Comments on the hypotheses on stock structure presented at the *pre-implementation assessment* of western North Pacific Bryde's whale

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ABSTRACT

This paper comments on the stock structure hypotheses presented at the *pre-implementation assessment* of western North Pacific Bryde`s whale in the light of the available scientific data. The hypothesis of a single stock scenario in sub-areas 1 and 2 (Hypothesis 1) is fully consistent with the available data and deserves to be considered in the trial specifications as a base case scenario. The hypotheses of two stock- scenario (Hypotheses 2 and 3) should be considered in the trials under a precautionary approach: although there is no scientific evidence supporting the occurrence of a second stock east of 180° (sub-area 2), DNA and mark-recapture data are very limited for that sub-area. The hypotheses involving sub-stocks in sub-area 1 (Hypotheses 4 and 5) were already considered by the Workshop on *pre-implementation assessment* as having much smaller plausibility than the other hypotheses given the available data, particularly those that have become available since 1998. The scientific evidence examined here clearly does not support the stock structure hypotheses involving sub-stock scenario. In order to avoid waste of time, hypotheses involving sub-stocks can be ignored for the trial specifications.

KEYWORDS: BRYDE'S WHALES, STOCK STRUCTURE, IMPLEMENTATION, WESTERN NORTH PACIFIC

INTRODUCTION

Following the schedule for an *Implementation* and subsequent *Implementation Review* recommended in 2004 (IWC, 2005a), the Scientific Committee (SC) completed the *pre-implementation assessment* of western North Pacific Bryde's whale during a Workshop carried out early 2005 (IWC, 2005b). The Workshop considered all the aspects required under the 'Requirements and Guidelines' for *Implementations* to complete a *pre-implementation assessment* (IWC, 2005a), specifically a) abundance estimates; b) catches; c) stock structure hypotheses; d) dispersal rates; and e) data for conditioning. Based on the results of the examination, the Workshop recommended to the SC that it considered the *pre-implementation* process completed. The SC accepted the Workshop report and agreed that the *pre-implementation assessment* for western North Pacific Bryde's whales was completed and recommended that *Implementation* can commence (IWC, 2005c).

With regard to stock structure of western North Pacific Bryde's whales, the Workshop had identified five alternative hypotheses, which considered sufficiently inclusive that collection of new data during the *Implementation* process is unlikely to suggest a new stock hypothesis (IWC, 2005b). The Workshop had agreed that the various stock hypotheses were not equally plausible, but did not assign plausibility weights to these hypotheses as this is scheduled for the 'First Annual Meeting'.

The primary objective of the 'First Intersessional Workshop' is to develop an appropriate *Implementation Simulation Trials* structure and to specify the associated conditioning so that it can be carried out before the 'First Annual Meeting'.

As specified in the Workshop report (IWC, 2005b), a plausibility rank would need to be assigned to each simulation trial during the 'First Annual Meeting'. Notwithstanding a review of the hypotheses on stock structure will be carried out during the 'First Intersessional Workshop' with the aim to eliminate any hypotheses that are inconsistent with the data. This means that only the hypotheses consistent with the data should be considered for developing *Implementation Simulation Trials*.

The objective of this paper is to review the hypotheses on stock structure identified during the *pre-implementation assessment* of western North Pacific Bryde's whale in view of the available data, and to evaluate whether or not these hypotheses deserve to be considered in the trial specifications.

DESCRIPTION OF THE HYPOTHESES ON STOCK STRUCTURE

The five hypotheses on stock structure agreed during the *pre-implementation assessment* are summarized in Figure 1.

Hypothesis 1: this is a single stock hypothesis under which only one stock of Bryde's whale distributes in the feeding area from 130°E and 160°W (excluding the area of distribution of the East China Sea Stock, around Kochi) as shown in Figure 1(1). Under this hypothesis there is no sub-stock scenario.

Hypothesis 2: this is a two-stock hypothesis under which Stock 1 is found in sub-area 1 and Stock 2 in sub-area 2 as shown in Figure 1(2). Sub-areas 1 and 2 are divided at 180° longitude. Under this hypothesis there is no sub-stock scenario.

Hypothesis 3: this is a two-stock hypothesis under which Stock 1 is found in sub-areas 1 and 2 and Stock 2 only in sub-area 2 as shown in Figure 1(3). Under this hypothesis there is no sub-stock scenario.

