

**Report of the Workshop
on the *Implementation Review*
of Western North Pacific
Bryde's Whales**

Report of the Workshop on the *Implementation Review* of Western North Pacific Bryde's Whales¹

EXECUTIVE SUMMARY

The Workshop on the RMP *Implementation Review* of offshore western North Pacific Bryde's whales, chaired by Donovan, was held in Tokyo from 21-24 March 2017 at the Ministry of Agriculture, Forestry and Fisheries Sanbancho Branch Office.

The Workshop made considerable progress with this, the first *Implementation Review* since the completion of the *Implementation* in 2007, as summarised below.

- (1) The Workshop reviewed the new information relevant to stock structure and agreed to take forwards two stock structure hypotheses (see Fig. 5 below) - one of the four considered at the 2007 *Implementation* and one new hypothesis:
 - (a) *Hypothesis 2*: There are two stocks, one feeding in sub-area 1 and the second feeding in sub-area 2.
 - (b) *Hypothesis 5*: There are two stocks, one feeding in sub-area 1 and the second feeding in sub-area 2 with mixing occurring in sub-area 1E. There are more animals from stock 1 than stock 2 in the mixing area.
- (2) The Workshop reviewed new information on abundance estimates and developed a workplan to try to obtain agreed abundance estimates (including additional variance) for use in conditioning the trials and the *CLA*.
- (3) The Workshop developed a new set of simulation trials for the *Implementation Review* that involve testing for uncertainty in stock structure, stock boundaries, MSYR, removals and additional variance.
- (4) The Workshop developed an ambitious work plan to try to complete the *Implementation Review* at SC/67a in May 2017.

The Workshop was held in Tokyo, from 21-24 March 2017 at the Sanbancho Branch Office of the Ministry of Agriculture, Forestry and Fisheries. The list of participants is given as Annex A.

1. INTRODUCTORY ITEMS

1.1 Convenor's opening remarks

Donovan welcomed the participants to Tokyo. He thanked the Fisheries Agency of Japan and the Institute of Cetacean Research for hosting the Workshop in such excellent facilities.

The purpose of the Workshop was to facilitate the first *Implementation Review* of western North Pacific Bryde's whales; the *Implementation* was completed in 2007 (IWC, 2008b, pp.91-115). The RMP states that:

'... an *Implementation Review* for a species and *Region* should normally be scheduled no later than six years since the completion of the previous *Implementation (Review)*. In some cases, an *Implementation (Review)* may require the specification and running of further *Implementation Simulation Trials*, especially when major changes to *Management Area* boundaries or the selection of different options for *Catch-capping* and/or *Catch-cascading* than those currently used is contemplated. In such cases the *Implementation Review* would probably not be completed at a single meeting.'

The Scientific Committee had agreed that the *Implementation Review* would take place later than six years in light of the additional information expected to become available from the JARPN II review (IWC, 2010; 2017a) and to avoid overlap with ongoing *Implementation Reviews*.

The objective of the Workshop was to examine any new information available (including that on stock structure, catch and abundance) and determine whether the existing trials (and by extension hypotheses) are adequate, whether further trials are necessary (and if so develop them) or whether some existing trials are no longer required. If additional work is necessary, then the Workshop will develop a timetable to complete the *Implementation Review*.

1.2 Election of Chair and appointment of rapporteurs

Donovan was elected Chair. Allison, Butterworth, Palka, Punt and Tiedemann acted as rapporteurs, assisted by Donovan.

1.3 Adoption of agenda

The adopted agenda is given as Annex B.

1.4 Documents and data available

The list of documents is given as Annex C.

2. SUMMARY OF THE INITIAL IMPLEMENTATION

The Initial *Implementation* completed in 2007 followed the timetable and process agreed for the RMP, including two intersessional workshops (IWC, 2007b; 2008a; 2008b, pp.91-115; 2008c).

2.1 Overview of hypotheses

The 2007 *Implementation* of western North Pacific offshore Bryde's whales (IWC, 2008c) identified four hypotheses about mixing and stock structure for the western North Pacific Bryde's whales. In developing these hypotheses, it had been assumed that:

- (1) the breeding grounds are in lower latitudes where no whaling will take place;
- (2) no whaling will occur during migration to the feeding grounds; and
- (3) the hypotheses could be represented using three spatial cells (sub-areas 1W, 1E and 2; see Fig. 1.).

The four general hypotheses regarding stock structure considered in the *Implementation* are illustrated in Fig. 2, Hypotheses 1-4.

- (1) Hypothesis 1 is that there is only one stock in sub-areas 1 and 2.
- (2) Hypothesis 2 comprises two stocks, one stock in sub-area 1 and the other in sub-area 2.
- (3) Hypothesis 3 also involves two stocks in sub-areas 1 and 2. One stock is found in both sub-areas whilst the other is found in sub-area 2 only.
- (4) Hypothesis 4 involves two stocks in sub-areas 1 and 2. Stock 1 consists of two sub-stocks that mix in sub-areas 1W and 1E. Stock 2 is only found in sub-area 2. Sub-stocks are modelled as stocks (i.e. there is no permanent transfer of animals among sub-stocks).

¹Presented to the Scientific Committee as SC/67a/Rep07.

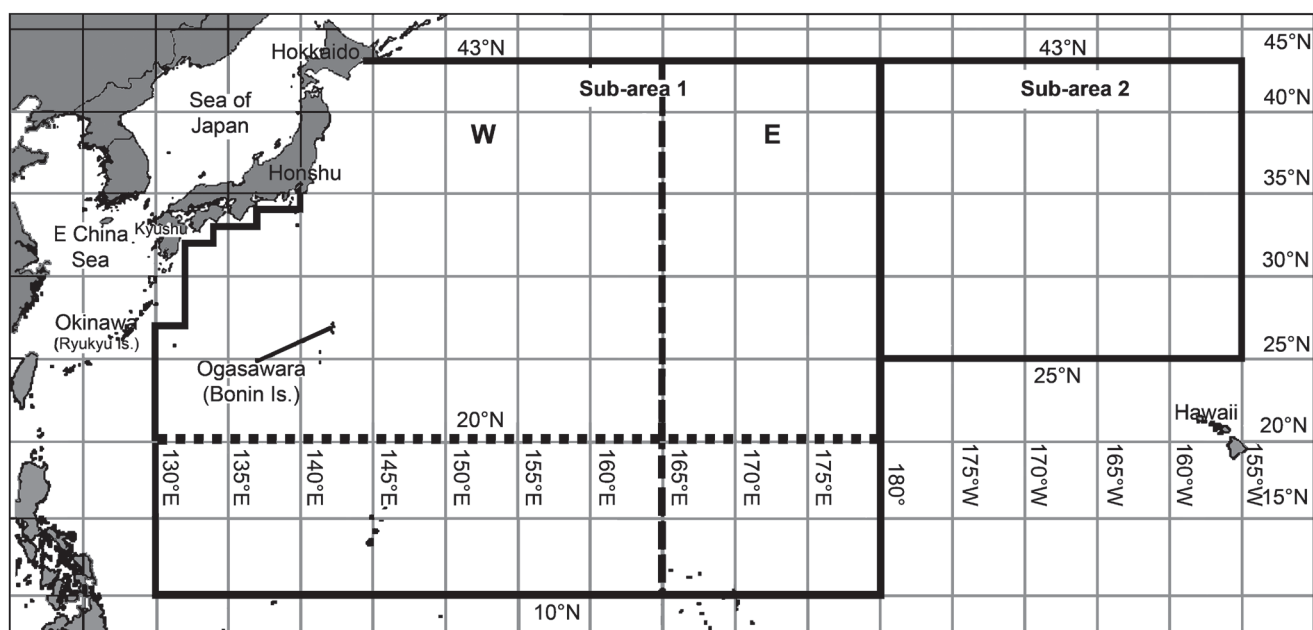


Fig. 1. Map of the western North Pacific showing the sub-areas defined for the western North Pacific Bryde's whales during the *Implementation* (IWC, 2008b, pp.91-115). The staggered border to the south of Japan is used to ensure that no catches of the inshore form occur. The dotted line at 20°N shows the revised southern border of sub-area 1 agreed at this Workshop (see Item 4.2) to avoid the breeding grounds.

Table 1
Management variants considered in the 2007 *Implementation*.

Variant	Description
Variant 1	Sub-areas 1W, 1E and 2 are <i>Small Areas</i> .
Variant 2	Sub-area 2 is taken to be a <i>Small Area</i> and the complete sub-area 1 is treated as a <i>Small Area</i> .
Variant 3	Sub-area 2 is taken as a <i>Small Area</i> and sub-area 1 is a <i>Combination Area</i> . Sub-areas 1W and 1E are <i>Small Areas</i> , with catch-cascading applied.
Variant 4	Sub-areas 1 and 2 (combined) are a <i>Combination Area</i> , and sub-areas 1W, 1E and 2 are <i>Small Areas</i> , with catch-cascading applied.

The data used in the trials included historical catches, abundance estimates, ages (commercial, 1971-79 and special permit, 2000-03) and marking (animals marked 1972-84, recovered 1976-86). The full trial specifications and list of trials are given in (IWC, 2008b, pp.91-115). In addition to the stock hypotheses, the following factors were tested:

- (1) uncertainty in historical catches (particularly regarding the allocation between sei and Bryde's whales as these whales were not differentiated in the data prior to 1954);
- (2) additional process error;
- (3) position of the boundary between sub-areas 1W and 1E;
- (4) age dependent mixing; and
- (5) stochastic mixing (Hypothesis 4).

2.2 Results and conclusions

The four management variants given in Table 1 were tested. Variants 1, 3 and 4 were considered 'acceptable' whereas Variant 2 was considered 'acceptable with research'. The last result was due to the poor performance of Variant 2 in some trials related to stock structure Hypothesis 4.

3. REVIEW OF NEW INFORMATION

3.1 Stock structure and movements

The Workshop noted that the *Implementation* had developed stock structure hypotheses based on genetic, mark-recapture and age data. Most of the new information relevant to stock structure considered in this *Implementation Review* related to additional genetic data (including refined analyses) and age data.

3.1.1 Movements

Kishiro (1996) examined movements of Bryde's whales in the western North Pacific using information from whale marks recovered by Japanese and Soviet whaling vessels until the end of the 1987 season. The data suggested that whales summering in the whaling grounds of sub-area 1, winter over a wide latitudinal range (1-25°S). The study did not find evidence of more than one stock of Bryde's whales in the western North Pacific whaling grounds of sub-area 1.

Murase *et al.* (2016) reported the movements of two individual Bryde's whales using satellite-monitored radio tags in offshore waters of the western North Pacific (sub-area 1). One whale was tracked for 13 days in July 2006 and the second whale was tracked for 20 days in July/August 2008. The first whale showed a north-south movement while the second one moved from west to east and then to the south.

The Workshop welcomed this information, noting that the marking data had also been considered in the 2007 *Implementation*.

It agreed that this information would be considered when evaluating potential stock structure hypotheses (see Item 3.1.4).

3.1.2 Age data

SC/M17/RMP03 reported on progress in earplug-based age determination and on the estimation of biological parameters for Bryde's whales sampled during the 2000 to 2014 JARPN II surveys. Age readability was reported, and the age distribution for JARPN II and commercial whaling was compared by sub-area, with no significant differences detected for whales of age 9 and older.

The comparison of age distributions by sub-area is important, as differences detected between sub-areas 1W and 1E during the original *Implementation* had been the primary basis for introducing stock structure hypothesis 4 (IWC, 2007a, pp.94-96; 2007b, pp.407-414), which assumes different stocks in those two sub-areas.

The Workshop examined the updated age data set, giving particular consideration to the consequences of a change in age reader (from Kato to Bando) over the period under consideration, and the locations and method of collection of the samples.

Annex D lists estimates of ages of the same earplug by the two readers, and provides associated comparative plots. The Workshop noted an appreciable systematic difference evident between Bando's age readings and the earlier readings of JARPN II by Kato, with the former being notably larger than the latter for most earplugs. Bando explained that Bryde's whale earplugs were particularly difficult to read. A careful study had revealed frequent cases of additional rings present that were particularly difficult to identify. He considered the fact that he was counting these additional rings to be the main reason for his readings frequently being greater than those by Kato.

The Workshop also noted differences (see Annex D2) in the latitudinal distribution of the commercial and JARPN II catches (the latter being further north). Furthermore, readability of earplugs from the commercial operations (around 17%) was much lower than that for JARPN II (around 65%), with the difference being attributed to the less careful extraction process possible during commercial whaling.

Given the above, the Workshop **agreed** that the data could not be pooled across the commercial and JARPN II activities, and that consequently comparisons of age distributions between sub-areas should be restricted to Bando's readings of the JARPN II earplugs (or Ohsumi and Masaki's readings of the commercial samples). To avoid possible confounding by selectivity effects, comparisons were restricted to whales aged 10 and above, with a sensitivity analysis for ages of 12 and above.

The results of χ^2 tests comparing these age distributions across sub-areas 1W and 1E are reported in Annex D. No differences significant at the 5% level were found. This contrasts with a difference significant at the close to the 1% level found previously (IWC, 2007b, pp.413-414) that provided the basis for stock structure Hypothesis 4. The Workshop **agreed** that the earlier result was probably an artefact caused by pooling non-comparable data that had been available in different proportions in the two sub-areas.

The desirability of an age reader calibration exercise, *inter alia* to allow the estimation of ageing error is discussed under Item 3.5.

3.1.3 Genetic data

Considerable new genetic information on North Pacific Bryde's whales was presented by Kanda *et al.* (2007), Pastene *et al.* (2016a; 2016b), SC/M17/RMP01 and Annex E, based on analysis of mitochondrial control region and 17 autosomal microsatellites, derived from sub-area 1W (SA1W), sub-area 1E (SA1E), and sub-area 2 (SA2).

Pastene *et al.* (2016b) examined a total of 1,019 and 1,026 samples of North Pacific Bryde's whales with microsatellite DNA (17 loci) and mtDNA sequences (299bp), respectively, to examine stock structure in sub-areas 1 and 2. Samples were from different sources: JARPN II (catches), Japanese dedicated sighting surveys (biopsy), IWC/POWER surveys (biopsy) and past commercial whaling (catches). No significant genetic heterogeneity was found between the western and eastern sectors of sub-area 1 divided at 165°E,

a result supported by high statistical power. However, both genetic markers showed significant differences (males, females and both sexes combined) between sub-areas 1 and 2. Phylogenetic analysis of mtDNA haplotypes revealed no sub-area specific clades. The authors concluded that the results are consistent with the occurrence of two stocks with a stock division around longitude 180°.

