOCK STRUCTURE HYPOTHESIS

Barbara L. Taylor and Karen K. Martien

Introduction

Baseline A suffers from the following problems.

(1) Results are compromised by arbitrary initial boundary placement.
(2) No statistical evidence for 'W' stock appearing only in one area and only sporadically, therefore use of data is selective.
(3) Selective use and exclusion of hypothesis test results.
(4) No evidence that sex ratios or age ratios across the mid-latitudes differ within a month.
(5) No explanation for differences in contaminants.

Genetic analyses

Inferences drawn from the genetic data to formulate Baseline A are based on hypothesis testing using *a posteriori* analysis. The analysis of the available data is compromised by the original stratification of the data into arbitrary predetermined geographical areas and by the subsequent interpretation of the data that picks and chooses among the many statistical results and makes some conclusions with no statistical support.

The Baseline A hypothesis is inconsistent with the results from many hypothesis tests which show significant genetic heterogeneity to the east of Japan (Goto *et al.*, 2002). In proposing the Baseline A hypothesis, one must disregard all of these significant test results in favour of the hypothesis that the only heterogeneity is due to the occasional appearance of W-stock whales in a small portion of sub-area 9. This 'intrusion' hypothesis is based on an analysis conducted during the JARPN review meeting in which Goto *et al.* (2000) sub-divided sub-area 9 and found that all other areas (7, 8 and 9E) differed from 9W. The basis for choosing the location of that boundary (which does not evenly divide sub-area 9) was given as optimising the differences between eastern and western sectors in a post-stratification step. The authors single out haplotype 9 to support the idea that the 'W' stock is only present in some years. However, a statistical analysis of the data used to support these claims reveals no significant difference in haplotype 9 within 9W by year ($p = 0.61$) or within 9E by year ($p = 0.225$). Their own paper states 'no significant yearly variation was found in sub-areas 7, 8, 9 and 11' (Goto *et al.*, 2002). Thus, there is no statistical basis for annual changes in haplotype frequencies used to support the periodic intrusion hypothesis.

Fig. 1 (from data in Table 1) shows why hypothesis tests are difficult to interpret with respect to stock structure. With the area to the east of Japan divided into six strata, each stratum has lower sample size than if the area were divided into the original three strata. Baseline A contends that hypothesis tests support 9W as being different from everything else. However, 9W does not differ (using their criterion of $\alpha = 0.05$) from 9E nor from 8W. Another scientist could use these results to say that 'W' stock was found in 9 and 8W and 'O' in 7 and 8E. But if we decide to 'pool' areas with non-significant results then we run into a logical difficulty with 8W because it does not differ from either 9W or 7E, suggesting it should be pooled with both of these areas. However, 9W and 7E differ from each other, and should therefore not be pooled.

The chances of detecting stock structure are improved comparing the three large strata (7, 8 and 9) because the increased sample size greatly improves our ability to detect differences. Sub-area 9 is significantly different from both 7 and 8 (Table 2). Although the 7-8 comparison is non-significant using $\alpha = 0.05$, Taylor and Chivers (2001) found that if 7 and 8 really are different, we would fail to detect that difference 36% of the time. In other words, a decision that there is no stock structure in the 7-8 region means that a manager is more than 7 times more willing to ignore stock structure when it is present than the reverse ((0.36)/0.05). Thus, using hypothesis testing results,

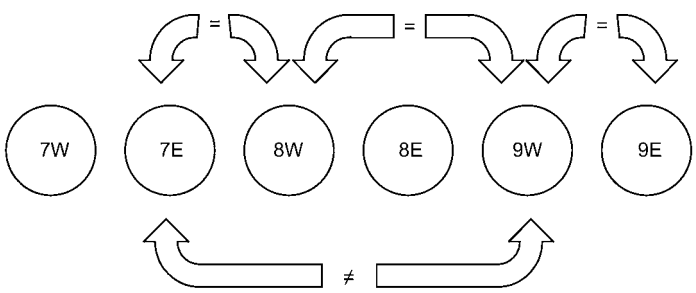

Fig. 1. A graphical representation of some of the results of hypothesis tests when samples are divided into six small strata. An equal (=) sign indicates that two strata did not differ significantly, while a not equal sign (≠) indicates that the strata are significantly differentiated. Comparisons of 8W to both 7E and 9W were not statistically significant, creating a logical problem if non-significant strata are to be pooled, since 7E and 9W differ significantly from each other. The figure also shows that 9W and 9E did not differ significantly, contrary to the hypothesis of Baseline A.

Table 1

Result of pairwise comparison between sub-areas by χ^2 test (SC/55/IST3). Significant p-values ($\alpha < 0.05$) are in **bold**. Sample size within strata are shown in parentheses.

	7W (174)	7E (39)	8W (46)	8E (66)	9W (149)	9E (84)
7W (174)		0.405	0.464	0.155	**0.003**	0.317
7E (39)			0.369	0.725	**0.044**	0.265
8W (46)				0.660	0.206	0.325
8E (66)					0.066	0.432
9W (149)						0.199

excluding a coastal stock has a strong bias towards inappropriately pooling stocks, and thus providing inadequate protection. Further, if the boundary should be placed in the middle of 7, then the above 7-8 comparison is compromised by mixing whales from two different stocks in the area 7 strata. This illustrates the impact of initial boundary placement when using hypothesis tests to detect population structure.

Table 2

p-values from χ^2 permutation tests comparing the three sub-areas east of Japan. Sub-area 9 is significantly different from the other two sub-areas.

	Sub-area 8	Sub-area 9
Sub-area 7	0.15	0.01
Sub-area 8		0.05

These problems with hypothesis testing are not unique to North Pacific minke whales. Last year (IWC, 2003, p.51) it was stated that:

> The Committee reiterates its concerns about the value of conclusions based solely on the results of hypothesis tests, expressed in IWC (2001f, p.236). In brief, it is often not clear *a priori* what hypotheses should be tested; multiple hypothesis tests are a poor way of doing exploratory data analyses; stock definition analyses should begin with exploratory data analysis and proceed, where possible, to estimation (e.g. of dispersal rates between areas) rather than to hypothesis testing.

Both market and bycatch data (SC/55/RMP7; Goto *et al.*, 2001; Pastene *et al.*, 2001) are consistent with a situation in coastal waters where multiple coastal stocks are likely. The current implementations that suggest only occasional and low number of J-stock whales in waters to the east of Japan are not consistent with the recent market data. RMP variants that concentrate on coastal catches (like variant 6) could base their catch on a '*Small Area*' representing Baseline A with an abundance of 25,454 when the actual stock size hunted under the Baseline C hypothesis would be 3,533. This would effectively overestimate the abundance of the hunted population by a factor of over 7 times. SC/55/IST7 found very low statistical power to detect declines given the precision of estimates for minke whales near coastal Japan using preliminary analyses and suggested that it was not safe to assume that serious mistakes could be easily detected before declines of serious concern would occur.