Hypothesis 4: this is a two-stock hypothesis under which Stock 1 is found in sub-area 1 and Stock 2 in sub-area 2. Stock 1 consists of two sub-stocks that mix in sub-area 1 as shown in Figure 1(4).

Hypothesis 5: this is a two-stock hypothesis under which Stock 1 is found in sub-areas 1 and 2 and Stock 2 in sub-area 2 only. Stock 1 consists of two sub-stocks, one found in sub-area 1 and the other in sub-areas 1 and 2 as shown in Figure 1(5).

EVALUATION OF THE STOCK STRUCTURE HYPOTHESES IN THE CONTEXT OF AVAILABLE DATA

During the *pre-implementation assessment* Workshop, it was agreed that the various hypotheses shown in Figure 1 are not equally plausible, particularly given the data and analyses that have become available since 1998 (IWC, 2005b). In this section the stock structure hypotheses are reviewed in the context of the available scientific data.

Hypothesis 1

Hypothesis 1 is largely supported by the available biological data as shown in Annex E of IWC (2005b). There is a genetic study, based on allozymes, which covered most of the longitudinal range depicted in Figure 1 (1) (Wada, 1996). This study showed a notable stability of the frequencies of a particular allozyme (*Got-1*^{f}) in the area comprised between latitudes 20°N and 40°N and between longitudes 140°E and 160°W (Figure 2). This result provided no evidence of more than one stock in that longitudinal sector. It could be argued on the low power of using just a single locus. However statistical test for heterogeneity using this single locus showed significant differences when the sample of the western North Pacific was compared with other recognized stocks of Bryde's whales in the Pacific Ocean (Wada and Numachi, 1991) so if the level of genetic differentiation between putative stocks in sub-areas 1 and 2 is similar to that between Western North Pacific Stock and other Pacific stocks, this single locus should recognize such differences.

Apart from the genetics, analysis of sighting distribution showed no gaps in the longitudinal sector depicted in the Figure 1 (1). Shimada and Miyashita (1996) examined sighting data for western North Pacific Bryde's whale obtained between 1988 and 1995. There was no clear discontinuity in distribution in the pelagic western North Pacific west of 160°W (Figure 3). More recently Shimada (2004) examined sighting data obtained in the western North Pacific between 1998 and 2002. Distribution of sighting data showed no discontinuity in the longitudinal sector comprised between 140°E and 160°W (Figure 4).

Other biological information derived from body proportion and biological parameter analyses (Kato and Yoshioka, 1995) conducted for whales sampled along all longitudinal range shown in Figure 1 (1) showed no evidence of heterogeneity. Again these data provided no evidence of more than one stock in the longitudinal range 140°E-160°W.

DNA analyses have been confined to the western part of the area (sub-area 1). Mitochondrial DNA and microsatellite data were analyzed using different kinds of clustering methods (Martien and Taylor, 2004) and hypothesis testing (Pastene *et al*. 2004a) and none of these methods revealed significant degree of heterogeneity within that sub-area. During the *pre-implementation assessment* Workshop three different methods for evaluating the power of the genetic analyses based on hypothesis testing, were presented. The Workshop believed that in particular one of these methods (Kitakado *et al*., 2005) provided a more defensible means of identifying the power of hypothesis testing (IWC, 2005b). Results from the three methods showed that for the samples sizes available the power to detect genetic differences for western North Pacific Bryde's whale is high.

Same as DNA analyses, mark-recapture analyses have been confined to sub-area 1 (Kishiro, 1996; 1998). Results were consistent with those from the genetic analysis, and no evidences were found of more than one stock of Bryde's whale in sub-area 1.

Hypotheses 2 and 3
These hypotheses involve different stocks in sub-areas 1 and 2. These were proposed under a precautionary approach. Currently there is no scientific evidence supporting a separate stock east of 180° (sub-area 2). On the contrary, genetic analyses based on allozymes (Wada, 1996), body proportion and biological parameters analyses (Kato and Yoshioka, 1995) and sighting distribution (Shimada and Miyashita, 1996; Shimada, 2004) showed no differentiation between sub-areas 1 and 2 (see Figures 2, 3 and 4). However it is recognized that two important information components (genetic analysis based on DNA and mark-recapture) are not available for whales in sub-area 2.