Pastene *et al.* (2016a) presented the results of a STRUCTURE analysis based on the same Bryde's whale data set used in Pastene *et al.* (2016b). The results of the analyses revealed no structuring of the Bryde's whale within sub-areas 1 and 2. The STRUCTURE approach showed structure at the oceanic basin level (western North Pacific, eastern South Pacific off Peru, western South Pacific off Fiji and eastern Indian Ocean off Java; Kanda *et al.*, 2007).

SC/M17/RMP01 examined the stock structure of Bryde's whale in the North Pacific using a Discriminant Analysis of Principal Component (DAPC), based on the same data set used in Pastene *et al.* (2016b) and Kanda *et al.* (2007). The DAPC analysis revealed no structure in the North Pacific region involving sub-areas 1 and 2. However, the DAPC analysis showed differentiation of Bryde's whales among western North Pacific, eastern South Pacific off Peru, western South Pacific off Fiji and eastern Indian Ocean off Java. The lack of an evident structure within the North Pacific analysis was explained by the low *Fst* estimates among whales in sub-areas 1W, 1E and 2.

The Workshop thanked the authors of these papers. The results of three additional analyses of these data that could assist in examining stock structure are presented in Annex E:

- heterogeneity test between sub-areas 1 and 2 by year;
- heterogeneity test between sub-areas 1 and 2 by moving the longitudinal boundaries between the two sub-areas (150°E, 155°E, 160°E, 165°E, 170°E, 175°E, 180° and 175°W); and
- test for Hardy-Weinberg (HW) equilibrium.

Regarding (a), tests were conducted for the years 1979 to 2014 and in 12 cases significant differences were found for both genetic markers. Regarding (b) significant differences were found for both markers when the boundaries were 165°E, 170°E, 175°E and 180°. The test for HW equilibrium (c) was not considered informative with respect to stock structure. Based on these results, the following evaluation of the stock structure hypotheses from the 2007 *Implementation* was made by the authors of Annex E:- Hypothesis 1: not consistent with the current genetic data; Hypotheses 2 and 3: consistent with the current genetic data; Hypothesis 4: not specifically supported by the current genetic data. In addition, an additional hypothesis was proposed that is also consistent with the genetic data: Hypothesis 5, which proposes two stocks, one in sub-area 1W and the other in sub-area 2 with the two stocks mixing in sub-area 1E. These are illustrated in Fig.2.

In order to evaluate the five stock structure hypotheses, the Workshop identified a number of additional analyses. These are discussed below (and see Annex E). As well as the material on ages and movements, a series of genetic diversity measures were considered (arising from analyses included in presented papers, complemented by analyses described in Annex E and summarised in Table 2):

- for microsatellites: observed heterozygosity, H_o , expected heterozygosity, H_e , test for departure from Hardy-Weinberg-equilibrium, HWE; and
- for mtDNA: haplotype diversity, HD , and haplotype frequencies.

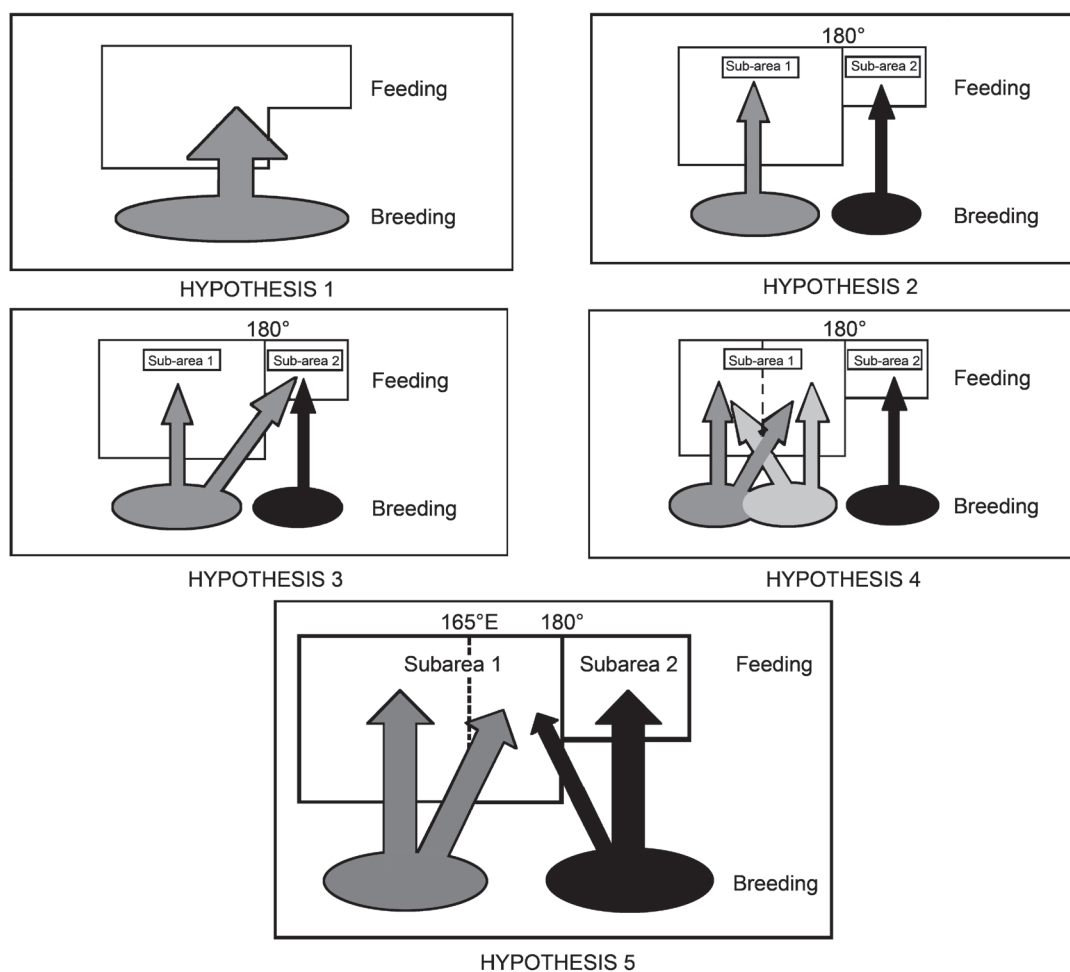


Fig. 2. Schematic showing the stock structure hypotheses considered during this *Implementation Review*. Hypotheses 1-4 were also used in the 2007 *Implementation*. Hypothesis 5 is the hypothesis developed at this Workshop.

Table 2
Measures of genetic diversity and haplotype frequencies (+/- 1SD).

Genetic diversity measures	SA1W	SA1E	SA1	SA2	SA1E+SA2	Total
H_O	0.67+/-0.15	0.68+/-0.16	0.67+/-0.15	0.70+/-0.14	0.68+/-0.15	0.67+/-0.15
H_E	0.68+/-0.15	0.69+/-0.14	0.68+/-0.15	0.68+/-0.14	0.69+/-0.14	0.68+/-0.15
HWE	0.713	0.111	0.419	0.370	0.157	0.407
HD	0.82+/- 0.01	0.82+/- 0.03	0.90+/- 0.02	0.82+/- 0.01	0.85+/- 0.02	0.83+/- 0.01
Sample size for microsatellites	847	119	966	53	172	1,019
Sample size for mtDNA	855	117	972	53	190	1,025

Microsatellites: H_O , observed heterozygosity; H_E , expected heterozygosity; HWE, p-value for Hardy-Weinberg-Equilibrium; mitochondrial DNA: HD, haplotype diversity

Table 3
Genetic divergence measures.

	SA1W vs SA1E vs SA2	SA1W vs SA1E	SA1E vs SA2	SA1 vs SA2	SA1W vs combined SA1E/SA2	SA1W vs SA2
Microsatellite F_{ST}	0.002 p=0.002	0.000 p=0.155	0.003 p=0.029	0.004 p<0.001	0.001 p=0.010	0.004 p<0.001
mtDNA F_{ST}	0.009 p=0.002	0.002 p=0.090	0.017 p=0.045	0.022 p<0.001	0.011 p=0.004	0.023 p=0.003
mtDNA exact test	p=0.001	p=0.148	p=0.010	p<0.001	p<0.001	p<0.001

Bold text indicates a statistical significance at $\alpha=0.05$ after FDR correction.

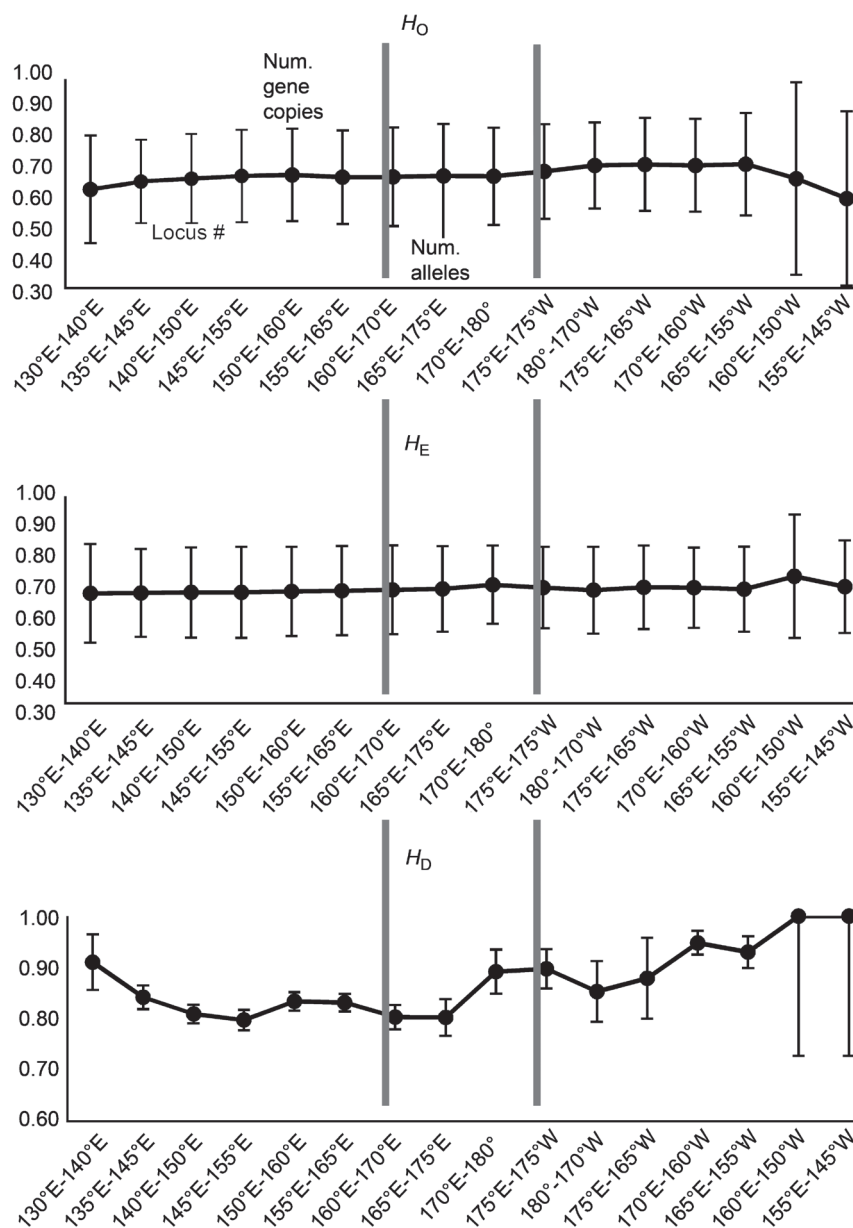


Fig. 3. Genetic diversity relative to longitude of sample origin (calculated for 5° intervals; plotted as moving averages over 10° intervals). The vertical grey lines indicate the management boundaries.

The following strata were considered: sub-area 1W, sub-area 1E, and sub-area 2 separately, sub-area 1, combination of sub-area 1E and sub-area 2, total (combination of sub-area 1 and sub-area 2).

Table 3 summarises the results of cross-comparison of several estimates of genetic divergence (i.e. for microsatellites F_{ST} ; for mtDNA F_{ST} and p-values of an exact test of population differentiation (i.e. test of non-random distribution of haplotypes into population samples under the hypothesis of panmixia).

Fig. 3. and Fig. 4. illustrate the diversity and DAPC data by longitude. Further details are provided in Annex E.

With regard to sampling strategy, the Workshop noted that:

- the sample number is highest in sub-area 1W, and much lower in sub-area 2;
- the temporal spread in sampling is larger in areas of former commercial whaling (sub-area 1); and
- 5 samples assigned to sub-area 2 actually originated from east of sub-area 2 (between 155°W and 145°W).

The possible implications of these issues were discussed and the Workshop **recommends** that prior to SC/67a, analyses are conducted to test for the effect of inclusion vs exclusion of:

- the old samples from commercial whaling; and
- samples east of 155°W.

It is not expected that these issues will substantially change the plausibility of the stock structure hypotheses.

With respect to statistical power, Pastene *et al.* (2016b) had evaluated the power to detect population structure using hypothesis testing (i.e. F_{ST}). The Workshop noted that power analysis confirms high statistical power to detect population structure for migration rates up to 0.01 (translating into an F_{ST} of about 0.005), but power drops considerably with higher migration rates (power is below 10% at migration rate 0.1). Actual power to detect structure on feeding grounds may be lower if breeding stocks mix on feeding grounds (stock structure hypothesis 3 to 5), in particular, if mixing proportions are uneven.