Other data

Stocks that are separated in space for part or all of the year may carry other biological indicators correlated with this separation. For example, many such factors differ between J-stock and whales to the east of Japan: peak breeding season, colouration patterns, scarring/parasite patterns, etc. While such differences are likely to indicate separation, a lack of differences does not indicate that there is no population structure. The physical environment imposes strong constraints on migratory animals. For example, even though humpback whales in the North Pacific have breeding grounds separated by thousands of miles and many feeding grounds spread across the entire northern perimeter of the North Pacific basin, all have the same breeding and migration times. Generally, marine mammal stocks that are confined during part or all of the year to bodies of water separate from the main body of the Pacific are more likely to have altered biological patterns to fit the specific attributes of that habitat. To date there is no evidence for strong selective differences for large baleen whales inhabiting the main body of the North Pacific basin.

Contaminants are a special case because they do not involve selection over long periods and may, therefore, indicate spatial segregation and not be constrained by the evolutionary forces expected to constrain morphology. Interpretation of contaminants as indicators of separateness can be difficult because patterns are confounded by the age and sex of the individual and may carry the pattern of the prey rather than the predator. Nonetheless, there were striking differences between both Cd and Hg levels in an early comparison of males from sub-areas 7 ($n = 23$) and 9 ($n = 109$) (Fujise, 1996). Although no statistics were done to compare these areas, these preliminary results are consistent with figs 1-4 from Yasunaga *et al.* (2002) that reveal higher levels of contaminants in offshore animals.

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Appendix 8e

PROBLEMS WITH THE BASELINE C STOCK STRUCTURE HYPOTHESIS

M. Goto and L.A. Pastene

There are several reasons why Baseline C should not be supported.

Genetics

Baseline C is based on the results of boundary rank (BR). BR can only be considered as an exploratory technique. Hypothesised boundaries derived from this technique should be further evaluated by means of parameters estimate (dispersal rates) or by the use of independent data to check these boundaries. Both approaches have failed to provide any support for Baseline C.

Dispersal rates were estimated for putative stocks 'O_w' and 'O_e' at 0.001 (low) and 0.0045 (best). It is noted that the high interval for this estimate included infinity (SC/55/IST8), which corresponds to complete mixing. Such estimates were based on an observed Fst value of 0.0018 (two-site criteria to exclude 'J' stock). These estimations were made based on boundaries, which are different to those used in *ISTs* (Fig. 1). This important detail was omitted by the authors of Baseline C during the most recent *ISTs* Workshop.

When the estimation is made considering the right *ISTs* boundaries for this scenario (147°E and 157°E), the Fst value is −0.0004 (two-site criteria for excluding 'J' stock). This substantially lower Fst value implies higher dispersal rates, which corresponds to complete mixing which is the same as for Baselines A and B.

The underlying hypothesis of Baseline C has failed a test using independent data. SC/55/IST2 conducted a microsatellite analysis using JARPN II samples. There were no significant differences among putative 'O_w', 'O_e' and 'W'. Recognising the differences in the effect size between nuclear and mtDNA, the microsatellite analysis was made using a large number of loci (17).

Baseline C is inconsistent with the results of hypothesis testing using mtDNA. Using the two-site criteria to exclude 'J' stock animals, the results of the comparison between 'O_w' and 'O_e' (using the boundaries used in *ISTs*) for chi-square and Fst were the following:

Chi-square: P value = 0.392

Fst = −0.0004, P value = 0.5013

We do not support the Baseline C scenario because it is based on incorrect placement of boundaries followed by incorrect sample groupings for statistical tests. These tests then produced a completely incorrect interpretation of the stock structure.

Significant differences between 'O_w' and 'O_e' stocks in SC/55/IST8 and SC/55/IST9 occurred because both papers included some of the samples taken from sub-area 9W, which were located east of 157°E, as 'O_e' samples for their analyses (Fig. 1a). Previous genetic studies have shown that the genetic heterogeneity found in the western North Pacific was only due to the genetic difference attributable to the minke whales taken from sub-area 9W.

No significant difference existed between 'O_w' and 'O_e' when the boundary was correctly placed along 147°E and 157°E lines, respectively. In other words, when the minke whales representing the 'W' stock are not included in the 'O_e' stock, significant difference no longer exists between the 'O_w' and 'O_e' stock (Fig. 1b). When appropriate groupings were applied to the BR, it showed no significant difference between 'O_e' and 'O_w' stocks as expected. It is clear, therefore, that available genetic data do not support Baseline C.

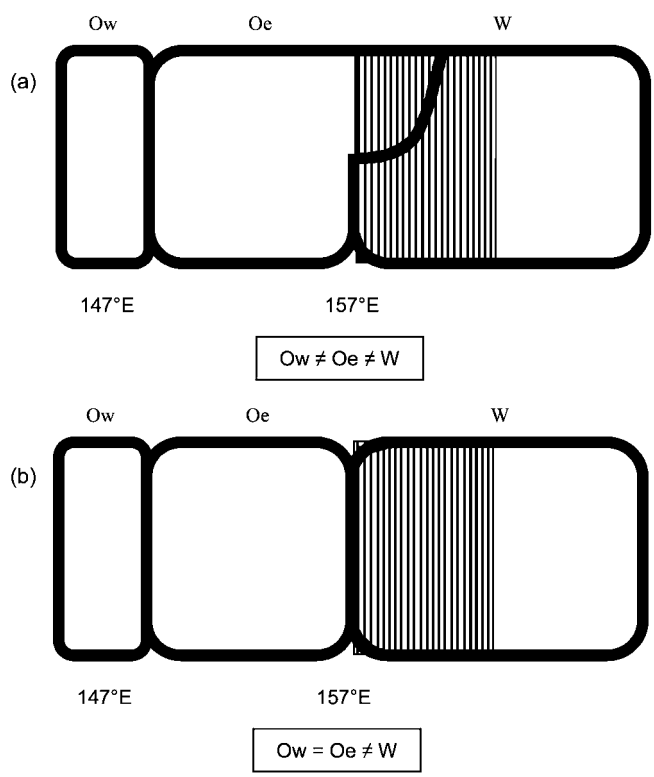

Fig. 1. Scheme of result from SC/55/IST8, IST9 (a) and from analysis conducted using the boundaries used in *IST*s (b). The shaded area shows W stock showing heterogeneity from all other areas.