Hypotheses 4 and 5
The Workshop on *pre-implementation assessment* agreed that the currently available data on genetics, mark-recapture and sightings indicate that the hypotheses in which there are two sub-stocks in sub-area 1 (Hypotheses 4 and 5 in Figure 1) are likely to be assigned much smaller plausibility weights than the other hypotheses (IWC, 2005b). Actually there is no scientific evidence supporting the occurrence of sub-stocks in sub-area 1.

Argument used in proposing the sub-stock scenario
According to Annex E of IWC (2005b), the possibility of sub-stock structure in sub-area 1 cannot be ignored because there are no genetic data for the breeding grounds. If two breeding sub-stocks mix uniformly to each other in the feeding ground of sub-area 1, then it will be difficult to detect differences in biological characters, included the genetics, between the west and east part of that sub-area. Such differences would be detected between different localities in the breeding ground because in those localities sub-stocks are not mixed.

It could be argued that Hypotheses 2 and 3 (two-stocks in sub-areas 1 and 2) are based on similar arguments to those used to postulate Hypotheses 4 and 5 (two sub-stocks in sub-area 1). In the first case it is argued that no available DNA and mark-recapture data exist for sub-area 2. In the second case it is argued that no available DNA data exist for low latitude breeding grounds. However it is much more plausible that additional stock structure occur when a wide longitudinal span is involved, as in the case of Hypotheses 2 and 3.

Arguments against the sub-stock scenario based on genetic data
Testing for Hardy-Weinberg (HW) equilibrium in nuclear markers can sometime be useful to detect situations of mixing of stocks/sub-stocks because deviation from HW provides the evidence of non-random mating as well as selection or migration i.e. the situation at which genetically different populations are mistakenly sampled as one population. This has been the case of the North Pacific common minke whale where a significant departure from the HW equilibrium for allozyme loci was found for samples obtained in the southern part of the Okhotsk Sea where J and O stocks of common minke whale mix to each other in some months (Wada, 1991). By examining microsatellite loci, a significant departure from HW equilibrium was also found for the autumn samples of the BCB stock of bowhead whale and one of the possible explanations for such result is that two different stocks mix to each other in Point Barrow during the autumn migration (Pastene *et al*. 2004b).

Analysis of nuclear markers for western North Pacific Bryde's whale have been conducted by Wada (1996) using allozymes and Pastene *et al* (2004a) using a set of 17 microsatellites. None of these studies detected significant deviation from HW equilibrium for samples in sub-areas 1 providing no support for mixing of sub-stocks in that sub-area (see also Table 1).

Argument against the sub-stock scenario based on the pattern of mixing
The results of no genetic differences in gene frequencies between Bryde's whales in sub-areas 1W and 1E (see Table 1) could indicate that two sub-stocks mixed equally in either sub-area. If mixing rates are different it is likely that genetic differences could be detected between the sub-areas, which is not the case (Martien and Taylor, 2004; Pastene *et al*., 2004a). However, the exactly same mixing rate in two different sub-areas is implausible considering the knowledge we have on the pattern of movement and mixing of large whales. Mixing of genetically differentiated whale stocks has been documented for migratory corridors and feeding grounds, and a marked variability in the mixing rate has been detected among geographical regions or among years (e.g. Pastene *et al*., 1998).

Results for JARPN II samples, which were taken approximately in a same sub-area, showed no significant genetic differences among years (see Table 4 of Pastene *et al*., 2004a). In the context of the sub-stock scenario this results means that the mixing rates of sub-stocks in each sub-area is exactly the same in each year. Again by taking into consideration the pattern of movement and mixing of whales this is biologically implausible.

Therefore by considering the pattern of movement and mixing exhibited by whales and the results of the genetics showing no significant differences between sub-areas 1W and 1E (Table 1), the scenario of sub-stocks in Hypotheses 4 and 5 is considered implausible.

Necessity of samples from the breeding ground
In several opportunities the Scientific Committee has noted the importance of obtaining samples from breeding grounds for a comprehensive understanding of the stock structure of migratory whales. This makes sense from the scientific point of view, however the logistic difficulties in getting such samples should be considered. The case of the B-C-B stock of bowhead whale is mentioned here as an example. As mentioned earlier, significant genetic heterogeneity has been detected for migrating bowhead whales, for both mtDNA and microsatellites (e.g. Pastene *et al*. 2004b). For this specific case samples from the breeding grounds would assist largely to understand the pattern of genetic differentiation found in the migratory corridor. By recognizing the logistic difficulties in obtaining samples from the breeding grounds, the Committee has not insisted in such a sampling neither has adopted stock structure hypotheses to cover for the lack of samples from the breeding ground. In this particular case analyses and hypothesis on stock structure are based on samples obtained in the migratory corridor (e.g. Rugh *et al*., 2003).