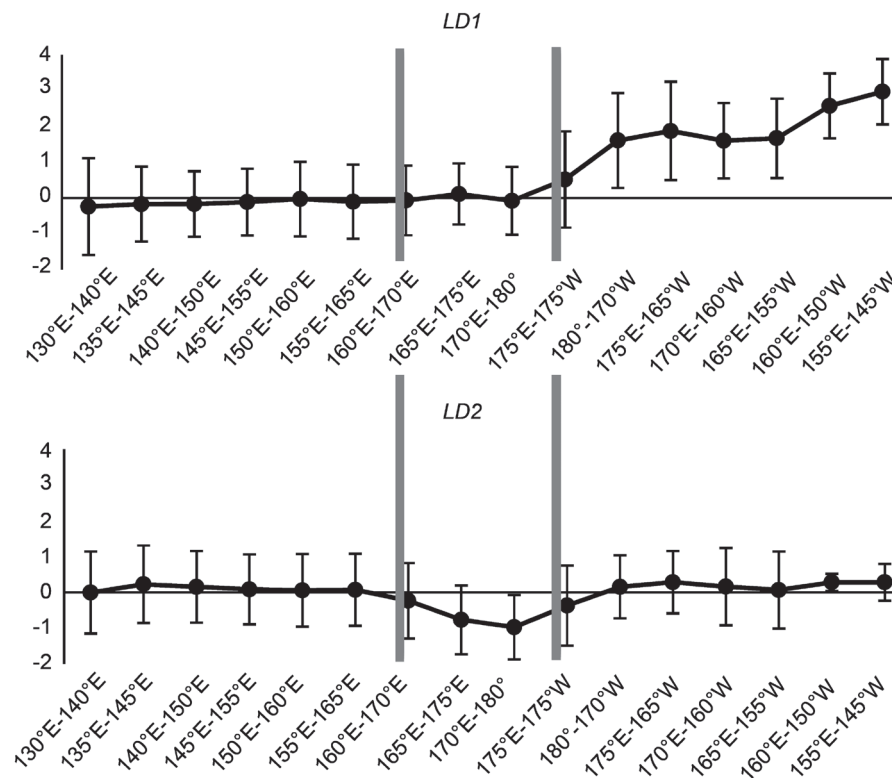


Fig. 4. Mean values of the first two principal components of the DAPC, conditional on longitude (calculated for 5° intervals; plotted as moving averages over 10° intervals). The vertical grey lines indicate the management boundaries.

Table 4

General summary of the information useful to assess plausibility of alternative stock-structure hypotheses (*cf* Fig. 2). A '+' indicates evidence in favour of a hypothesis, '-' indicates evidence against a hypothesis, '(+)' indicates weak evidence in favour of a hypothesis, '(-)' indicates weak evidence against a hypothesis, a '(+/-)' indicates ambiguous information, and 'NIW' indicates that the evidence is not inconsistent with the hypothesis. Note that the designation NIW often reflects the asymmetrical nature of information on stock structure (i.e., existence of differences can be viewed as positive evidence for multiple stocks, but absence of differences provides no information, and cannot be viewed as positive evidence for a single stock).

Evidence	Hypothesis 1	Hypothesis 2	Hypothesis 3	Hypothesis 4	Hypothesis 5 (new)
mtDNA-HD	-	-	(+)	- ^a	+
mtDNA-F _{ST}	-	+	-	- ^a	(+)
mtDNA-haplotype distribution (exact test)	-	+	NIW	- ^a	(-) ^d
Microsatellite H _O /H _E	NIW ^b	(-) ^b	- ^b	- ^{a,b}	(-) ^b
Microsatellite-F _{ST}	-	+	-	- ^a	(+) ^c
Microsatellite DAPC	-	+	(-)	NIW	NIW
Overall assessment	-	+	-	- ^a	(+) ^d

^aAssumes two stocks in SA1, one predominantly feeding in SA1W, the other in SA1E, with mixing. With small divergence among these stocks/high mixing rates, this hypothesis will become indistinguishable from hypothesis 2. ^bHeterozygosity estimates were almost identical across all strata, even if stratified by longitude and were considered uninformative with regard to stock structure. ^cUnder the assumption of uneven mixing proportions in SA1E, biased towards the more western stock. ^dIf mixing proportions are strongly biased towards the more western stock, difficult to distinguish from hypothesis 2.

3.1.4 Conclusions

The genetic information used in the evaluation of the five stock structure hypotheses is summarised in Table 4.

HYPOTHESIS 1

This hypothesis constitutes the null hypothesis of no stock structure. It was rejected with high statistical support by various divergence measures indicative of genetic structure. It is further contradicted by increased haplotype diversity, when combining strata (Table 2).

The Workshop **recommends** that Hypothesis 1 is not considered further.

HYPOTHESIS 2

This hypothesis was supported by all statistical analyses of genetic divergence, both for mtDNA and microsatellites. It

can however not fully explain the stratum-specific pattern of haplotype diversity, i.e., increased HD when sub-area 1W and sub-area 1E are combined (Table 2), nor the increase in HD east of 175°E (i.e., within sub-area 1E).

The Workshop **recommends** that Hypothesis 2 is included in the *Implementation Simulation Trials*. However, it also **recommends** that sensitivity to the position of the border between sub-area 1 and sub-area 2 is investigated in the trials.

HYPOTHESIS 3

This hypothesis did not receive explicit support by any of the performed analyses. There is no indication for a mixing of stocks in sub-area 2.

The Workshop **recommends** that Hypothesis 3 is not considered further.

Table 5
Potential abundance estimates for consideration for use in the *Implementation Review*.

Area	Date stamp	Range of years	Estimate	CV	Approx. 95% CI	IWC reference	Original reference	Status/notes
1W	1995	1988-96	8,152	0.329	4,300-15,500	IWC (2007)	Kitakado <i>et al</i> (2005); Kitakado <i>et al</i> (2007)	See 1
1E	1995	1988-96	10,814	0.342	5,500-21,100	IWC (2007)	As for 1W	See 1
2	1995	1988-96	2,860	0.372	1,400-5,900	IWC (2007)	As for 1W	See 1
1+2	1995	1988-96	21,826	0.295	11,000-38,000	IWC (2007)	As for 1W	Add SD of 0.673
1W	2000	1998-2002	4,957	0.398	2,300-10,800	IWC (2009a, pp.6-7)	Kitakado <i>et al</i> (2008); Shimada <i>et al</i> (2008)	See 2
1E	1999	1998-2002	11,213	0.498	4,200-29,800	As for 1W	As for 1W	See 2
2	2002	1998-2002	4,331	0.553	1,500-12,800	As for 1W	As for 1W	See 2
1+2	2000	1998-2002	20,501	0.337	11,000-38,000	As for 1W	As for 1W	See 2
1W	2012	2008-14	16,511	0.25	10,200-26,800	This report	SC/M17/RMP02	See 3
1E	2012	2008-15	7,074	0.24	4,500-11,200	As for 1W	As for 1W	See 3
2 extended	2014	2013-15	4,861	0.24	3,100-7,700	As for 1W	As for 1W	See 3

Notes:

¹The 1988-96 surveys were not oversighted. The estimates were used for conditioning the *Implementation* but have not been agreed for use in an actual application of the RMP.

²1998-2002 estimates agreed for use in conditioning and for use in an actual application of the RMP.

³2008-15 estimates: status to be confirmed – see discussion in main text.

HYPOTHESIS 4

The inference from age data previously taken to support this hypothesis is no longer considered valid (see Item 3.1.2). Furthermore, the genetic data do not provide any indication for three stocks, one each feeding in sub-area 1W, sub-area 1E, and sub-area 2, with an unknown degree of mixing of the first two stocks. While recognising that the existence of two stocks occurring in sub-area 1 cannot be formally disproved, the Workshop **agrees** that the lack of specific support suggests that if two stocks exist in sub-area 1, they are genetically very similar and/or mix at high rates, such that the emerging stock structure may sufficiently approximated by Hypothesis 2.

The Workshop **recommends** that Hypothesis 4 is not considered further.

HYPOTHESIS 5

While the genetic data are not indicative of an equal mixing of two stocks in sub-area 1E, Hypothesis 5 may explain some of the genetic patterns not reconciled by Hypothesis 2, namely the increased HD when combining sub-area 1W and sub-area 1E. Maximum likelihood estimates of mixing proportions in sub-area 1E based on mtDNA haplotype frequencies (Annex F) suggest mixing proportions of 80-100% for the western stock, depending on whether the JARPN II/POWER or commercial samples are used to specify the haplotype frequencies for sub-areas 1E (at 100%, the pattern becomes identical to Hypothesis 2). As for Hypothesis 2, the evidence for Hypothesis 5 was not unequivocal, but it was noted that: (a) it is always difficult to prove given very uneven mixing proportions and shallow divergence between stocks (as here); and (b) it provides an explanation for genetic patterns not captured by Hypothesis 2.

The Workshop **recommends** that Hypothesis 5 is included in the *Implementation Simulation Trials*. However, it also **recommends** that sensitivity to the position of the border between sub-area 1 and sub-area 2 is investigated in the trials.

3.2 Abundance

There are three series of abundance estimates (see Table 5) to consider and evaluate:

- (1) the original series used in the *Implementation* were collected during 1988-96 and time stamped at 1995;

- (2) a series agreed to by the Committee (IWC, 2009b) for use in the *CLA* was collected during 1998-2002 (Kitakado *et al.*, 2008) and time stamped at 2000; and
- (3) a new series using data collected during 2008-15, which was the focus of discussions at this Workshop.

These three series of estimates will be used for conditioning trials and potentially for actual applications of the RMP.

SC/M17/RMP02 presents abundance estimates for the new time series using data from the recent IWC-POWER and JARPN II line transect surveys. The IWC-POWER series of surveys that detected Bryde's whales were conducted during three surveys, 2013-15 which were in sub-areas 1E, 2 and 20° longitude farther west of the original sub-area 2 (referred to as 'sub-area 2 extended'). The JARPN II series of surveys was conducted during 2008, 2012 and 2014 and were in sub-areas 1W and 1E. The two series were analysed separately using the Multiple Covariate Distance Sampling (MCDS) module in the DISTANCE program, where the potential covariates were group size, Beaufort and Year. Based on the best models, abundance estimates were 16,511 (CV=0.25), 7,074 (CV=0.24) and 4,861 (CV=0.24) for sub-areas 1W, 1E, and 2 extended, respectively.

The Workshop thanked the authors and discussed the additional work that would be needed to finalise abundance estimates for the entire surveyed area for the recent time series and for the sub-areas as defined in the *Implementation*. It requested additional details on the methodology and results, many of which were provided during the meeting (see Annex G).

The Workshop **recommends** that a new paper be provided to the Scientific Committee meeting in May 2017. This must include more details on the survey collection modes and data used (e.g. how were group sizes confirmed in independent observer (IO) mode, distance and angle corrections), analytical methods (e.g. how were the CV's calculated, model averaging, use of alternative covariates) and reported results (such as the complete maps of track lines along with on-effort and off-effort Bryde's whale sightings, estimates of the effective half strip width or $p(0)$, average group sizes).

More substantially, the Workshop **recommends** that the paper includes the additional analyses that need to be undertaken before the estimates can be agreed. These additional analyses relate to:

- (a) including sightings that were identified as 'Bryde's like' and 'unidentified large baleen whales'; and
- (b) attempting to estimate $g(0)$.

A previous IWC-POWER Technical Advisory Group (TAG) meeting (IWC, 2017b), had **agreed** that, since so few other positively identified baleen whales were detected in the 2014 and 2015 IWC-POWER cruises (only one sighting of a blue whale and one of a sei whale in 2014), the unidentified large baleen whale sightings during these two years were very probably Bryde's whales. The Workshop **concurs** with this view, and **recommends** that these sightings be included for comparison with estimates where they are excluded.

The Workshop also **concurs** with the TAG that the 2015 and 2016 IWC-POWER surveys that used the IO data collection mode should be analysed to attempt to estimate $g(0)$ for Bryde's whales using the MRDS module in the DISTANCE program. The TAG had noted that a preliminary analysis (although with low sample size) had suggested that $g(0)$ might be considerably below 1.

The Workshop also discussed the additional analyses that would be needed to develop abundance estimates to be used in the conditioning and for simulated application of the *CLA* in the trials. It is important that the three sets of abundance estimates are as consistent as possible to avoid 'spurious' trends being considered. The Workshop **recommends** that the abundance paper presented to SC/67a also includes:

- (1) abundance estimates for the recent series of surveys for the sub-areas that correspond to the stock structure hypotheses above²;
- (2) estimation of additional variance at the sub-area level using all three series; and
- (3) consideration of whether the value of $g(0)$ estimated for the most recent series of cruises is appropriate for application to the earlier surveys.

With respect to (1), the Workshop **agreed** that the post-stratified components from the updated abundance estimates developed for the entire survey area in a revised SC/M17/RMP02 could be used to develop estimates for the sub-areas needed to condition the *Implementation Simulation* trials. For example, use sub-area specific estimates of the encounter rate (n/L) and group size, together with the pooled estimate of $g(0)$ to estimate abundance for the desired sub-areas. Although spatial modelling was discussed as another potential method to derive the required abundance estimates, the Workshop noted spatial modelling techniques and guidelines for their use will be discussed at SC/67a. It will be appropriate, after these discussions, to evaluate whether such techniques would result in more precise and accurate abundance estimates for the sub-areas needed. However, at least for the conditioning, the Workshop **agreed** that the simpler post-stratification method was sufficient.

With respect to (2), the Workshop **agreed** that multiple abundance estimates for common blocks are required. The previous two series of surveys met this requirement, and so the additional variance was estimated using block-wise abundance estimates from those surveys and are reflected in the CVs of the abundance estimates (Kitakado *et al.*, 2008). The abundance estimates for all series of surveys should be examined to allow an evaluation of comparability.

With respect to (3), the nature of the earlier series of cruises (methods, vessels, etc.) should be examined to see

if the recent estimate of $g(0)$ is applicable for one or more series. The Workshop also **recommends** that a more general discussion of the use data from series for which correction factors (e.g. estimates of $g(0)$) are available only for more recent surveys and not for historical surveys.

The Workshop **agreed** to establish an Advisory Group to assist in the work on abundance (Palka [Chair], Hakamada, Kitakado, Donovan, Butterworth, Allison, Miyashita).

3.3 Removals data

3.3.1 Catch data

Allison reported that there are no changes to the catch series developed for the 2007 *Implementation* except for some minor revisions over the 1938-45 period and the addition of catches for the 2006-16 period.

3.3.2 Bycatch data

Four incidental catches between 1975 and 2003 were identified in the 2007 *Implementation* (see *pre-Implementation assessment* Workshop report, (IWC, 2006, p.338), of which one (in October 2003 from a trap net in Shizuoka) was identified as an offshore type Bryde's whale based on DNA analysis (L. Pastene, pers. comm.). The remaining three (in August 1978 from Oita, April 1988 from Hyogo and March 1995 from Kochi [released]) are all thought to have been inshore forms, although no DNA data are available to confirm this.