Biology

As animals in sub-areas 7E, 8 and 9 are composed mainly of mature males, it is assumed that other animals of these three stocks migrate further north to the Okhotsk Sea. Although it seems that mature females migrate further north and immature animals of 'O_w' stock migrate to coastal areas, the feeding area of immature animals of 'O_w' and 'W' stock

cannot be explained by this hypothesis. Baseline C hypothesis is therefore an incomplete representation of the biology of these immature animals.

The density hiatus pointed out by the proposers of Baseline C has been already been denied by the GAM-based analysis using sightings data (Okamura *et al.*, 2001). The apparent hiatus observed around 147°E (border line of 'O_w' and 'O_e') is caused by the southern penetration of the Russian EEZ where we were unable to collect the information.

From the biological point of view, the 'O_w'/'O_e' boundary suggested in Appendix 8b is not a realistic one, because samples from these areas were taken from animals on the way to the feeding area located in higher latitudes. If this bending boundary is correct, the direction suggests that minke whales ought to migrate through this area not to the Sea of Okhotsk but to the Bering Sea. This means that 'W' stock animals will not migrate to the Sea of Okhotsk.

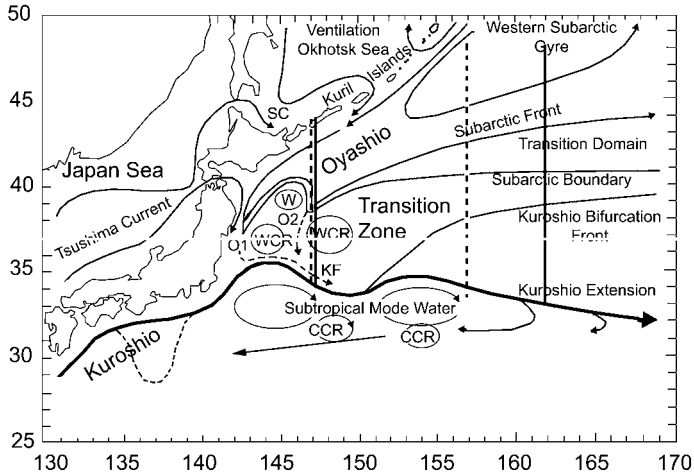

Fig. 2. Schematic representation of the currents and frontal systems in the western North Pacific (Yasuda *et al.*, 1996 modified from Endo, 2000). WCR: warm core ring; CCR: cold core ring. Black dotted solid lines are particular longitude lines used in Baseline C and D, respectively.

Ecology

Baseline C proposes new stocks 'O_w' and 'O_e' instead of 'O' stock with the hard boundaries at 147°E (no mixing across them), making the distributional area of each stock limited. This would seem to require ecological barriers to hinder the mixing between stocks around the longitude line. Minke whales are known to feed on pelagic fishes, krill and squid. Tamura and Fujise (2002) reported the geographical, seasonal and yearly changes of prey species of minke whales and suggested these changes probably reflect the availability of prey species. The availability of prey to minke whale, is determined by the abundance of prey species and the space-time overlap in their distribution. Pelagic fishes have shown drastic fluctuations for the past 100 years. Some prey species have a short lifespan. The waters off the east coast of northern Japan are dynamic (Yasuda *et al.*, 1996; Fig. 2), where minke whales and prey species conduct the seasonal north-south migration. The degree of space-time overlap in their distribution changes yearly as well as seasonally. The prey availability and oceanographic conditions in this area have changed in both the long and short terms. There are no ecological barriers separating stocks 'O_w' from 'O_e' in the environment implied in Baseline C. Therefore the plausibility of Baseline C is low from the ecological point of view.

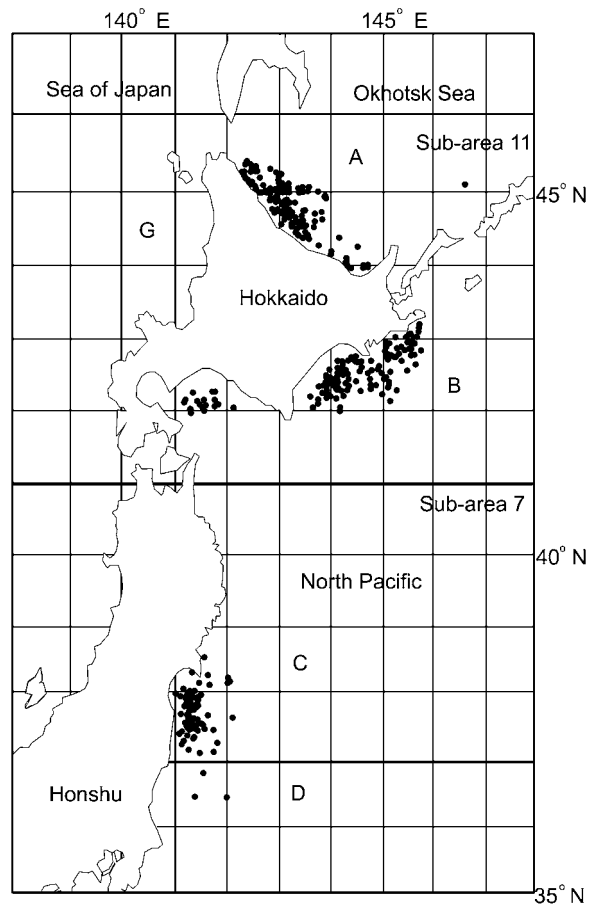

Fig. 3. Sub-areas and regions used, and the position of minke whale catches in 1984 (from Wada, 1986).

Small-type whaling and CPUE

Baseline C proposes new small 'O_w' and 'O_e' stocks, replacing 'O' stock, with the hard boundary at 147°E (no mixing across them). It means that the small 'O_w' stock in the coastal areas had been exclusively taken by Japan's small-type whaling for more than 40 years (Fig. 3). The annual catches of minke whales have been 200-500 (Fig. 4). As a result, the abundance of minke whales in sub-areas 7W and 11 would decline considerably, in some cases, to one third of the initial size. SC/55/IST7 shows, if Baseline C and the management variant 6 which is similar to the past operation patterns of the small-type whaling, are combined, it results in the extinction of the stock in a few decades. That was not the case. SC/55/IST16 reviewed the small-type whaling and CPUE analyses. Two types of CPUE series, CPUE1 and CPUE2 were used (Ohsumi, 1975; Wada, 1986). Judging from the corrected CPUE1 trend for about 35 years, the drastic decline of abundance seems unlikely (Fig. 5). CPUE2 analysis in 1977-1987 with operation hours by area also does not suggest that 'O' stock has declined (Fig. 6). As no considerable decline was detected in either CPUE series, the plausibility of Baseline C was considered low.