Same as in the case of the bowhead whale, the sole reason of absence of samples from low latitude breeding ground should not be a reason for establishing new stock hypotheses in the case of the North Pacific Bryde's whale. Otherwise the Scientific Committee criterion to adopt hypotheses on stock structure could be considered again as inconsistent (e.g. Pastene, 2003).

Is the longitudinal line at 155°E biologically plausible?

During the 1998 Scientific Committee meeting there was a concern on an apparent gap in the catch distribution of Bryde’s whale between 150°E and 160°E (see IWC, 1999 p. 116). Catch distribution analysis was based on past land-based and pelagic commercial catches (Figure 5). On that opportunity it was explained that such gap in catch distribution was a result of catch regulations; the western boundary to pelagic whaling set by the Government of Japan at that time was 159°E and the eastern extent of coastal whaling was restricted by distance from the land station (IWC, 1999).

Since 2000 JARPN II surveys have covered new regions in the western North Pacific included the longitudinal sector around 155°E. The catches of Bryde’s whales in the western North Pacific for both past pelagic commercial operations (1971-1979) and recent JARPN II catches (2000-2005), were plotted (Figure 6). As evident from this figure there is no gap between 150°E and 160°E. Further no discontinuity in the catch distribution is observed for the sector comprised between approximately 140°E and 160°W, which cover most of sub-areas 1 and 2. Whales taken by past land-based operations around the Ogasawara Island (data not shown) would cover the blank space in the south west region in Figure 6. Therefore the explanation given in 1998 to explain the gap observed in catch distribution between 150°E-160°E has been corroborated.

A statistical test based on the randomized chi-square (Roff and Bentzen, 1989) was conducted using all available genetic samples (Figure 6), to test for differences between whales distributed west (sub-area 1W) and east (sub-area 1E) of 155°E (Table 1). Analysis based on mtDNA involved 261 samples for sub-area 1W and 140 for sub-area 1E. A large P-value resulted from this comparison suggesting no significant differences between these sub-areas. A similar result was found in the microsatellite analysis for 17 loci (Table 1). This is consistent with the results found by Martien and Taylor (2004) and Pastene *et al*. (2004a), which conducted more detailed genetic analyses based in different groupings in sub-area 1

Analysis of sighting distribution (Miyashita and Shimada, 1996; Shimada, 2004, Figures 3 and 4) and mark-recapture (Kishiro, 1996; 1998) suggested no discontinuity around 155°E.

Given these results the longitudinal line at 155°E is not supported by available scientific data.

CONCLUSIONS

The single stock scenario (Hypothesis 1) is fully consistent with the available data. This hypothesis should be given high plausibility and it should be considered as base case scenario in the trials specifications. Although DNA and mark-recapture data are limited for sub-area 2, results based on allozymes, sighting and catch distribution and biological parameters suggest no differences between whales in sub-areas 1 and 2. Hypotheses 2 and 3 should be considered in the trials under a precautionary approach (to cover for the absence of DNA and mark-recapture data in sub-area 2). However these hypotheses should not be considered as base case because there is no scientific evidence supporting the existence of a second stock east of 180°E.

Hypotheses 4 and 5 are not supported or explained by the available scientific data. Furthermore the application of the `simple model filter` to mark-recapture data for western North Pacific Bryde`s whales (Punt *et al*., 2005) suggested that if there are two sub-stocks in sub-area 1, they are very well mixed. The high mixing rates implied by the available data meant that trials based on stock hypotheses with two-sub-stocks that mix would behave in a manner very similar to trials based on stock hypotheses with only one stock in sub-area 1. In order to avoid waste of time, hypotheses involving sub-stocks can be ignored for the trial specifications.

The possibility of additional stock structure in sub-area 1 emerged during the 1998 Scientific Committee, not because of supporting evidence but rather by the concern by some members of the Committee that sub-area 1 is very large and there is limited information for some part of it (IWC, 1999 p. 14). The spatial distribution of genetic samples in sub-area 1 has been enhanced since 1998 through the addition of the samples from the JARPN II. Different genetic methods were used to examine these data and no significant degree of genetic heterogeneity was found. Also JARPN II catches covered for the apparent geographical gap observed when only past commercial samples were plotted.