Yoshida reported that a Bryde's whale caught in a trap net at Nagasaki in 2004 was from the East China Sea stock; one offshore type was caught in a stationary uncovered pound net at Mie in 2010.

The Workshop **agreed** that there was no evidence to suggest that any appreciable number of Bryde's whales is caught incidentally, so that (as in the 2007 *Implementation*) there is no need to model incidental catches in the *Implementation Simulation Trials*.

3.3.3 Ship strikes data

Kato informed the Workshop that there were no confirmed ship strikes of Bryde's whales in Japan with 'normal' vessels for the period 2003-16 according to the website of the Japanese Coast Guard³. On the other hand, there have been 25 records of hydrofoil collisions with large marine organisms for that period including eight cases confirmed as large cetaceans (five common minke whales, one humpback whale and two sperm whales).

As hydrofoils operate only in close coastal waters, The Workshop **agreed** that there was no need to model ship strikes in the revised *Implementation Simulation Trials*.

3.4 Future likely whaling operations

Future harvesting of Bryde's whales by Japan (Annex H) is proposed from May to September in Japanese coastal waters and high seas but excluding:

- (1) 40 n.mile zone off the coast of southern Japan west of 140°E;
- (2) the 200 n.mile zone round countries other than Japan; and
- (3) the area south of 20°N.

The proposed timing will avoid both the expected breeding (December-April) and calving (October-March) seasons (Ohsumi, 1995). The proposed harvest area (see Fig. 1) ensures that catches will be taken from the offshore form only. The main area that Japan wishes to operate for whaling is sub-area 1 (especially sub-area 1W).

²Following the guidelines developed for *Implementations*, the appropriate time stamps for the abundance estimate for each sub-area should be the average year of the surveys that covered that sub-area i.e. 2011 for sub-area 1W, 2011 for sub-area 1E and 2014 for sub-area 2.

³<http://www6.kaiho.mlit.go.jp/info/marinesafety/jikojouhou.html>.

3.5 Other data that might assist in the *Implementation Review*

3.5.1 Biological data

SC/M17/RMP03 reported on progress in earplug-based age determination and on the estimation of biological parameters for Bryde's whales sampled during the 2000 to 2014 JARPN II surveys. The apparent pregnancy rate over a whole year was estimated to be 0.615. von Bertalanffy growth curves were estimated separately for males and females, with their respective ages at sexual maturity estimated to be 9.99 and 8.72 years.

Matters related to the age readings relevant to stock structure were considered under Item 3.1.2.

The meeting noted that an analysis of the existing Kato-Bando pairs of age readings (see Annex D) would not be appropriate for evaluating ageing errors as the methods used by the two readers had differences. The Workshop **agrees** that undertaking such an analysis (similar to that undertaken for Antarctic minke whales, see Butterworth and Punt, 2009, and Kitakado and Punt, 2010) was important and Bando advised that Japan was planning such an exercise, which was hoped to be completed by SC/67b in 2018.

With respect to biological parameters, the Workshop received a revised estimate (Annex I) of the age-at-50%-maturity for females from application of the method of Punt (2008) to the JARPN II data, for the ages obtained by Bando. This resulted in a value of 8.6 years compared to the value of 6 years used for previous *Implementation Simulation Trials*. This change was primarily ascribed to differences in age readings as detailed above, and the Workshop **agreed** to use the higher new value in revised *Implementation Simulation Trials*, although it will be advisable to take ageing error into account when the appropriate experiment has taken place. However, the Workshop **agrees** that the lack of sensitivity to age at sexual maturity in the trials means that the lack of an analysis including ageing error will not influence the choice of variants.

4. CONSIDERATION OF THE NEED FOR NEW TRIALS

4.1 Need for new trials

The Workshop conclusions with respect to stock structure hypotheses are given under Item 3.1.4, i.e. that Hypotheses 2 and 5 (a new hypothesis) should be considered in the trials. Variant 2 was considered 'unacceptable' in the 2007 *Implementation* due to its poor performance for three trials based on stock structure Hypothesis 4 (IWC, 2008b, pp.91-115).

The Scientific Committee agreed in 2013 that $MSYR_{+}=1\%$ be adopted as a pragmatic and precautionary lower bound for use in trials (IWC, 2014). In contrast, $MSYR_{mat}=1\%$ was considered during the 2008 *Implementation*.

The Workshop **agreed** that the new information and its implications warranted the development and running of new trials.

4.2 Trial specifications

Table 6 lists the factors considered in the new trials. Compared to the 2007 *Implementation*, the new trials explore a new factor, the boundary between sub-areas 1E and 2, and eliminate two factors: stochastic mixing (included in the earlier trials owing to lack of data), and age-dependent mixing (dropped owing to the lack of difference in age structure within sub-area 1). The new trials are based on two rather than four stock structure hypotheses (hypotheses 2 and 5; see Item 3.1.4 and Fig. 5). Table 6 lists the set of factors on which the new trials are based and their levels.

Table 6

Factors considered in the revised trials.
The values in bold are the baseline values.

Factor	Values considered
Stock structure hypotheses	2, 5
$MSYR$	$MSYR_{+}=1\%$; $MSYR_{mat}=4\%$
Catch series	Low, Best , High
Additional variance	Baseline , Upper 5%ile
1W/1E boundary	160°E, 165°E , 170°E
1E/2 boundary	175°E, 180° , 175°W

Table 7 summarises the revised set of trials (see Annex J for full technical specifications). Most of the trials are based on stock structure hypothesis 5 because stock structure hypothesis 2 is a bounding case of stock structure hypothesis 5, with the mtDNA haplotype data supporting a high proportion of stock 1 (the stock found in sub-area 1W) in sub-area 1E. Other modifications to the 2008 trials are:

- (1) the age-at-maturity has been updated (see Item 3.5)
- (2) the set of catches and abundance estimates used for conditioning and when applying the *CLA* has been updated (see Item 3.3);
- (3) age and marking data are no longer used for conditioning as they pertained to stock structure hypothesis 4, which is no longer considered plausible (see Item 3.1.4);
- (4) the data on mixing proportions are used when conditioning the trials based on stock-structure hypothesis 5 (see Annex F);
- (5) the plan for future surveys has been updated (see Annex H); and
- (6) The southern boundary of sub-area 1 was changed from 10°N to 20°N in order to avoid the breeding grounds.

The Workshop noted that the trials assumed $g(0)=1$. Additional trials may be needed if estimates of $g(0)$ are calculated and approved by the Scientific Committee (see Item 3.2).

5. CONCLUSIONS AND WORK PLAN

5.1 Summary

The Workshop made considerable progress with the *Implementation Review*. The major conclusions are summarised below.

- (1) The new information relevant to stock structure was reviewed and the Workshop agreed to take forward two stock structure hypotheses (see Fig. 5) - one of the four considered at the 2007 *Implementation* and one new hypothesis. These are:
 - (a) *Hypothesis 2*: there are two stocks, one feeding in sub-area 1 and one feeding in sub-area 2.
 - (b) *Hypothesis 5*: there are two stocks, one feeding in sub-area 1 and one feeding in sub-area 2 with mixing occurring in sub-area 1E. There are more stock 1 than stock 2 animals in the mixing area.
- (2) The Workshop reviewed new information on abundance estimates and developed a workplan to try to obtain agreed abundance estimates (including additional variance) for use in conditioning and the *CLA*.
- (3) The Workshop developed a new set of simulation trials for the *Implementation Review* that involve testing for uncertainty in stock structure, stock boundaries, $MSYR$, removals and additional variance.
- (4) The Workshop developed an ambitious workplan to try to complete the *Implementation Review* at SC/67a in May 2017.

Table 7
The *Implementation Simulation Trials* for the Western North Pacific Bryde's whales.

Trial	Stock structure hypothesis	MSYR ¹	Additional variance	Catch series	1W/1E boundary	1E/2 boundary	Comment
Br1-1	2	1	Baseline	Best	165°E	180°	Baseline stock structure hypothesis 2
Br1-4	2	4	Baseline	Best	165°E	180°	Baseline stock structure hypothesis 2
Br2-1	5	1	Baseline	Best	165°E	180°	Baseline stock structure hypothesis 5
Br2-4	5	4	Baseline	Best	165°E	180°	Baseline stock structure hypothesis 5
Br3-1	5	1	Baseline	Low	165°E	180°	Stock hypothesis 5 with low catches
Br3-4	5	4	Baseline	Low	165°E	180°	Stock hypothesis 5 with low catches
Br4-1	5	1	Baseline	High	165°E	180°	Stock hypothesis 5 with high catches
Br4-4	5	4	Baseline	High	165°E	180°	Stock hypothesis 5 with high catches
Br5-1	5	1	Upper CI	Best	165°E	180°	Stock hypothesis 5 with higher additional variance
Br5-4	5	4	Upper CI	Best	165°E	180°	Stock hypothesis 5 with higher additional variance
Br6-1	2	1	Baseline	Best	160°E	175°E	Stock hypothesis 2 with alternative boundaries 1 ²
Br6-4	2	4	Baseline	Best	160°E	175°E	Stock hypothesis 2 with alternative boundaries 1 ²
Br7-1	5	1	Baseline	Best	160°E	175°E	Stock hypothesis 5 with alternative boundaries 1 ²
Br7-4	5	4	Baseline	Best	160°E	175°E	Stock hypothesis 5 with alternative boundaries 1 ²
Br8-1	5	1	Baseline	Best	170°E	175°W	Stock hypothesis 5 with alternative boundaries 2 ²
Br8-4	5	4	Baseline	Best	170°E	175°W	Stock hypothesis 5 with alternative boundaries 2 ²

¹MSYR=1% is related to the 1+ component; MSYR =4% is related to mature component. ²Based on alternative mixing proportion data.

Table 8

Work plan to try to complete the *Implementation Review* at SC/67a in May 2017. If this is not possible, the Workshop agrees that it should be possible to complete the *Implementation Review* at SC/67b without the need for an additional Workshop.

Item	Responsibility	Time
Develop new abundance estimates for the most recent surveys	Hakamada with assistance from the advisory group chaired by Palka	24/04/17
Develop additional variance estimate	Kitakado with assistance from the advisory group chaired by Palka	24/04/17
Code the <i>Implementation Simulation Trials</i>	Allison and de Moor with assistance from Punt	By SC/67a
Condition and run the <i>Implementation Simulation Trials</i>	Allison and de Moor with assistance from the Bryde's whale steering group	By SC/67a

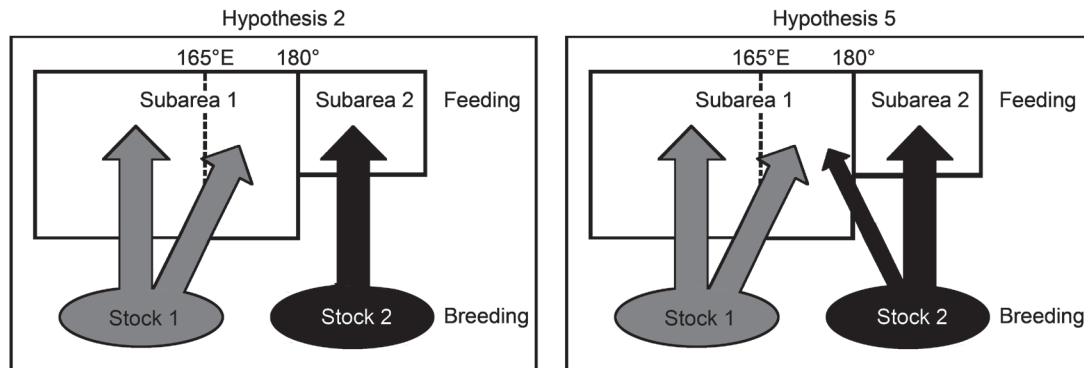


Fig. 5. The two hypotheses that will be considered in the *Implementation Simulation Trials*.

5.2 Work plan

The work plan is shown in Table 8. The Workshop recognises:

- that the work plan is ambitious; and
- the abundance estimates will need to be adopted formally by the Scientific Committee.

If it is not possible to meet the work plan, the Workshop believes that it should be possible to complete the *Implementation Review* at SC/67b without the need for an additional workshop.

6. ADOPTION OF REPORT

The Workshop finished its work at 13:00 on 25 March 2017. Apart from editorial corrections the report was adopted at that time. Donovan thanked the participants for their positive co-operation and hard work, especially in terms of carrying out additional analyses during the meeting. He also thanked the rapporteurs for their conscientious work that enabled

a painless adoption of the report and the interpreters who worked so effectively. Finally, he thanked the Government of Japan for the excellent facilities. The participants thanked the Chair for his usual fair and effective Chairing.

REFERENCES

- Allison, C. 2008. Report of the second Intersessional Workshop on the western North Pacific Bryde's whale *Implementation*, Yokohama, 10-14 December 2006. Annex C. Catch series for western North Pacific Bryde's whales. *J. Cetacean Res. Manage. (Suppl.)* 10: 457-67.
- Butterworth, D.S. and Punt, A.E. 2009. Report of the Scientific Committee. Annex G. Report of the sub-committee on in-depth assessment (IA). Appendix 4. Proposed further work to aid resolution of questions concerning ageing of Antarctic minke whales. *J. Cetacean Res. Manage. (Suppl.)* 11: 209.
- International Whaling Commission. 2006. Report of the Workshop on the *pre-Implementation assessment* of western North Pacific Bryde's whales. *J. Cetacean Res. Manage. (Suppl.)* 8:337-55.
- International Whaling Commission. 2007a. Report of the Scientific Committee. Annex D. Report of the Sub-Committee on the Revised Management Procedure. *J. Cetacean Res. Manage. (Suppl.)* 9:88-128.