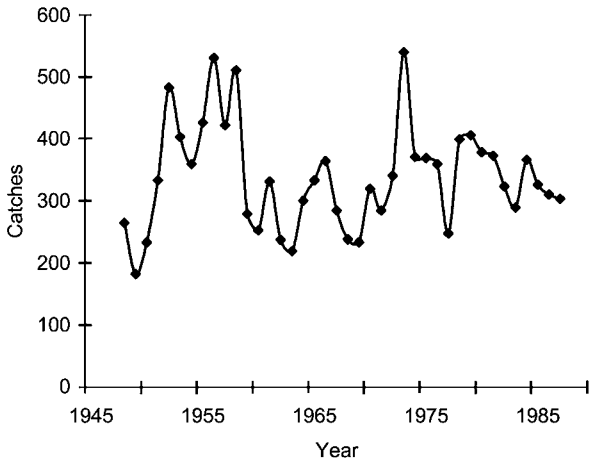

Fig. 4. Yearly changes of catches of minke whales by small-type whaling.

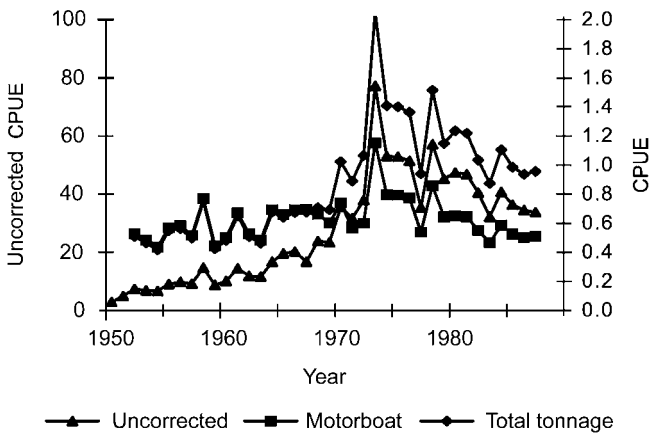

Fig. 5. Yearly changes of catches of uncorrected, total tonnage + motorboat corrected CPUE1 of minke whales by small-type whaling.

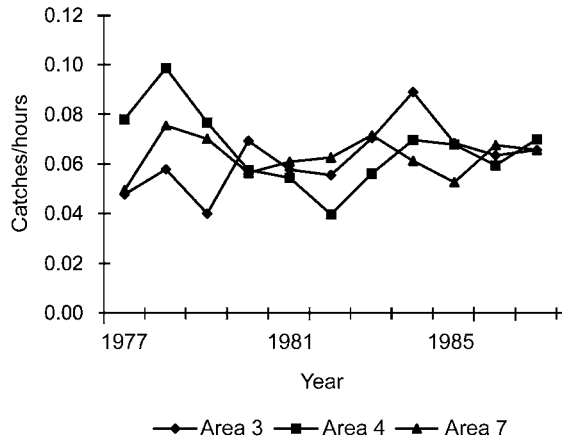

Fig. 6. CPUE2 in each area of small-type whaling in 1977-1987.

Conclusion

In conclusion, there is no independent information supporting this hypothesis. Animals from 9W which are the source of heterogeneity were incorrectly included into sub-area 8 at the start of the Boundary Rank method application, resulting in an apparent difference in animals between sub-areas 7 and 8. The history of the Japanese coastal whaling clearly proves that Baseline C is not reality because the stock collapse suggested by it has not occurred.

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Appendix 8f

PROBLEMS WITH THE BASELINE D STOCK STRUCTURE HYPOTHESIS

M. Goto and L.A. Pastene

There are several reasons why Baseline D should not be supported.

Genetics

We strongly disagree with the Baseline D scenario simply because its assumption that 'W' stock minke whales occupy the whole of sub-area 9 has never been supported by real data. 'W' stock was detected only east of 162°E in sub-area 9 (9W) in some years.

SC/55/IST3 described the results of heterogeneity tests conducted using mtDNA haplotype frequency data among the samples taken from sub-areas 7W, 7E, 8W, 8E, 9W and 9E. The heterogeneity found in SC/55/IST3 was due to the samples from the western part of sub-area 9 (9W) rather than from the eastern part of sub-area 9 (9E). This clearly indicates that sub-area 9E should not be a representative sample of 'W' stock.

SC/55/IST2 described the results of microsatellite analysis showing no significant departure from the

Hardy-Weinberg equilibrium within the sector 147°-162°E. This is not the case we could expect from a situation of mixing between different stocks as proposed by Baseline D.

Statistical analysis

According to Baseline D, the mixing rates of O-stock and W-stock in sub-areas 7E, 8W, 8E and 9W were estimated from mtDNA sequencing data treating sub-areas 7W and 9E as baseline stocks of O and W. In addition, the selection between the constant mixing rate model and the freely estimated mixing rate model was carried out by AIC. All the mixing rates of 'O' stock were more than 0.5 and AIC selected the model with the constant mixing rate (Table 2 of SC/55/IST3). Furthermore, the authors investigated change in density of O-stock under the free mixing rate model. The density estimate of O-stock in each sub-area did not show monotonic decrease towards offshore, whereas Baseline D postulated a rapidly decreasing density of O-stock from 7E to 9W (Table 1). This raises a strong doubt about the Baseline D scenario. Population structures with mixing can be appropriately identified using AIC when there are moderately sufficient data (as is the case for the present western North Pacific minke whale sample size) and a reasonable model is used (Table 2). We therefore conclude that Baseline D neglects the importance of evidence obtained from DNA data.

Table 1

Density estimates of 'O' stock in each sub-area. These were estimated from the mixing rates of the full model multiplied by the density estimate of each sub-area obtained from sightings surveys. The catch mixing matrix of O-stock in August and September under Baseline D (Females (age >= 10), J1 and *MSYR* = 1%.

	7E	8W	8E	9W
Area (IWC, 2004)	58,272	69,410	93,134	118,972
Total abundance (IWC, 2003)	791	472	585	3,226
Abundance of O-stock	624	319	466	1,990
Mixing rate of O-stock	0.788	0.675	0.797	0.617
Density of O-stock	**0.011**	**0.005**	**0.005**	**0.017**
Standard Error	0.020	0.004	0.006	0.011
Catch mixing matrix	7E	8W	8E	9W
Females (age >= 10)	0.055	0.009	0.006	0.003

Ecology

Baseline D proposes 'O' and 'W' stocks to the east of Japan, with the highest densities of 'O' stock at 147°E declining to the east and 'W' stock at 162°E declining to the west monotonically. Baseline D would seem to need a stable environment to support the monotonic density changes of minke whales. As explained in arguments against Baseline C, the prey availability and oceanographic conditions surrounding minke whales have changed in both the long and short terms. Monotonic changes in the environment implied in Baseline D have not been shown. Therefore the plausibility of Baseline D is low from the ecological point of view.