The possibility of a sub-stocks occurring in sub-area 1 has been weakened considerably with the new information accumulated since 1998 and therefore hypotheses based on sub-stocks (Hypotheses 4 and 5) can be ignored for the process of trial specifications.

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ACKNOWLEDGEMENTS

I would like to thank T. Tamura and K. Konishi (ICR) for their assistance in making Figure 6 and M. Goto and N. Kanda (ICR) for their help in the update of DNA data. H. Hatanaka and S. Ohsumi (ICR) read the manuscript and provided valuable comments.

Table 1: Results of a genetic comparison between Bryde's whales west of 155°E (sub-area 1W) and east of 155°E (sub-area 1E) based on mtDNA and microsatellite, and chi-square test. In parenthesis are the sample sizes for 1W and 1E, respectively. Results for the Hardy-Weinberg equilibrium test, by sub-area and locus, are also shown. Figures shown are the P-values after 10,000 randomizations. All the samples involved in this analysis are from the larger, pelagic form Bryde's whale (Goto *et al*., 2004).

Locus	Heterogeneity test	Test for Hardy-Weinberg Equilibrium	
	P-value	Sub-area 1W	Sub-area 1E
mtDNA (261, 140)	**0.716**		
GATA98	0.154	0.720	0.148
EV104	0.764	0.829	0.671
GT011	0.860	0.958	0.465
GATA53	0.578	0.823	0.294
GATA417	0.784	0.954	0.504
DlrFCB14	0.348	0.619	0.856
DlrFCB17	0.968	0.909	0.915
GT23	0.488	0.218	0.328
EV14	0.608	0.731	0.331
GT310	0.188	0.231	0.641
EV1	0.455	0.038	0.360
EV94	0.674	0.792	0.005
GGAA520	0.351	0.253	0.247
EV21	0.430	0.138	0.250
GT575	0.342	0.607	0.803
GATA28	0.454	0.227	0.243
TAA31	0.740	0.502	0.232
All microsatellite loci (260, 125)	**0.882**	**0.737**	**0.209**