- International Whaling Commission. 2007b. Western North Pacific Bryde's *Implementation*: Report of the First Intersessional Workshop, 25-29 October 2005, Shizuoka, Japan. *J. Cetacean Res. Manage. (Suppl.)* 9:407-27.
- International Whaling Commission. 2008a. Report of the Scientific Committee. *J. Cetacean Res. Manage. (Suppl.)* 10:1-74.
- International Whaling Commission. 2008b. Report of the Scientific Committee. Annex D. Report of the Sub-Committee on the Revised Management Procedure. *J. Cetacean Res. Manage. (Suppl.)* 10:90-120.
- International Whaling Commission. 2008c. Report of the second Intersessional Workshop on the western North Pacific Bryde's whale *Implementation*, Yokohama, 10-14 December 2006. *J. Cetacean Res. Manage. (Suppl.)* 10:449-510.
- International Whaling Commission. 2009a. Report of the Scientific Committee. *J. Cetacean Res. Manage. (Suppl.)* 11:1-74.
- International Whaling Commission. 2009b. Report of the Scientific Committee. Annex D. Report of the Sub-Committee on the Revised Management Procedure (RMP). *J. Cetacean Res. Manage. (Suppl.)* 11:91-144.
- International Whaling Commission. 2010. Report of the Expert Workshop to Review the Ongoing JARPN II Programme, 26-30 January 2009, Yokohama, Japan. *J. Cetacean Res. Manage. (Suppl.)* 11(2):405-50.
- International Whaling Commission. 2014. Report of the Scientific Committee. Annex D. Report of the sub-committee on the Revised Management Procedure (RMP). *J. Cetacean Res. Manage. (Suppl.)* 15.
- International Whaling Commission. 2017a. Report of the Expert Panel of the Final Review on the Western North Pacific Japanese Special Permit Programme (JARPN II), 22-26 February 2016, Tokyo, Japan. *J. Cetacean Res. Manage. (Suppl.)* 18:527-92.
- International Whaling Commission. 2017b. Report of the Meeting of the IWC-POWER Technical Advisory Group (TAG), 7-9 October 2015, Tokyo, Japan. *J. Cetacean Res. Manage. (Suppl.)* 18:459-76.
- Kanda, N., Goto, M., Kato, H., McPhee, M.V. and Pastene, L. 2007. Population genetic structure of Bryde's whales (*Balaenoptera brydei*) at the inter-oceanic and trans-equatorial levels. *Cons. Genet.* 8: 853-64.
- Kishiro, T. 1996. Movements of marked Bryde's whales in the western North Pacific. *Rep. Int. Whal. Comm.* 46: 421-28.
- Kitakado, T., Butterworth, D.S. and Okamura, H. 2007. Western North Pacific Bryde's *Implementation*: Report of the First Intersessional Workshop, 25-29 October 2005, Shizuoka, Japan. Annex H. An integrated approach for the estimation of abundance through a random-effects model. *J. Cetacean Res. Manage. (Suppl.)* 9: 424-25.
- Kitakado, T. and Punt, A.E. 2010. Examination of the period/reader effect on the age-determination for the Antarctic minke whales and its implications to the statistical catch-at-age analyses. Paper SC/62/IA2 presented to the IWC Scientific Committee, June 2010, Agadir, Morocco (unpublished). 12pp. [Paper available from the Office of this Journal].
- Kitakado, T., Shimada, H., Okamura, H. and Miyashita, T. 2005. Update of additional variance estimate for the western North Pacific stock of Bryde's whales. Paper SC/O05/BW16 presented to the First Intersessional Workshop on the western North Pacific Bryde's whale *Implementation*, Shizuoka, Japan, 25-29 October 2005 (unpublished). 16pp. [Paper available from the Office of this Journal].
- Kitakado, T., Shimada, H., Okamura, H. and Miyashita, T. 2008. CLA abundance estimates for western North Pacific Bryde's whales and their associated CVs with taking the additional variance into account. Paper SC/60/PFI3 presented to the IWC Scientific Committee, June 2008, Santiago, Chile (unpublished). 27pp. [Paper available from the Office of this Journal].
- Murase, H., Tamura, T., Otani, S. and Nishiwaki, S. 2016. Satellite tracking of Bryde's whales *Balaenoptera edeni* in the offshore western North Pacific in summer 2006 and 2008. *Fish. Sci.* 82(1): 35-45.
- Ohsumi, S. 1995. A review of population studies of the North Pacific Bryde's whale stocks (revised). Paper SC/47/NP14 presented to the IWC Scientific Committee, May 1995, Dublin, Ireland (unpublished). 35pp. [Paper available from the Office of this Journal].
- Pastene, L.A., Goto, M. and Taguchi, M. 2016a. Additional genetic analyses on stock structure in North Pacific Bryde's and sei whales. Paper SC/66b/SD01 presented to the IWC Scientific Committee, June 2016, Bled, Slovenia (unpublished). 12pp. [Paper available from the Office of this Journal].
- Pastene, L.A., Goto, M., Taguchi, M. and Kitakado, T. 2016b. Updated genetic analyses based on mtDNA and microsatellite DNA suggest possible stock differentiation of Bryde's whales between management sub-areas 1 and 2 in the North Pacific. Paper SC/F16/JR44 presented to the Expert Panel Workshop of the Final Review on the Western North Pacific Japanese Special Permit Programme (JARPN II), 22-26 February 2016, Tokyo, Japan (unpublished). 18pp. [Paper available from the Office of this Journal].
- Punt, A.E. 2008. Report of the Scientific Committee. Annex D. Report of the sub-committee on the revised management procedure. Appendix 4. The specification for the *Implementation Simulation Trials* for western North Pacific Bryde's whales (final). Adjunct 3. Estimation of age-at-maturity for female Brude's whales. *J. Cetacean Res. Manage. (Suppl.)* 10: 114.
- Shimada, H., Okamura, H., Kitakado, T. and Miyashita, T. 2008. Abundance estimate of western North Pacific Bryde's whales for the estimation of additional variance and CLA application. Paper SC/60/PFI2 presented to the IWC Scientific Committee, June 2008, Santiago, Chile (unpublished). 34pp. [Paper available from the Office of this Journal].

Annex A

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Annex B

Agenda

1. Introductory items
 - 1.1 Convenor's opening remarks
 - 1.2 Election of Chair and appointment of rapporteurs
 - 1.3 Adoption of agenda
 - 1.4 Review of documents and data available
 2. The initial *Implementation*
 - 2.1 Overview of hypotheses
 - 2.2 Results and conclusions
 3. Review of new information
 - 3.1 Stock structure and movements
 - 3.2 Abundance
 - 3.3 Removals data
 - 3.3.1 Catch data
 - 3.3.2 Bycatch data
 - 3.3.3 Ship strikes data
 - 3.4 Future likely whaling operations
 - 3.5 Other data that might assist in the *Implementation Review*
 - 3.5.1 Biological data
 - 3.5.2 Operational data
 4. Consideration of the need for new trials
 - 4.1 Need for new trials (if yes, specify)
 5. Conclusions and work plan
 6. Adoption of Report
-

Annex C

List of Documents

SC/M17/RMP

1. Taguchi, M., Goto, M., Takahashi, M., Kitakado, T., Pastene, L.A. DAPC analysis for Bryde's whales in the North Pacific using microsatellite DNA data.
 2. Hakamada, T., Takahashi, M., Matsuoka, K. and Miyashita, T. Abundance estimate for western North Pacific Bryde's whale by sub-areas based on IWC-POWER and JARPN II sighting surveys.
 3. Bando, T. and Kato, H. Report on progress in earplug-based age determination and estimation of biological parameters of Bryde's whales collected during 2000 to 2014 JARPN II surveys.
-

Annex D

Further Investigations of Age Data

T. Bando

1. COMPARISON OF AGE DATA OF BRYDE'S WHALES READ BY TWO READERS

Earplug age reading of Bryde's whales collected by 2000-03 JARPN II was conducted by Kato (Reader-K) and analyses using these age data were presented to the *Implementation* meeting (Bando *et al.*, 2005). Subsequently the task of

earplug reading switched to Bando (Reader-B). In order to reduce the influence of inter-reader variability, all (2000-14) samples including the previously read 2000-03 samples were read by Reader-B. This Annex summarises age data read by two readers.

Table 1
Age data of Bryde's whales read by two readers (K and B).

Age				Age				Age				Age			
Year	No	K	B	Year	No	K	B	Year	No	K	B	Year	No	K	B
2000	B001	6	6	2001	B001	-	-	2002	B001	16	18	2003	B001	2	-
2000	B002	6	7	2001	B002	6	11	2002	B002	13	16	2003	B002	15	20
2000	B003	6	6	2001	B003	5	5	2002	B003	5	9	2003	B003	20	26
2000	B004	8	-	2001	B004	-	12	2002	B004	16	18	2003	B004	3	5
2000	B005	-	-	2001	B005	-	-	2002	B005	17	18	2003	B005	-	-
2000	B006	9	14	2001	B006	1	-	2002	B006	-	-	2003	B006	5	-
2000	B007	29	30	2001	B007	3	3	2002	B007	11	11	2003	B007	12	-
2000	B008	9	16	2001	B008	3	-	2002	B008	10	9	2003	B008	14	-
2000	B009	7	9	2001	B009	-	1	2002	B009	6	8	2003	B009	-	-
2000	B010	7	-	2001	B010	-	-	2002	B010	-	5	2003	B010	6	8
2000	B011	-	5	2001	B011	-	-	2002	B011	17	19	2003	B011	18	13
2000	B012	3	3	2001	B012	13	20	2002	B012	22	30	2003	B012	6	6
2000	B013	11	21	2001	B013	22	33	2002	B013	7	11	2003	B013	7	-
2000	B014	9	10	2001	B014	32	32	2002	B014	-	-	2003	B014	4	5
2000	B015	15	21	2001	B015	-	-	2002	B015	3	5	2003	B015	8	13
2000	B016	-	-	2001	B016	17	23	2002	B016	5	-	2003	B016	15	18
2000	B017	10	12	2001	B017	-	-	2002	B017	7	9	2003	B017	11	13
2000	B018	10	26	2001	B018	16	-	2002	B018	39	45	2003	B018	-	-
2000	B019	-	-	2001	B019	19	27	2002	B019	3	5	2003	B019	6	16
2000	B020	-	7	2001	B020	20	19	2002	B020	8	8	2003	B020	-	-
2000	B021	-	6	2001	B021	-	-	2002	B021	14	16	2003	B021	12	14
2000	B022	16	16	2001	B022	2	3	2002	B022	21	7	2003	B022	-	-
2000	B023	21	21	2001	B023	6	17	2002	B023	13	10	2003	B023	-	-
2000	B024	-	-	2001	B024	13	13	2002	B024	10	13	2003	B024	16	17
2000	B025	4	-	2001	B025	-	-	2002	B025	-	-	2003	B025	-	-
2000	B026	32	27	2001	B026	-	-	2002	B026	15	10	2003	B026	11	19
2000	B027	7	10	2001	B027	8	-	2002	B027	8	11	2003	B027	18	31
2000	B028	28	31	2001	B028	-	-	2002	B028	4	6	2003	B028	4	6
2000	B029	12	11	2001	B029	-	-	2002	B029	-	-	2003	B029	-	-
2000	B030	29	18	2001	B030	-	-	2002	B030	-	-	2003	B030	14	26
2000	B031	14	14	2001	B031	-	-	2002	B031	17	24	2003	B031	-	-
2000	B032	11	16	2001	B032	-	-	2002	B032	10	12	2003	B032	-	-
2000	B033	10	22	2001	B033	-	-	2002	B033	14	21	2003	B033	31	41
2000	B034	-	-	2001	B034	-	-	2002	B034	-	-	2003	B034	5	5
2000	B035	6	8	2001	B035	-	-	2002	B035	4	-	2003	B035	14	27
2000	B036	20	25	2001	B036	4	4	2002	B036	-	-	2003	B036	-	-
2000	B037	14	15	2001	B037	8	10	2002	B037	12	10	2003	B037	-	4
2000	B038	15	17	2001	B038	16	20	2002	B038	-	-	2003	B038	3	6
2000	B039	-	-	2001	B039	15	23	2002	B039	-	-	2003	B039	3	4
2000	B040	12	15	2001	B040	10	19	2002	B040	-	-	2003	B040	18	-
2000	B041	4	5	2001	B041	-	-	2002	B041	-	-	2003	B041	22	23
2000	B042	11	13	2001	B042	-	-	2002	B042	13	13	2003	B042	-	18
2000	B043	10	16	2001	B043	-	-	2002	B043	5	-	2003	B043	20	18
				2001	B044	9	11	2002	B044	10	13	2003	B044	-	-
				2001	B045	-	17	2002	B045	10	11	2003	B045	4	5
				2001	B046	-	-	2002	B046	4	4	2003	B046	29	26
				2001	B047	9	9	2002	B047	26	21	2003	B047	-	12
				2001	B048	9	9	2002	B048	-	4	2003	B048	8	13
				2001	B049	-	-	2002	B049	16	26	2003	B049	-	15
				2001	B050	1	-	2002	B050	-	-	2003	B050	11	17

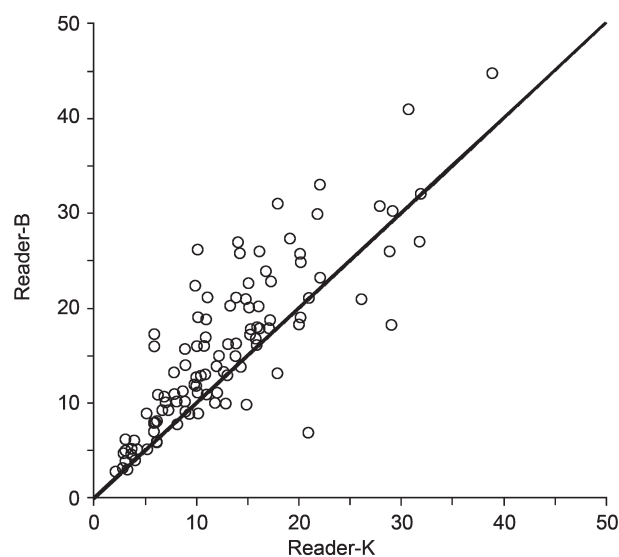


Fig. 1. Scatter plot of the ages from the earplug readings for the two readers. The solid line shows the 45° line.