Table 2

Probability that the correct model was selected by AIC. Two types of population structures were assumed: one is a single-stock structure and the other is a two-stock structure with gradient mixing rate. Six stepping-stone sampling areas were assumed. Two haplotypes were considered. In the single stock scenario, the frequency of the first haplotype is $p_1 = 0.7$ and the other $1 - p_1 = 0.3$. In the two stock case, one stock (stock 1) has the haplotype frequency $p_1 = 0.7$, $1 - p_1 = 0.3$ and the other (stock 2) has $p_2 = 0.3$ or 0.5, $1 - p_2 = 0.7$ or 0.5. Then, the proportion of stock 1 in sampling areas are $(a_1, a_2, a_3, a_4, a_5, a_6) = (1, 0.8, 0.6, 0.4, 0.2, 0)$. Generation of data were repeated 1,000 times and the number that true model was selected by AIC was counted for each population structure. The sample size $\underline{n} = (150, 50, 50, 50, 50, 150)$ was assumed to roughly imitate the sample size of the western North Pacific minke whales.

p_2=0.3	
n high:low:high	150:50:150
1 stock	**0.983**
2 stock	**1.000**
p_2=0.5	
n high:low:high	150:50:150
1 stock	**0.985**
2 stock	**0.854**

Small-type whaling and CPUE

Baseline D proposes 'O' and 'W' stocks to the east of Japan, with the highest densities of 'O' stock at 147°E declining to the east and 'W' stock at 162°E declining to the west monotonically. Baseline D may imply that 'O' stock is small. Minke whales have been exploited by Japan's small-type whaling in the coastal areas for more than 40 years. If 'O' stock was small, abundance would have declined considerably. SC/55/IST16 reviewed the small-type whaling and two types of CPUE analyses. As no considerable decline was detected in either CPUE series as shown in the arguments against Baseline C, the plausibility of Baseline D was considered low.

Conclusion

The Baseline D hypothesis was made recently by simple speculation. There is no supportive information for this hypothesis. The proposers thought that 'differences in genetic frequency have been demonstrated on a variety of spatial scales in the area from near the Japan coastline as far offshore as sub-area 9' (Appendix 8c). However, this is not correct because genetic data clearly showed that heterogeneities were observed only in sub-area 9W and that there was no significant difference among other areas. In conclusion, we could not support Baseline D.

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Appendix 8g

RESPONSES BY TAYLOR AND MARTIEN

Barbara L. Taylor and Karen K. Martien

Support for Baselines A and B

As stated in Appendix 8d, there is no statistical evidence given to support the assertion that 'data showed sporadic appearance of 'W' stock in sub-area 9W' nor that there is cause to separate 9W out from 9E (which when compared have a p-value = 0.199). Excluding data in the three years chosen for 9W excludes 22% of the entire JARPN dataset. Thus, the 'disappearance' of stock structure is consistent with reduced statistical power to detect such structure. The claim is that haplotype 9 is responsible for the temporal differences within sub-area 9. There is no statistical support for this claim (Table 1, $p = 0.61$).

Table 1

Frequency of haplotype 9 in sub-areas 9W as a function of the year in which samples were taken. The p-value for contingency table analyses of temporal variation with each of the sub-areas is shown in the last column. Data are from SC/55/IST9.

	Year					
Sub-area	1994	1995	1997	2000	2001	p-value
9W	0.143	0.231	0.158	0.375	0.241	0.61

Contaminant data are cited as supporting Baselines A and B. In Appendix 8a, fig. 2 has few samples from the two areas at the same length. Because contaminants are positively correlated by age, further analyses needed to be done when an appropriate number of comparable samples were available. Hatanaka shows a figure with contaminant levels by longitude. This comparison is improper because whale hunts in the coastal sub-area 7 occurred predominantly early in the year and included more immature animals, while those offshore are predominantly late with mainly mature males. Appendix 8b, fig. 2 shows an example that correctly compares contaminants by age for the different sub-area strata. Although no statistical analysis was done with this correct stratification, it is likely that levels would differ by sub-area. This disagrees with the statement that non-genetic markers (like contaminants) show no evidence of stock structure.

Response to argument against Baseline C

BR is a method that uses the genetic data to suggest boundary placement instead of requiring the scientist to place arbitrary boundaries based on no data. The argument against BR shows exactly its advantage over arbitrary boundary placement. Hatanaka claims that a group of animals that straddle the northern 8-9 boundary are 'W' stock whales that have been mistakenly placed into the 'O_e' stock. On the contrary, BR and supporting analyses suggest that this group of whales is actually part of the 'O_e' stock that has, in the past, been mistakenly included with 'W' stock. BR operates by placing the most related groups of animals together. Interestingly, the 'disputed' group is among the first that is placed with another group to their west. Although they could group with whale groups to the south (within 9W) or east (into 9E), they are most genetically similar to whales to their west (8E). These genetic similarities between groups of whales can be overlooked by placing arbitrary boundaries that run right through the middle of a geographical cluster of samples. This is exactly what happens with the boundary between sub-areas 8 and 9 that runs through the middle of the highest offshore density of whales killed in the JARPN research programme. It is completely inappropriate to suggest that the analyses done with the strata suggested by BR are in any way invalidated by comparing these results to those obtained with an arbitrary boundary placement.

The level of genetic differentiation and dispersal rates calculated for the Baseline C hypothesis accurately represent the genetic data. The best estimates for these dispersal rates are low across both boundaries (less than 0.5% per year), which is consistent with finding pairwise statistical significance between all stocks. Uncertainty in these estimates results from genetic data providing only a crude tool to detect population structure, not from any fault of the analyses. To detect the difference between two stocks of 5,000 females with a 0.5% per year dispersal rate a scientist has to try to tell the difference between 0.000 and 0.001. Genetic data are used because even though they have limited power, they provide the only clear data for North Pacific minke whales. A similar situation would be trying to estimate abundance using mark-recapture photo-identification for a population of 10,000 and a recapture probability of 0.001. Any abundance estimate would be expected to have low precision but the technique is still unbiased and a valid technique. For abundance estimation, scientists would likely recommend a more appropriate technique like line-transect abundance estimation. For stock structure there are currently no other techniques to offer and we must accept low precision.