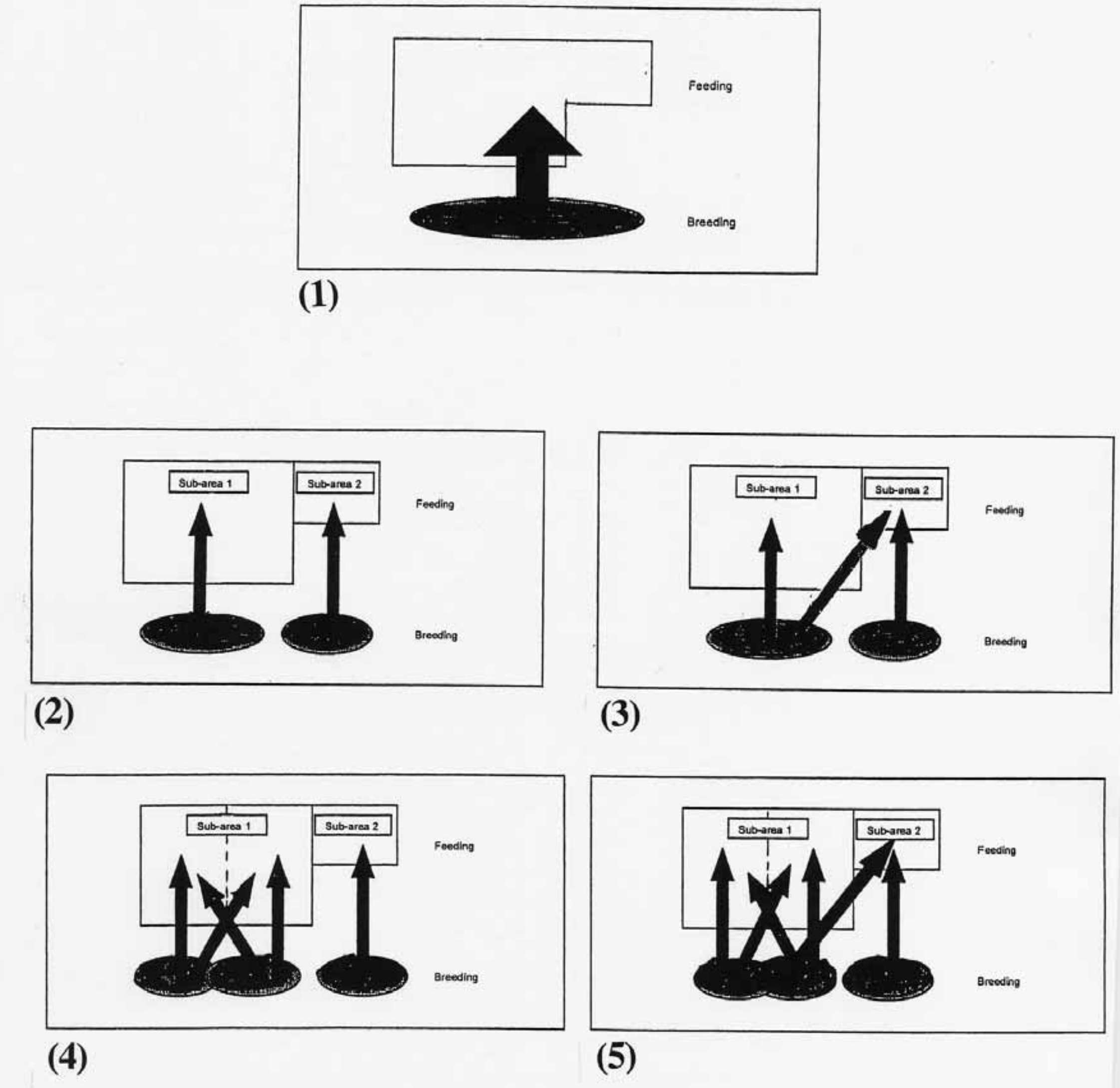

Figure 1: Hypotheses on stock structure presented at the *pre-implementation assessment* of western North Pacific Bryde's whale. The illustration was modified from that in the Workshop report for clarity. See text for explanation.

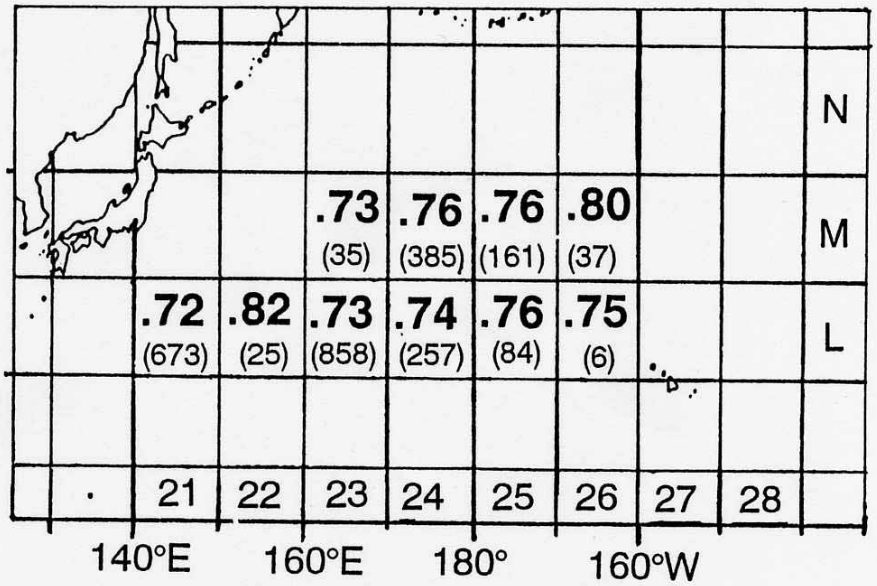

Figure 2: Spatial distribution of *Got1*^{f} frequencies by 10° squares for the western North Pacific Bryde's whales. In parenthesis are the sample sizes (taken from Wada, 1996).