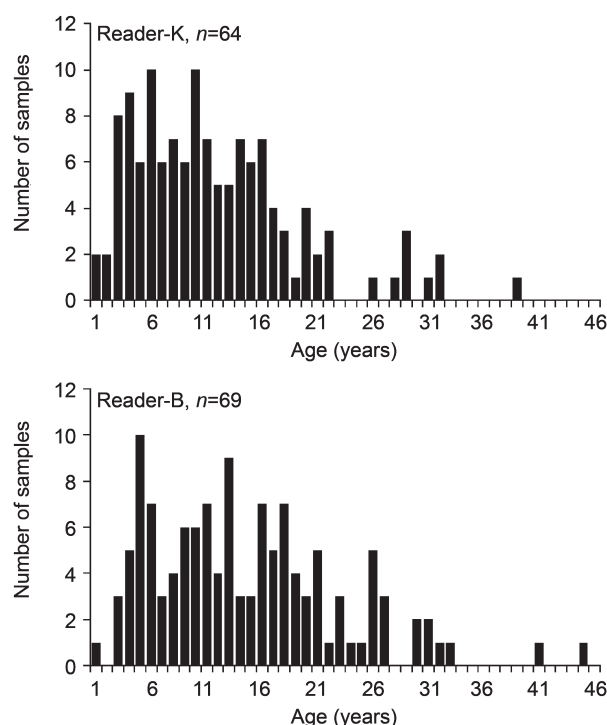


Fig. 2. Age distribution of Bryde's whales collected by 2000-03 JARPN II read by Reader-K (upper) and Reader-B (lower).

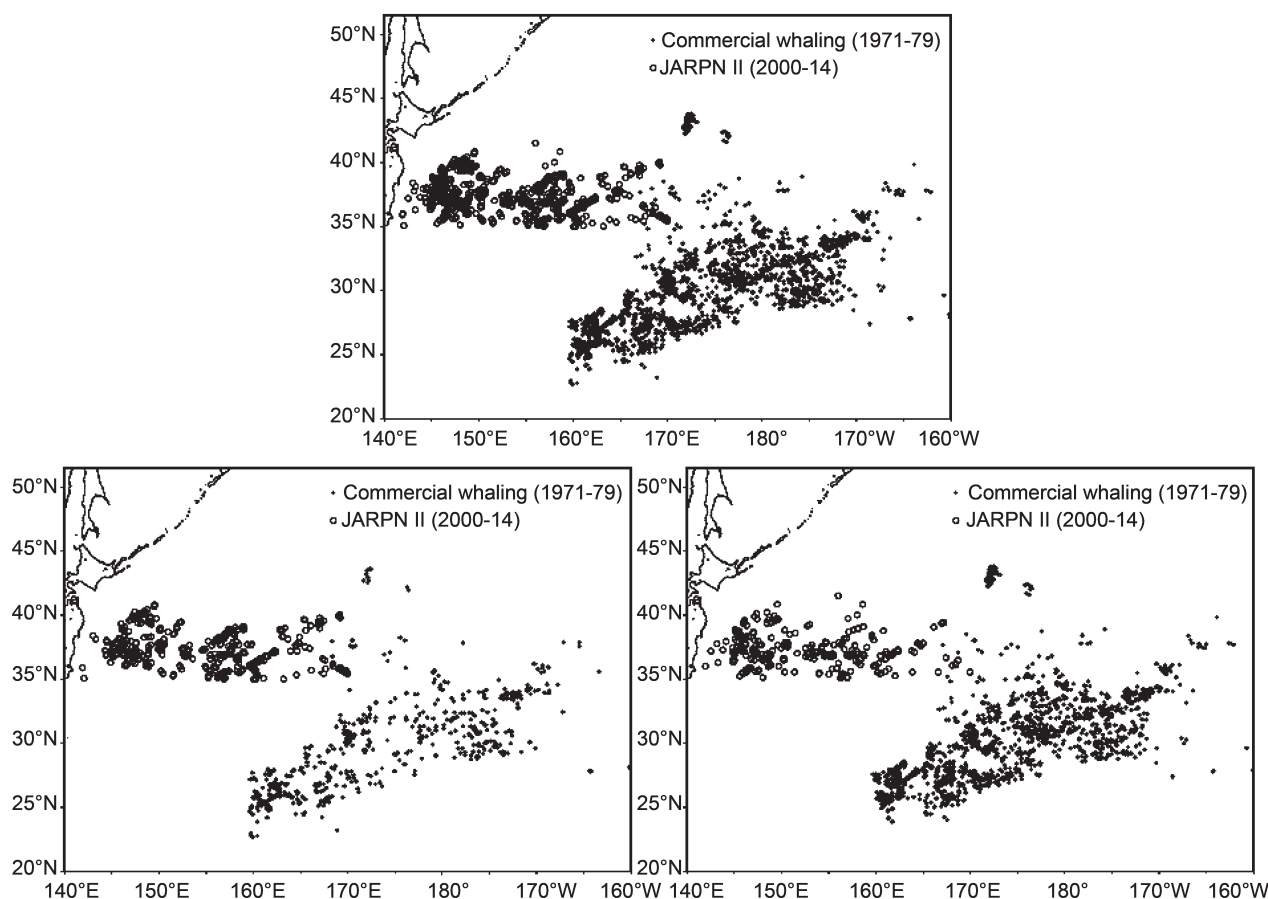


Fig. 3. Sampling position of all (upper), aged (lower, left) and unaged with unreadable earplug (lower right) Bryde's whales collect during 1971-79 Japanese pelagic commercial whaling and 2000-14 JARPNII surveys.

2. FURTHER ANALYSIS OF AGE DISTRIBUTION OF BRYDE'S WHALES BETWEEN SUB-AREAS

In order to investigate stock structure of western North Pacific Bryde's whales, the following analyses were performed using age and other biological data obtained by 1971-79 Japanese pelagic commercial whaling and 2000-14 JARPNII samples.

REFERENCE

- Bando, T., Kishiro, T., Ohsumi, S., Zenitani, R. and Kato, H. 2005. Estimation of some biological parameters of western North Pacific Bryde's whales by age distribution. Paper SC/O05/BW17 presented at the Bryde's whale *Implementation* workshop, Tokyo, 25-29 October 2005. 10pp. [Paper available from the Office of this Journal].

Table 2
Age distribution of Bryde's whales collected by JARPNI and commercial whaling by 5° longitude sector.

Longitude	Source	Ages					Age>9			
		10-11	12-13	14-15	16-20	21+	<i>n</i>	Mean	SD	SE
140°E-145°E	JARPNI	1	1	0	1	3	6	20.00	8.00	3.27
145°E-150°E	JARPNI	7	9	12	26	44	98	21.00	7.84	0.79
150°E-155°E	JARPNI	5	8	0	9	17	39	20.87	9.60	1.54
155°E-160°E	JARPNI	13	5	5	35	54	112	22.45	9.27	0.88
160°E-165°E	JARPNI	3	5	7	6	21	42	21.93	8.80	1.36
165°E-170°E	JARPNI	0	3	2	8	26	39	23.59	7.42	1.19
Total	JARPNI	29	31	26	85	165	336	21.87	8.62	0.47
155°E-160°E	Commercial	4	0	1	4	7	16	19.56	8.33	2.08
160°E-165°E	Commercial	14	14	9	26	49	112	20.71	8.79	0.83
165°E-170°E	Commercial	9	9	9	24	24	75	19.23	7.62	0.88
170°E-175°E	Commercial	16	8	9	19	23	75	18.67	8.24	0.95
175°E-180°	Commercial	11	6	7	17	11	52	17.31	6.79	0.94
180°-175°W	Commercial	8	9	9	17	36	79	21.04	8.88	1.00
175°W-170°W	Commercial	7	8	7	24	27	73	21.04	9.61	1.13
170°W-165°W	Commercial	2	1	2	4	9	18	21.78	9.98	2.35
165°W-160°W	Commercial	0	1	0	1	4	6	25.50	16.43	6.71
Total	Commercial	71	56	53	136	190	506	20.00	8.69	0.39

Table 3

Results of χ^2 test in age distribution of Bryde's whales between western and eastern (split at 155°E) sample of JARPNI (upper) and western and eastern (split at 180°) sample of commercial whaling. Age data were pooled and ages 0-9 were ignored because of the selectivity of commercial whaling following the method at previous *Implementation* meeting (IWC, 2007). P-value of χ^2 test is shown.

Area	Ages							Total
	10-11	12-13	14-15	16-20	21-25	26-30	31+	
JARPNI: West vs East of 155E (p=0.5381; df=6)								
Sample size	13	18	12	36	23	23	18	143
West of 155E	16	13	14	49	37	30	34	193
East of 155E	29	31	26	85	60	53	52	336
<i>Expected age-frequencies under the null hypothesis of independence</i>								
West of 155E	12	13	11	36	26	23	22	143
East of 155E	17	18	15	49	34	30	30	193
Total	29	31	26	85	60	53	52	336
Commercial whaling: West vs East of 180° (p=0.1763; df=6)								
Sample size	54	37	35	90	54	24	36	330
West of 180°	17	19	18	46	30	24	22	176
East of 180°	71	56	53	136	84	48	58	506
<i>Expected age-frequencies under the null hypothesis of independence</i>								
West of 180°	46	37	35	89	55	31	38	330
East of 180°	25	19	18	47	29	17	20	176
Total	71	56	53	136	84	48	58	506

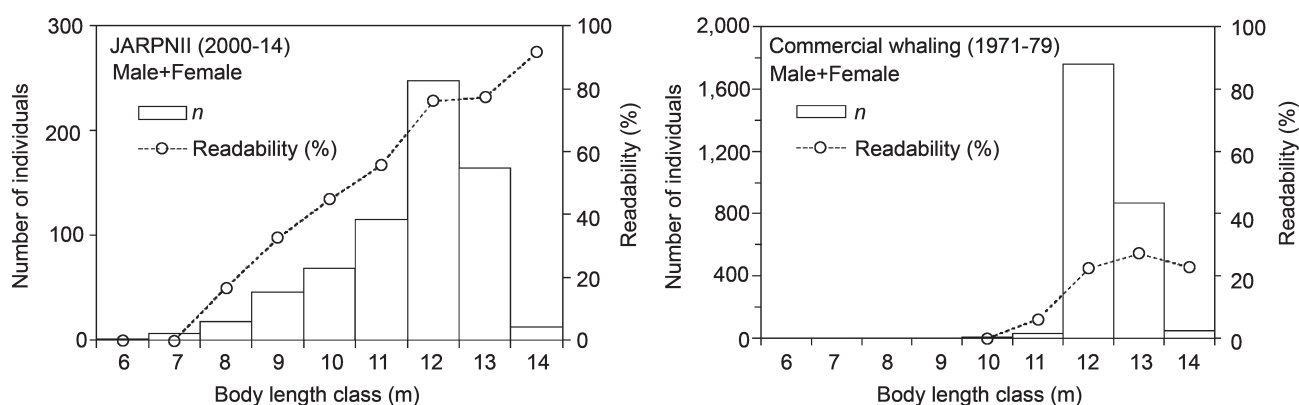


Fig. 4. Earplug age readability of Bryde's whales collected by JARPNI (left) and commercial whaling (right) by body length class.

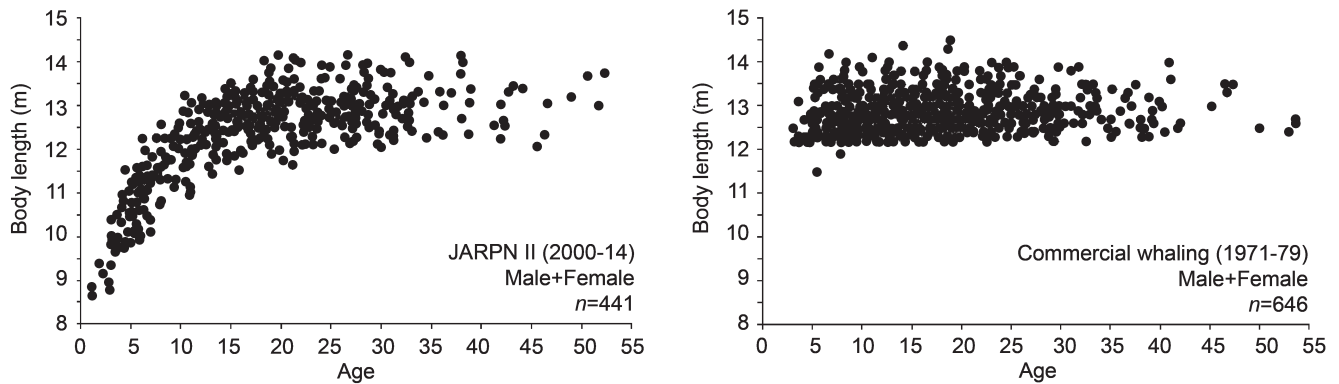


Fig. 5. Relationship between age and body length of Bryde's whales collected by JARPNII (left) and commercial whaling (right).

Annex E

Additional Analyses of Genetic Diversity

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Table 1

Results of the heterogeneity test for sub-areal differentiation by year.

Year	Microsatellites				Mitochondria			
	Sample size		<i>P</i> -values	<i>F_{ST}</i>	Sample size		<i>P</i> -values	<i>F_{ST}</i>
	SA1	SA2			SA1	SA2		
1979	97	53	0.001	0.003	112	53	0.001	0.038
1983	21	53	0.151	0.003	20	53	0.066	-0.008
1984	81	53	0.000	0.002	83	53	0.000	0.061
2000	43	53	0.001	0.005	39	53	0.007	0.069
2001	50	53	0.014	0.005	43	53	0.003	-0.001
2002	50	53	0.004	0.008	50	53	0.000	0.071
2003	50	53	0.008	0.006	50	53	0.004	0.024
2004	50	53	0.016	0.003	50	53	0.160	0.000
2005	50	53	0.015	0.004	49	53	0.000	0.051
2006	50	53	0.000	0.005	50	53	0.044	0.035
2007	50	53	0.000	0.007	50	53	0.005	0.028
2008	50	53	0.009	0.003	50	53	0.013	0.040
2009	50	53	0.012	0.004	50	53	0.144	-0.001
2010	50	53	0.007	0.002	50	53	0.094	0.011
2011	50	53	0.000	0.005	50	53	0.006	0.014
2012	76	53	0.005	0.002	75	53	0.000	0.059
2013	28	53	0.258	0.000	28	53	0.078	-0.011
2014	70	53	0.003	0.003	70	53	0.018	0.026

Bold text indicates statistical significance at alpha=0.05 after FDR correction.

Table 2

Results of the heterogeneity test for alternative boundaries.