The assertion has repeatedly been made that there cannot be stocks offshore from Japan because there is not complete demographic representation: specifically that immature whales and mature females are lacking in the offshore area. It has been pointed out since the JARPN review that the logic of this argument is flawed because of the seasonal migratory pattern of minke whales. Females are already far to the north in the period of JARPN whaling in offshore waters. Using Japanese data where sex ratios and maturity state can be compared within the same months no significant differences were found across the mid-latitudes (sub-areas 7, 8 and 9) (Table 2: sex ratio; Table 3: age ratio).

Table 2

Proportion of males in the catch (#males/total) by sub-area and month. No significant differences were found by area within a month (contingency table). However, comparisons of 8 to 9 in July were near significant with more females being found offshore in 9.

	Sub-Area			
Month	7	8	9	Contingency table p-value
May	0.88 (84)	0.88 (8)	0.74 (27)	0.20
June	0.91 (74)	0.91 (36)	0.91 (54)	0.98
July	-	0.96 (63)	0.89 (93)	0.07
August	0.95 (21)	1.00 (5)	0.91 (55)	0.66

Fig. 1 shows the density index of minke whales that is consistent with a coastal stock (from IWC, 2001, p.384).

Ecological arguments are made against the concept of both 'hard' boundaries and stock structure in general. There is no doubt that whales move to match their distribution with

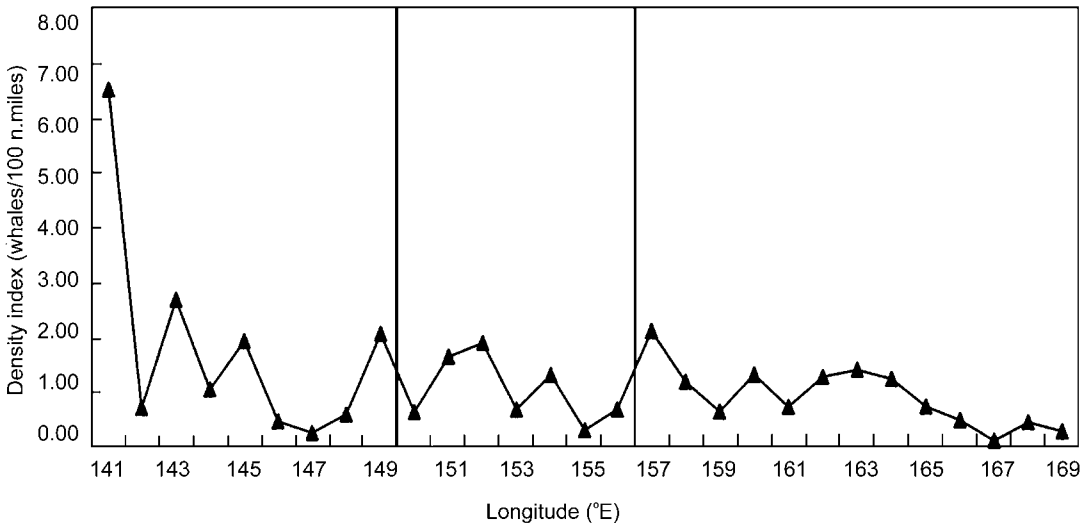

Fig. 1. Density index of minke whales (primary whale sightings/100 n.miles) by each 1 degree square using JARPN sightings from 1994-1999. Verical lines represent the boundaries between sub-areas 7, 8 and 9.

Table 3

Ratios of immature to total adult males with the total in parentheses. No significant differences were found (contingency table) between sub-areas 7 and 9. Data were taken from Zenitani *et al*. (2000) (table 7). Data for sub-area 8 were not available.

	Sub-area		Contingency table
Month	7	9	p-value
May	0.16 (49)	0.16 (20)	0.89
June	0.20 (45)	0.20 (49)	0.96
August	0.07 (15)	0.07 (29)	0.98

shifts in prey abundance. The boundaries in both Baseline A and C represent the concept of different stocks in different areas and were never meant to follow exact locations of whales. The models of whales used in the RMP capture whale stock structure and within season movements that are sufficient to ensure a safe level of hunting. There are now no ecological barriers between 'J' and 'O' stocks, which are known to mix while feeding in Japanese coastal waters and yet remain separate stocks. We understand little about population structure in whales, including in this case where the breeding grounds are for any minke whales and where the feeding ground destinations are for all the whales in sub-areas 7E-9. It makes little logical sense to conclude that there cannot be stock structure because we can detect no ecological barriers in the area through which minke whales are migrating.

The CPUE data were discussed during the Scientific Committee deliberations and found by many to be unconvincing because there was no statistical analysis affirming assertions about what the data were purported to demonstrate.

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Appendix 8h

RESPONSES BY GOTO AND PASTENE

M. Goto and L.A. Pastene

Appendix 8d suggests that 'Baseline A disregards all the significant differences found among sub-areas 7, 8 and 9 in favour that the only heterogeneity is due to the occasional appearance of W-stock whales in a small portion of sub-area 9'. It further argues on the difficulty to interpret results derived from hypothesis testing.

It is true that several hypothesis tests have been conducted in the past and that the different results could make the interpretation of the stock structure of minke whales difficult. However, it is important to focus on the aim of the original tests conducted at the JARPN review meeting. Results from these original tests should be examined to understand the development of subsequent tests and results.

The original tests presented to the JARPN review meeting were aimed to compare the sub-areas under the null hypothesis of panmixia. Taylor (2000) and Goto and Pastene (2000) used chi-square and Fst, respectively for comparing sub-areas 7, 8 and 9. The results for chi-square were the following:

	Sub-area 8	Sub-area 9
Sub-area 7	0.704	0.066
Sub-area 8		0.068

These pairwise comparisons show no significant differences among sub-areas, but it is noted that small P values were found in the comparison involving sub-area 9. The JARPN review workshop suggested further mtDNA analyses, which were conducted during the workshop. These analyses followed a post-stratification step that divided sub-area 9 into west and east at 162°E. In reviewing these results the Committee noted in 2000 the differences in mtDNA possibly arising from samples taken in the western part of sub-area 9 in 1995, and that further analyses should be carried out to explore those findings further (IWC, 2001a, p.59).

Following the advice from the Committee, the hypothesis of 'W' stock in sub-area 9W was tested using samples taken by JARPN in 2000 and 2001 and new hypothesis tests confirmed the occurrence of 'W' stock in that sector. These results gave us a background to support the occurrence of 'W' stock in sub-area 9W in some years. If you extract samples from sub-area 9W taken in 1995, 2000 and 2001 no significant differences are observed for several combinations of samples in sub-areas 7, 8 and 9 (Goto *et al.*, 2002 and SC/55/IST2).