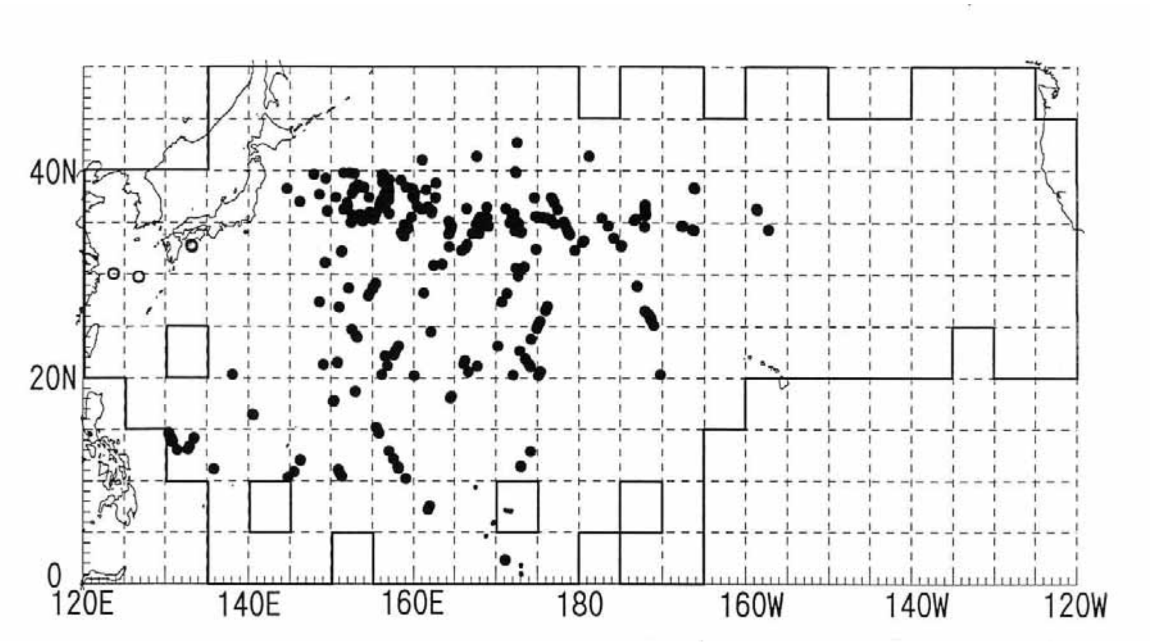

Figure 3: Positions of primary sightings of western North Pacific Bryde's whales in August and September in the period 1988-1995 (taken from Shimada and Miyashita, 1996).

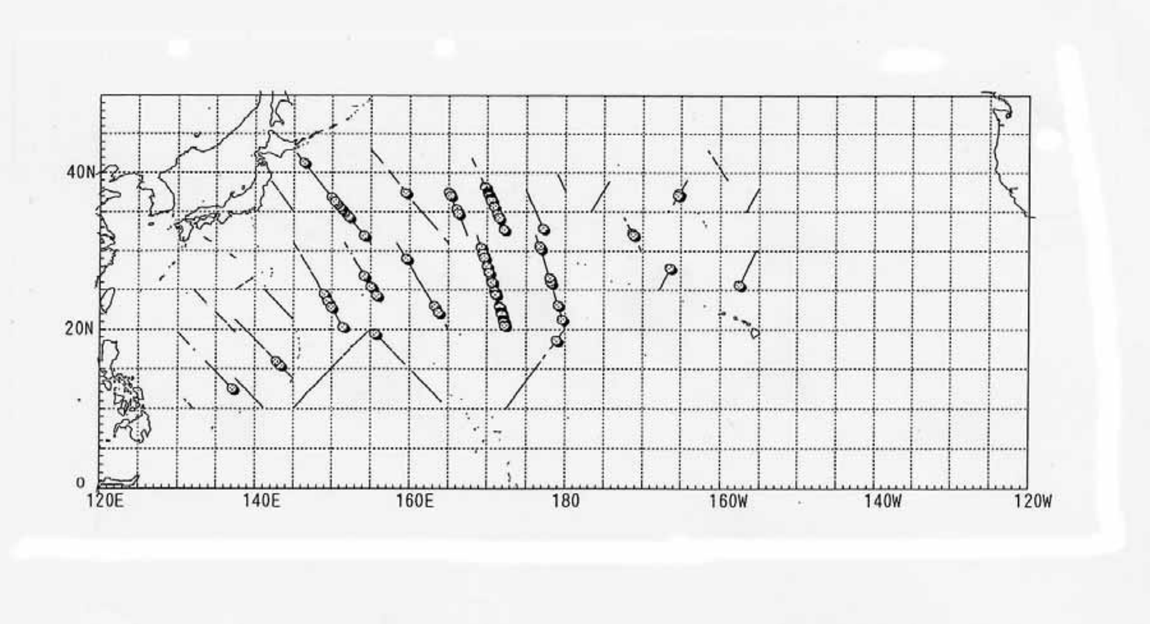

Figure 4: Distribution of primary sighting of western North Pacific Bryde's whales and track lines under passing mode effort for the period 1998-2002 (taken from Shimada, 2004).