Year	Microsatellites				Mitochondria			
	Sample size		<i>P</i> -values	<i>F_{ST}</i>	Sample size		<i>P</i> -values	<i>F_{ST}</i>
	SA1	SA2			SA1	SA2		
150E	390	629	0.017	0.000	382	643	0.094	0.003
155E	493	526	0.111	0.000	485	540	0.011	0.001
160E	706	313	0.144	0.000	698	327	0.018	0.008
165E	847	172	0.001	0.001	855	170	0.001	0.011
170E	936	83	0.000	0.002	942	83	0.000	0.029
175E	954	65	0.000	0.002	960	65	0.000	0.026
180	966	53	0.000	0.004	972	53	0.000	0.039
175W	981	38	0.000	0.005	987	38	0.056	0.034

Bold text indicates statistical significance at alpha=0.05 after FDR correction.

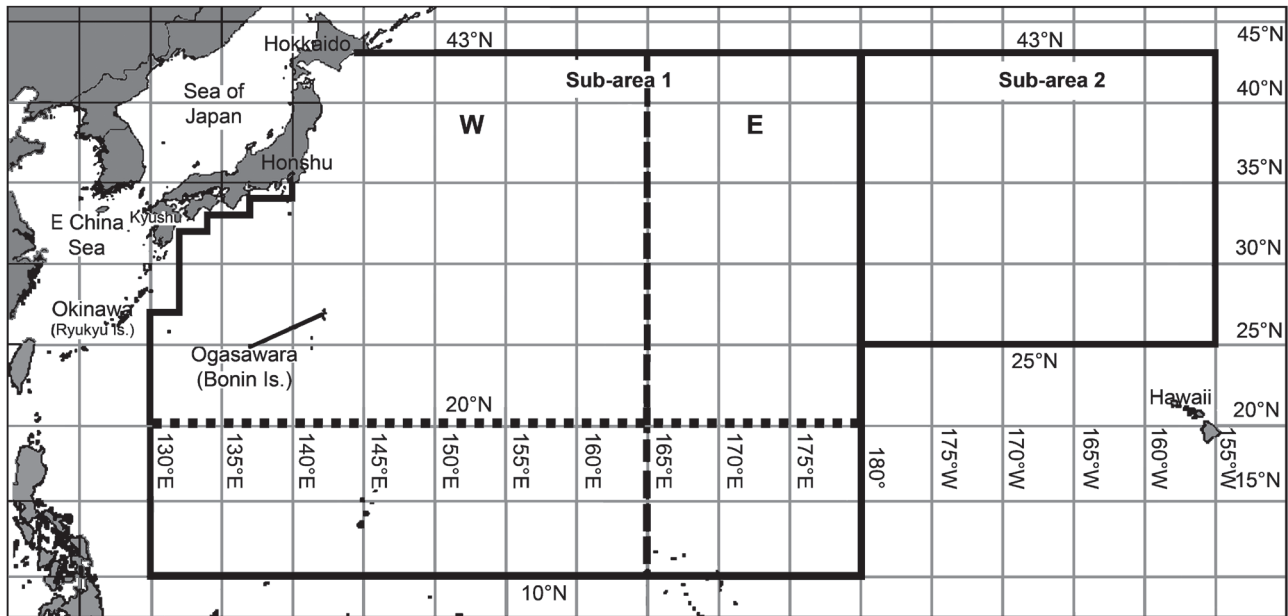


Fig. 1. Sub-areas of North Pacific Bryde's whale used in the 2007 RMP Implementation.

Table 3
Results of the HWE in each subarea (*P*-values).

Sub-area	HWE
SA1W	0.716
SA1E	0.106
SA2	0.371

Table 4
Results of the HWE for each alternative boundary in sub-areas 1 and 2 (*P*-values).

Microsatellite loci	150°E		155°E		160°E		165°E		170°E		175°E		180°		175°W	
	SA1	SA2	SA1	SA2	SA1	SA2	SA1	SA2	SA1	SA2	SA1	SA2	SA1	SA2	SA1	SA2
GATA98	0.60242	0.27889	0.78179	0.22538	0.79754	0.25931	0.56644	0.07416	0.64036	0.02507	0.60326	0.16121	0.63534	0.30919	0.64773	0.05752
EV104	0.69765	0.86664	0.61492	0.79479	0.76145	0.71276	0.86222	0.27564	0.90435	0.36500	0.90313	0.17021	0.90630	0.22488	0.80763	0.48440
GT011	0.90052	0.21796	0.57953	0.41133	0.75651	0.35425	0.70344	0.35766	0.36332	0.16985	0.35789	0.06666	0.34793	0.13861	0.29787	1.00000
GATA53	0.34814	0.31662	0.41515	0.47868	0.50430	0.57589	0.35374	0.46229	0.56272	0.05043	0.65399	0.08728	0.55881	0.14591	0.58716	0.15290
GATA417	0.16197	0.34113	0.45865	0.11445	0.34449	0.33794	0.49949	0.13747	0.30542	0.83837	0.33437	0.88742	0.29090	0.95416	0.21869	0.92122
DlrFCB14	1.00000	0.16673	1.00000	0.15245	0.70158	0.19876	0.62407	0.15171	0.42254	0.36676	0.29061	1.00000	0.32406	0.77522	0.32846	0.72606
DlrFCB17	0.83873	0.87329	0.86118	0.88084	0.84603	0.91995	0.77433	0.70125	0.85722	0.53221	0.80153	0.30300	0.76763	0.26350	0.83068	0.30423
GT23	0.36225	0.94815	0.63420	0.88577	0.43216	0.91086	0.33120	0.87266	0.65397	0.55805	0.67207	0.13364	0.61683	0.31634	0.57562	0.71666
EV14	0.35760	0.75080	0.52927	0.90978	0.63168	0.91173	0.58396	0.25982	0.69776	0.39905	0.67366	0.39273	0.75952	0.11219	0.76408	0.10111
GT310	0.29831	0.87821	0.24514	0.51597	0.67875	0.39946	0.79069	0.49146	0.58389	0.48425	0.64074	0.28743	0.64254	0.36302	0.60714	0.67449
EV1	0.05756	0.12852	0.01057	0.32321	0.09472	0.43816	0.10174	0.14180	0.04345	0.48785	0.07163	0.29883	0.03675	0.31781	0.07229	0.24058
EV94	0.20998	0.07935	0.26377	0.03463	0.77314	0.00001	0.69287	0.00312	0.48669	0.09118	0.36154	0.27729	0.42536	0.25342	0.39228	0.27178
GGAA520	0.14162	0.14858	0.10111	0.33195	0.04603	0.56309	0.05356	0.51697	0.02393	0.32093	0.02552	0.64817	0.02983	0.44626	0.01708	0.34020
EV21	0.19225	0.68899	0.27271	0.56053	0.34380	0.85232	0.44028	0.93955	0.25848	0.91696	0.24429	0.69424	0.23370	0.64893	0.29194	0.56210
GT575	0.69701	0.75404	0.86217	0.49615	0.92112	0.34821	0.78889	0.64863	0.66683	0.26822	0.62273	0.08310	0.59543	0.36945	0.60348	0.42483
GATA28	0.17757	0.88116	0.19077	0.83644	0.35126	0.76563	0.21977	0.78705	0.18704	0.71893	0.26491	0.48948	0.29199	0.54819	0.32300	0.75857
TAA31	0.62201	0.50635	0.79005	0.47341	0.58812	0.74591	0.40034	0.97904	0.45782	0.91787	0.46085	0.87340	0.50707	0.86805	0.56242	0.79360
Overall	0.38754	0.61350	0.45837	0.54621	0.82415	0.12307	0.71359	0.15043	0.42388	0.25081	0.45264	0.16941	0.41399	0.37060	0.41067	0.58437

Bold text indicates statistical significance at $\alpha=0.05$ after FDR correction.

Table 5

Measures of genetic diversities and haplotype frequency for several combinations of sub-areas.

Genetic diversities	SA1W	SA1E	SA1	SA2	SA1E+SA2	Total
H_O	0.67±0.15	0.68±0.16	0.67±0.15	0.70±0.14	0.68±0.15	0.67±0.15
H_E	0.68±0.15	0.69±0.14	0.68±0.15	0.68±0.14	0.69±0.14	0.68±0.15
HWE	0.713	0.111	0.419	0.370	0.157	0.407
HD	0.82±0.01	0.82±0.03	0.90±0.02	0.82±0.01	0.85±0.02	0.83±0.01
Sample size for msDNA	847	119	966	53	172	1019
Haplotype frequency						
3	333	47	380	13	60	393
4	87	3	90	3	6	93
6	81	11	92	1	12	93
7	37	7	44	5	12	49
9	33	11	44	6	17	50
8	31	5	36	4	9	40
2	20	3	23	0	3	23
19	18	2	20	3	5	23
28	18	1	19	3	4	22
11	17	3	20	0	3	20
18	16	2	18	0	2	18
16	14	0	14	0	0	14
13	13	1	14	2	3	16
14	13	1	14	0	1	14
1	11	2	13	0	2	13
15	11	1	12	0	1	12
23	11	0	11	0	0	11
27	10	1	11	0	1	11
21	9	4	13	2	6	15
33	7	2	9	0	2	9
29	6	1	7	0	1	7
17	6	0	6	0	0	6
31	6	0	6	0	0	6
5	5	2	7	0	2	7
25	5	0	5	1	1	6
20	4	1	5	0	1	5
26	4	0	4	1	1	5
32	3	1	4	0	1	4
39	2	1	3	5	6	8
47	2	1	3	0	1	3
22	2	0	2	1	1	3
30	2	0	2	0	0	2
45	2	0	2	0	0	2
46	2	0	2	0	0	2
36	1	0	1	1	1	2
10	1	0	1	0	0	1
12	1	0	1	0	0	1
24	1	0	1	0	0	1
34	1	0	1	0	0	1
35	1	0	1	0	0	1
37	1	0	1	0	0	1
40	1	0	1	0	0	1
41	1	0	1	0	0	1
42	1	0	1	0	0	1
43	1	0	1	0	0	1
44	1	0	1	0	0	1
48	1	0	1	0	0	1
51	1	0	1	0	0	1
49	0	2	2	0	2	2
38	0	1	1	0	1	1
50	0	0	0	2	2	2
Total	855	117	972	53	170	1,025

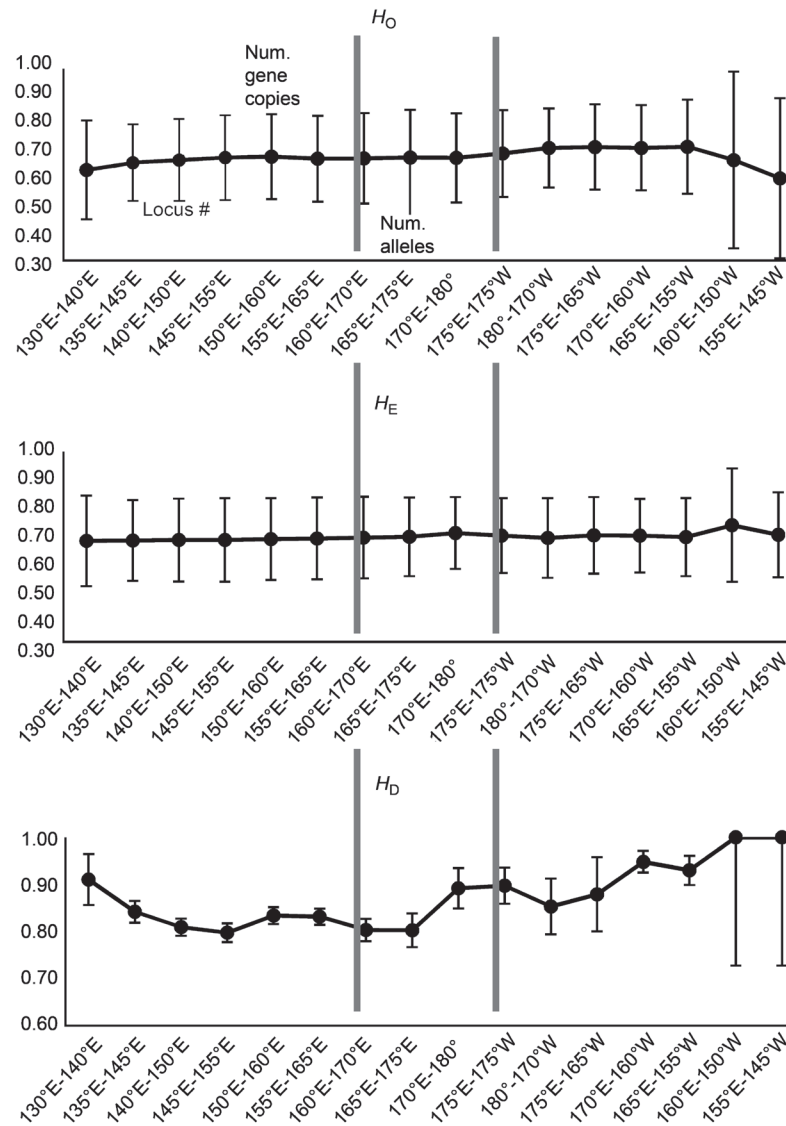


Fig. 2. Genetic diversity relative to longitude of sample origin (calculated for 5° intervals; plotted as moving averages over 10° intervals). H_0 : observed heterozygosity; H_E : expected heterozygosity; H_D : haplotype diversity.

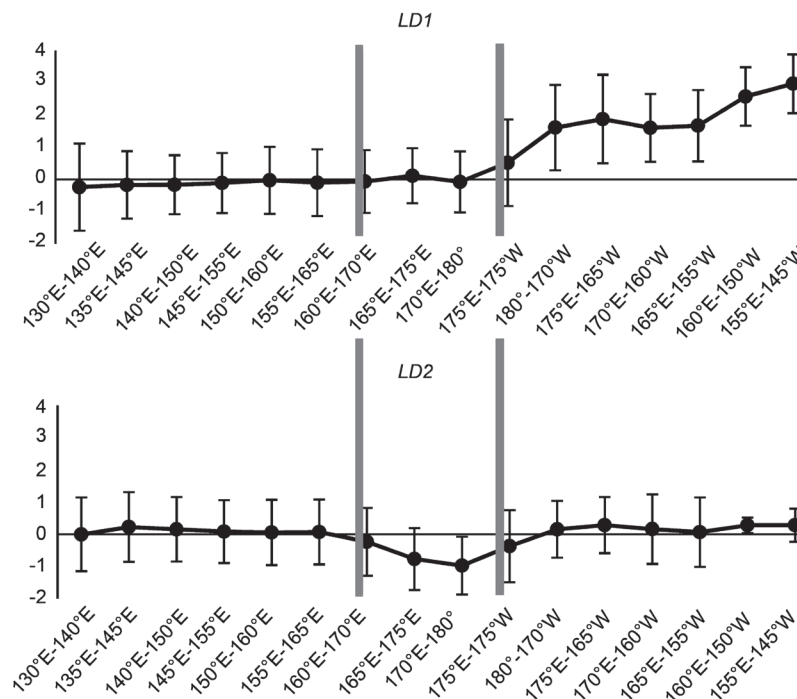


Fig. 3. Mean values of the first two principal components of the DAPC, conditional on longitude (calculated for 5° intervals; plotted as moving averages over 10° intervals). $LD1$: value of PC1; $LD2$: value of PC2.