It is important to note that the logic followed by the hypothesis testing analyses respond to suggestions by the Committee.

The haplotype frequencies of samples taken in sub-area 9W in 1995, 2000 and 2001 seem to be different from samples from other strata, and particularly the frequency of haplotype '9'. SC/55/IST9 used the frequencies of this particular haplotype to examine heterogeneity among years in sub-area 9W and 9E and no significant differences were found. During the *IST* Workshop conducted in 2002, AIC-based evaluations of different stock structure models were conducted to explain the frequency of this haplotype in various sub-areas. 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' (IWC, 2003, pp. 457-458). We believe that the power of the analysis is low due to the small sample size when the samples are divided on an annual basis.

When the samples in the western North Pacific are divided into six strata (7W, 7E, 8W, 8E, 9W and 9E), samples from 9W are differentiated from most of the others (see Table 1). On the other hand, samples from sub-areas 7 and 8 do not differ significantly from 9E. As noted in Appendix 8d, in two cases no significant differences are found in the comparison involving sub-area 9W (with 8W and 9E). What it is important here is the trend observed for sub-area 9W. Some comparisons might not derive significant results even if two different stocks are involved in the comparison. For example, in the case of sub-area 8W the sample size is not particularly large. The important issue here is that if we follow the logic of the hypothesis testing and exclude samples from sub-area 9W in 1995, 2000 and 2001, the P values in the comparisons among six sectors or comparison among sub-areas 7, 8 and 9 become larger. In the latter case the sample sizes are 213, 112 and 110, respectively and we think that small sample size is not a strong argument to explain the lack of differences between 7, 8 and 9 in this case.

Table 1

Result of pairwise comparison between sub-areas by chi-square test (SC/55/IST3). Boundaries of each sub-areas are drawn at 147°E in sub-area 7, 153°E in sub-area 8 and 162°E in sub-area 9, respectively. Figures shown are P values.

	7W (174)	7E (39)	8W (46)	8E (66)	9W (149)	9E (84)
7W		0.405	0.464	0.155	0.003	0.317
7E			0.369	0.725	0.044	0.265
8W				0.660	0.206	0.325
8E					0.066	0.432
9W						0.199

Appendix 8d cited a concern of the Committee about the value of conclusions based solely on the results of hypothesis testing and that analysis should begin with exploratory analysis followed by estimation of dispersal rate. Dispersal rates estimates for the Baseline A scenario were estimated considering the 'O' stock (all samples less sub-area 9W 1995, 2000 and 2001) and 'W' stock (sub-area 9W 1995, 2000 and 2001). The estimations are lower enough to support the underlying hypothesis of Baseline A that 'W' stock occurs in sub-area 9W in these years.

It is also suggested that market (SC/55/RMP7) and bycatch data (Goto *et al.*, 2001; Pastene *et al.*, 2001) are consistent with a situation in coastal waters where multiple coastal stocks are likely. Bycatch data only suggested the occurrence of J and O stocks. A market sampling scheme might include large biases as noted by the Committee several times (IWC, 2000, p.84; IWC, 2001b, p.96). Consequently, we cannot apply results from the market for the *IST*s.

It is also pointed out that 'the abundance of the coastal stock in Baseline A is seven times of that in Baseline C', and that 'it was not safe to assume that serious mistakes could be easily detected before serious declines'. However, the historic mature female population derived from *IST* conditioning clearly shows an extreme depletion of the coastal stock in the case of Baseline C. If it occurred in reality, we could easily find it. The CPUE series standardised using the GLM showed that the estimated yearly trend was an increasing function. The lower limit of 95% confidence interval indicated at most 20% decrease during 30 years. Therefore, the CPUE series have the consistency with the historical trajectories of Baseline A obtained from the conditioning. This result negates Baseline C, because such an extreme depletion of the coastal stock did not occur in the history of coastal whaling.

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Appendix 8i

DETERMINING PLAUSIBILITY AND DETERMINING RELATIVE PLAUSIBILITY OF THE FOUR WESTERN NORTH PACIFIC MINKE STOCK HYPOTHESES

Tim Smith and Tom Polacheck

Plausibility

The main purpose of conducting *IST*s is to ensure that a specific candidate RMP *Implementation* is robust to uncertainties about stock structure within the region in which harvesting is to occur. The reason for including more than one set of stock structure hypotheses (i.e. baseline trials) is to ensure that the set of trials considered actually reflect the plausible range of uncertainty about stock structure.

In this context, we consider that each of the four base case hypotheses address part of what some consider reasonably plausible for minke whales in the western North Pacific, derived either from hard data, or from general knowledge from having been in the field in the North Pacific, or from possibilities based on knowledge of minke and other cetaceans elsewhere. The purpose of developing the set of base case scenarios was to provide a representation of the uncertainty about North Pacific minke whale stock structure. We think that the *IST* Steering Group was successful in developing a set of hypotheses that provided a balanced and reasonably complete representation of this uncertainty, and that these are sufficient to ensure robust performance in any of the implementation variants for the RMP that were considered. The *IST* Steering group did this based on a careful consideration of the data before them. In this sense, all of the four base case stock hypotheses were plausible when they were proposed. Further, no additional information presented subsequently (including the information at this year's Scientific Committee meeting) provides a sufficient basis for changing that conclusion.

Relative plausibility

Relative plausibility entails ranking hypotheses. If data are sufficient, likelihood can be calculated for a data-based hypothesis. However, this is not possible for some North Pacific minke whale hypotheses because direct data are lacking on many influential factors. The Scientific Committee attempted to extend its agreement that all four hypotheses were plausible. However, despite strenuous attempts to agree on the relative plausibility among the hypotheses, there proved to be no basis for such ranking.

The attempt to assign rankings to hypotheses should not be seen as a contest to chose the 'best' base case scenario or one of trying to determine which is the 'most plausible'. Instead the process should be seen as one of determining whether any of the base cases are sufficiently implausible or unlikely that there is little need to be concerned about the performance under the RMP[1]. A hypothesis/base case should be given a high ranking if it has sufficient plausibility[2] that there is a need to ensure that the RMP will provide robust performance if in fact reality was close to the hypothesis.

We were not surprised by the failure to agree on rankings among the hypotheses because we feel the Steering Group in fact did its work well. Indeed, the fact that we were able to complete evaluating the *Implementation Simulation Trials* in the absence of agreeing relative plausibility of stock structure hypotheses suggests that doing so is not in fact required.