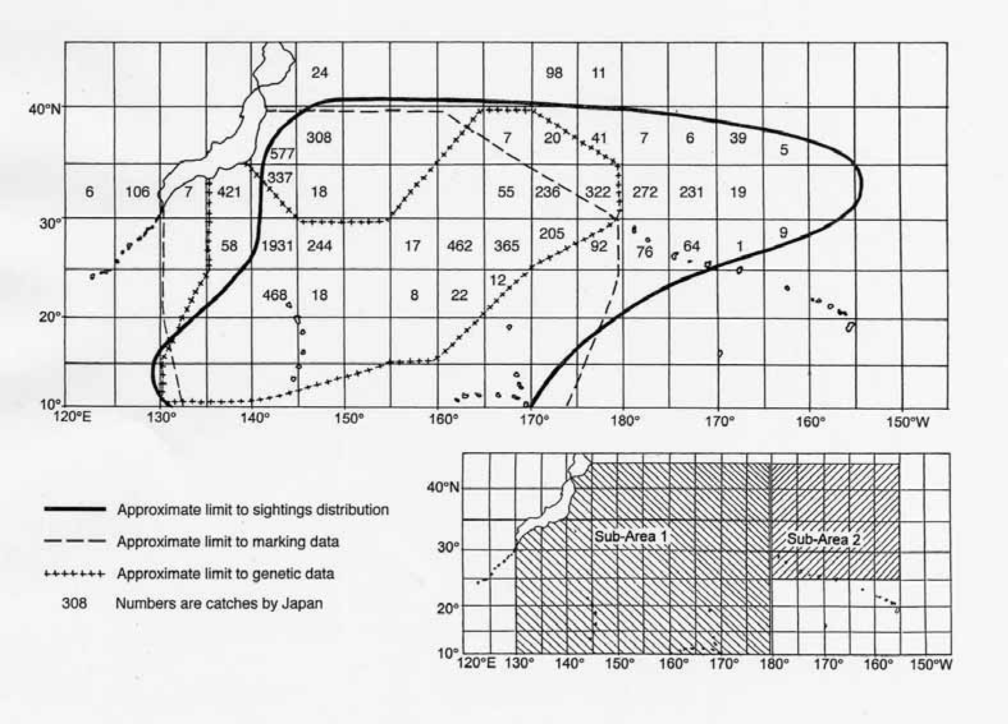

Figure 5: Summary of information for determining stock boundaries for *ISTs* for western North Pacific Bryde's whales and agreed boundaries for the Western Stock and two sub-areas. Note the apparent gap between 150°E and 160°E in catch distribution (taken from IWC, 1999).

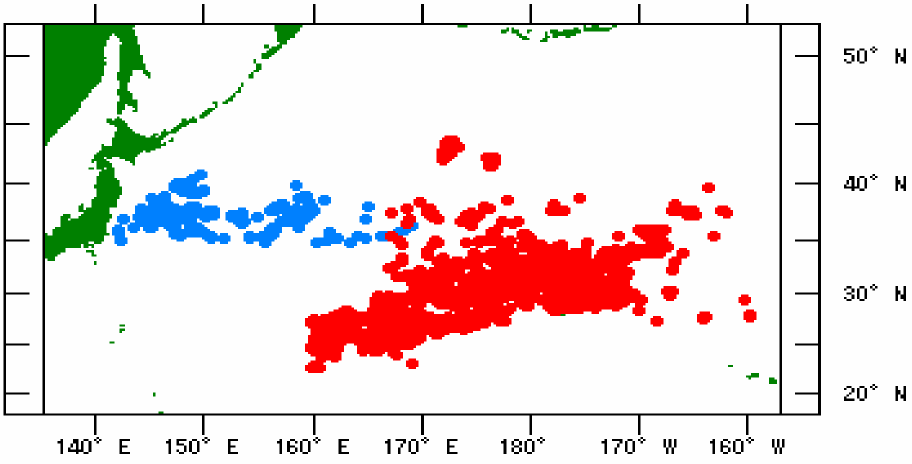

Figure 6: Catch distribution of Bryde's whales in the western North Pacific. Red corresponds to catch by pelagic whaling operations conducted between 1971 and 1979; blue corresponds to catch by JARPN II between 2000 and 2005.