Although the Steering Group did not verbalise all of the methods described in Appendix 5, it was inherent in its work that the sharp edges of Occam's Razor and the Reduction to the Absurd were in fact kept in balance by the frequent application of self-control. In the context of selecting a plausible range of hypotheses in implementing the RMP, we need to use *self-control* to avoid shaving too close with *Occam's razor*. The goal is not to establish the best hypothesis (as per Occam's Razor), but rather to establish a plausible set of stock hypotheses that include a balance between too close a shave and an absurdly long and tangled beard. Shaving to closely risks cutting oneself, while not shaving risks too long a beard that inhibits practical affairs.

[1] Note that no matter how rankings of plausibility are to be assigned, there will be an element of subjectivity and implicit judgements about acceptable levels of risks given the agreed decision framework for selecting a variant. Thus, the assignment of a low rank to a specific scenario constitutes a judgement that the risk in not ensuring robust performance is acceptable to the set of hypotheses that this specific scenario was meant to represent. Assignment of a high ranking entails a judgement that there is an unacceptable level of risk associated with non-robust performance for a particular scenario, while the assignment of a medium ranking constitutes an acceptance of some intermediate level of risk.

[2] Note that sufficient plausibility in this context is not equivalent to 'worst case scenario'.

Appendix 9

HIGH BYCATCH AND EVIDENCE OF MULTIPLE COASTAL STOCKS OF NORTH PACIFIC MINKE WHALE AROUND KOREA AND JAPAN: IMPLICATIONS FOR UNCERTAINTY AND PLAUSIBILITY IN CURRENT *IST*S

C.S. Baker, N. Funahashi and F. Cipriano

The unintentional hunting of a depleted or protected stock is a serious failing in management of whaling. The RMP protects against this potential failing by considering the impact of hunting, which is to be directed at an abundant stock, on adjacent stocks with different histories of exploitation. Plausible hypotheses about stock structure, boundaries, mixing, rates of increase and abundance are accommodated through *Implementation Simulation Trials* (*IST*s). These scenarios can be particularly complex for coastal stocks or non-migratory stocks that may overlap seasonally with migratory stocks.

The current *IST*s for North Pacific minke whales include Baseline scenarios with 2, 3 or 4 stocks. The four Baselines consider only a single, genetically distinct stock (J), in the Yellow Sea/East Sea/Sea of Japan and differ only in considering the number of stocks in the North Pacific east of Japan (O only, O and W, or 'O_w', 'O_e' and W). No Baseline gives consideration to more than one stock in the Yellow Sea/East Sea/Sea of Japan and none gives specific consideration to a non-migratory coastal stock around either Japan or Korea. Only Baseline C (four stocks) considers the hypothesis of a distinct coastal stock adjacent to the east coast of Japan.

Below, is a summary of information on high levels of minke whale bycatch in coastal waters of Japan and Korea. This information is taken directly from the national progress reports of these two countries and, as a minimum estimate of bycatch, is not in dispute. A summary is also given of evidence, presented to the Scientific Committee (SC) or published in international scientific journals over the last three years, of multiple stocks in the coastal waters of Japan and Korea. This information derives from genetic analyses of bycatch and market products, including those reported by the Institute of Cetacean Research, Tokyo, and the National Fisheries Research and Development Institute, Korea. The uncertainty in stock boundaries indicated by these data is not fully consistent with any of the current Baseline Scenarios in the *IST*s.

The high levels of bycatch raise serious concerns about potential depletion (or even extinction, see SC/55 RMP7 and Baker *et al*., 2000) of the J or other unrecognised coastal stocks. The uncertainty in boundaries and mixing of coastal stocks has important implications for management advice regarding:

(1) Japanese scientific hunting in coastal sub-area 7W (east of Hokkaido) under JARPNII;
(2) future commercial hunting in sub-areas 7W and 11 (e.g. management variant 6, SC/55/Rep2, p.51);
(3) the 'yields and risks' of restricting whaling to within the EEZ or other waters within 200 miles of the coast (IWC, 2003, p.27).

These issues can only be addressed fully by a revised in-depth assessment of the North Pacific minke whale (see IWC, 2002, p.99). However, the reported bycatch and evidence of multiple coastal stocks summarised here is best reflected in the hypothesis of four stocks in Baseline C and the J*ii* and K*ii* options for levels of incidental takes. Consequently, these are the only highly plausible hypotheses in the current *IST*s.

High levels of bycatch

(1) 2001: 249 entanglements or strandings of minke whales; 160 for Korea and 89 for Japan (SC/54 Progress Reports).
(2) 2002: 205 entanglements or strandings of minke whales; 89 for Korea and 116 for Japan (SC/55 Progress Reports).

Multiple coastal stocks

(1) Goto *et al*. (2001) shows mtDNA haplotype frequencies of Japanese bycatch (1993-2000) from the East Sea/Sea of Japan prefectures are similar to those for Korean bycatch (1998-2000) but more diverse and significantly different from a small sample ($n = 28$) derived from the Korean commercial catch in 1982. The latter sample, now known to be unrepresentative of the J stock (IWC, 2002, p.99), is the basis of the Assessment under which the *IST*s continue to operate.
(2) Baker *et al*. (2000), in an independent analysis of Korean bycatch as represented in market products, suggests that some of the heterogeneity in the East Sea/Sea of Japan is the result of O-stock haplotypes. This could indicate the migration or intrusion of some 'O' stock animals into the East Sea/Sea of Japan, or multiple stocks with intermediate haplotype frequencies.
(3) SC/55/BC6 summarises haplotype frequencies for Korean bycatch (1998-2003) confirming substantial differences compared with the 1982 commercial catch and suggesting mixing of different stocks (e.g. O and J or other).
(4) Pastene *et al*. (2001) show 'J' and 'O' stock haplotype frequencies for market surveys conducted by the Government of Japan (1995-2001). More than 50% of North Pacific minke whale products (15 of 26 individual whales represented in 20 of 31 products) did not match DNA profiles from the scientific hunt (JARPN). Many of the products purchased in prefectures along the eastern coast of Japan (bordering sub-areas 2 and 7W) had J-like haplotypes. Because regulations in effect at the time required 'local distribution' of bycatch, the J-like products in the eastern prefectures could represent takes from a coastal stock with some genetic similarity to the true J stock.
(5) Dalebout *et al*. (2002) confirmed findings of Pastene *et al*. (2001), showing widespread distribution of J-stock products on Japanese markets, including along the eastern coast of Japan (bordering sub-areas 2 and 7W).
(6) SC/55/RMP7 summarises market surveys of products purchased from 1993-2003, showing highly significant differences in frequencies of J-type haplotypes and sex ratios (82% female in Japan, 40% female in Korea) between North Pacific minke whale products from Japanese ($n = 217$) and Korean ($n = 310$) markets.