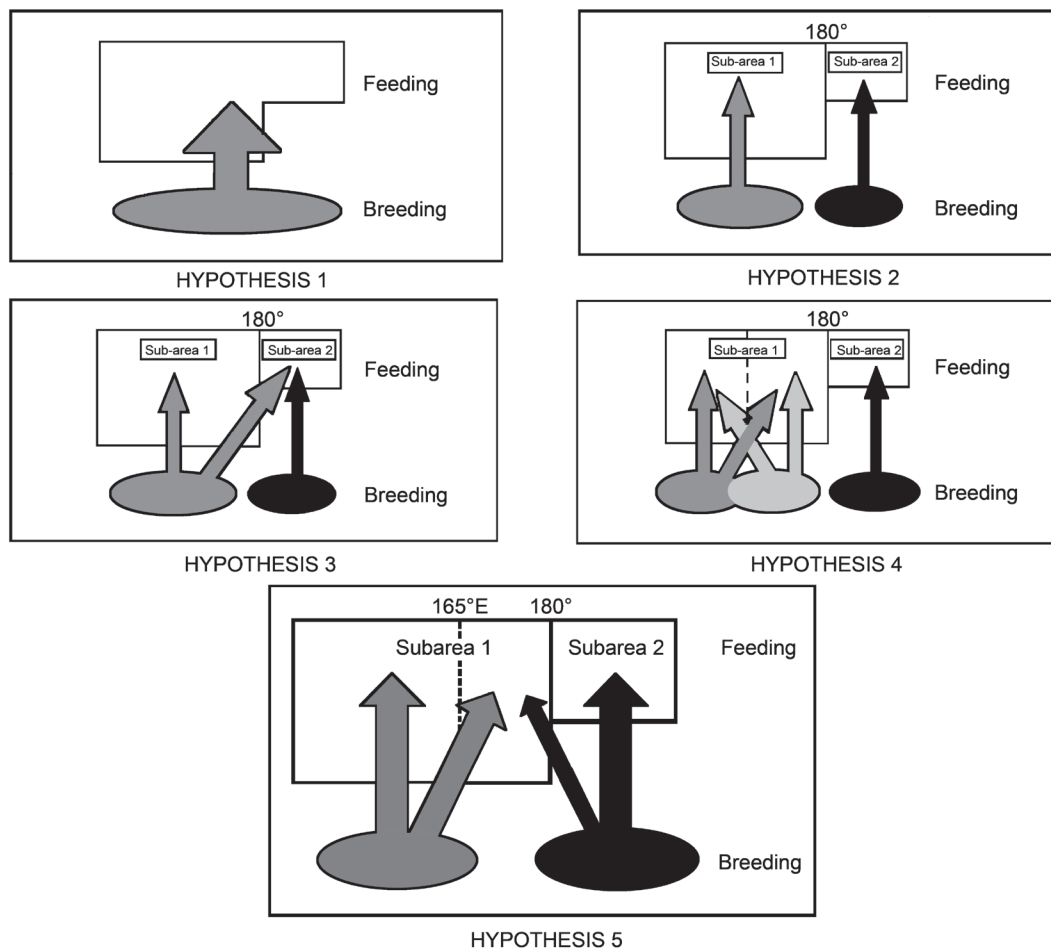


Fig. 4. The stock structure hypotheses: Hypotheses 1-4 were used in the 2007 *Implementation*. Hypothesis 5 is the hypothesis newly developed for this *Implementation*.

Table 6

Sample size for the analysis of genetic diversities in alternative boundaries (moving boundaries) in sub-areas 1 and 2.

Sectors	Microsatellites	Mitochondria
130°E-140°E	21	20
135°E-145°E	133	134
140°E-150°E	369	362
145°E-155°E	360	351
150°E-160°E	316	316
155°E-165°E	354	370
160°E-170°E	230	244
165°E-175°E	107	105
170°E-180°	30	30
175°E-175°W	27	27
180°-170°W	25	25
175°W-165°W	14	14
170°W-160°W	22	22
165°W-155°W	19	19
160°W-150°W	3	3
155°W-145°W	5	3

Table 7

Genetic divergence (F_{ST}) for different groupings of Bryde's whales in sub-areas 1 and 2.

F_{ST}	SA1W vs SA2	SA1W vs SA1E+SA2	SA1W vs SA1E	SA1 vs SA2
Microsatellites	0.004	0.001	0.000	0.004
Mitochondria	0.023	0.011	0.002	0.022

Table 8

Results of Exact Tests for different groupings of Bryde's whales in sub-areas 1 and 2.

Grouping of sub-areas	P-values
SA1W vs SA1E vs SA2	0.001±0.001
SA1W+SA1E vs SA2	0.000±0.000
SA1W vs SA2	0.000±0.000
SA1W vs SA1E+SA2	0.000±0.000

Suggested revision of the original hypotheses (see main report)

Hypothesis 1: deletion suggested because this hypothesis is no longer supported by the DNA analyses.

Hypothesis 2: keep this hypothesis because both mtDNA and microsatellite DNA suggest higher F_{ST} values around longitude 180°, and mixing proposed under 'new' hypothesis 1 can be proved only with samples from breeding grounds.

Hypothesis 3: keep this hypothesis because sample size in SA 2 is still low to reject this possibility.

Hypothesis 4: deletion suggested because new genetic data are better explained by the existence of two stocks. No significant genetic differences were found when SA 1W was compared with SA 1E, for both genetic markers (high statistical power was estimated). Significant differences only emerge when samples from SA 2 are included.

Hypothesis 5: Alternative 'new' hypothesis proposed based on the additional analyses of genetic diversity.

Annex F

Estimates of Mixing Proportions for Sub-area 1E using mtDNA Haplotype Data

André E. Punt

Mixing proportions for sub-area 1E (defined here as the proportion of stock 1 in sub-area 1E) are required to condition the trials based on Stock Structure Hypothesis 5. These proportions can be estimated by assuming that sub-area 1E is a mixing area and the mtDNA haplotype frequencies for sub-areas 1W and 2 are respectively representative of stocks 1 and 2. The mixing proportion of stock 1 in sub-area 1E can be estimated by maximising the following log-likelihood:

$$LnL = \sum_i O_i \ln(p_i) \quad (1)$$

where O_i is the number of animals in sub-area 1E with haplotype i , and p_i is the estimate of the proportion of animals with haplotype i in sub-area 1E, i.e.:

$$p_i = \chi p_i^1 + (1 - \chi) p_i^2 \quad (2)$$

where χ is the proportion of the animals in sub-area 1E that are from stock 1, and $p_i^{1/2}$ are the proportions of animals in stocks 1 and 2 that have haplotype i .

The above algorithm was applied for two cases: (a) the haplotype proportions for stocks 1 and 2 and the numbers of animals in sub-area 1E with each haplotype are based on the JARPN/POWER data; and (b) the numbers of animals in sub-area 1E with each haplotype are based on the commercial

samples for sub-area 1E. Results are provided for three definitions for sub-area 1E (165°E-180°; 160°E-175°E; 170°E-175°W).

Fig. 1 shows likelihood profiles for the two cases and three definitions for sub-area 1E. Table 1 lists the estimates and their asymptotic standard errors. The estimate of χ for two combinations of sub-area 1E definition and data source are 1.00. It is not possible to estimate a standard error for these combinations because the estimates are on a boundary. An approximate standard error can be derived by calculating a lower 95% confidence bound for the proportion using the likelihood profile, which if equated to 1.96 standard errors, allows the calculation of a standard error.

Table 1

Estimates and asymptotic standard errors for the mixing proportion for sub-area 1E.

Sub-area definition	Basis for analysis	
	JARPN/POWER	Commercial
165°E-180°	1.000 (0.114*)	0.851 (0.132)
160°E-175°E	0.900 (0.065)	0.933 (0.057)
170°E-175°W	0.644 (0.144)	1.000 (0.467*)

*Calculated using the likelihood profile.

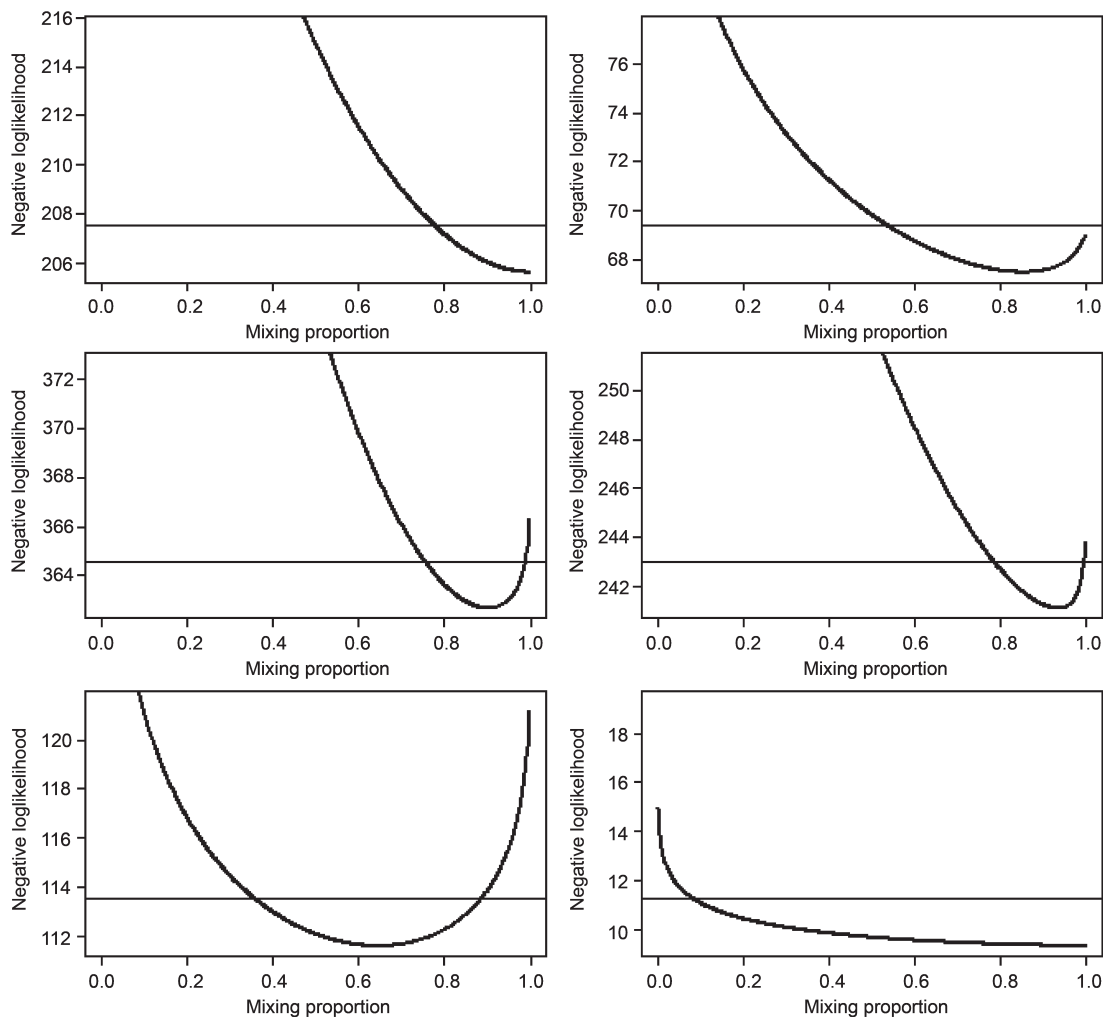


Fig. 1. Likelihood profiles for the proportion of sub-area 1E animals that are from stock 1 for cases: (a) [left panel]; and (b) [right panel]. Results are shown for three definitions for sub-area 1E: 165°E-180° (upper panels); 160°E-175°E (centre panels); 170°E-175°W (lower panels).

Annex G

Additional Information on Abundance Estimate in SC/M17/RMP02

T. Hakamada, M. Takahashi, K. Matsuoka and T. Miyashita

This Annex gives supplemental information on abundance estimates in response to questions and comments made during discussions regarding paper SC/M17/RMP02.

Parameter estimates on detectability

Table 1 shows coefficients and their standard errors for the best models of detection function for POWER and JARPN II data. For JARPN II, the effect of covariates on detectability can be seen from the table. Table 2 shows average $p(z_i)$ over all detection and effective search half width within 3 n.miles of perpendicular distance. Table 3 shows the expected mean school size and its CV for each stratum for both POWER and JARPN II.

Table 1

Coefficients for the best models of detection function for IWC-POWER (left) and JARPN II (right) data.

Parameter	Estimate	SE	Parameter	Estimate	SE
a	1.940	0.298	a	0.862	0.121
			Size	0.328	0.107
			Beaufort: bad	-0.196	0.083
			Year: 2012 and 2014	0.302	0.094

Table 2

Average $p(z_i)$ over all detections and effective search half width (ESW) for the best model of the detection function for IWC-POWER (left) and JARPN II (right) data.

Average p	ESW	CV	Average p	ESW	CV
0.712	2.135	0.088	0.550	1.649	0.034

Table 3

Expected mean school size and its CV by strata for POWER (left) and JARPN II (right).

Year	$E(s)$	CV	Year	Stratum	$E(s)$	CV
2013	1.00	0.000	2008	7	1.39	0.038
2014W	1.22	0.057	2008	8	1.53	0.204
2014E	1.12	0.064	2008	9W	1.42	0.048
2015E	1.38	0.121	2008	9E	1.36	0.053
2015W	1.14	0.125	2012	W	1.00	0.000
			2012	E	-	-
			2014	SW	1.17	0.053
			2014	SE	1.17	0.007
			2014	NW	1.30	0.035
			2014	NE	1.17	0.053

Weighted average of abundance estimate

Average weighted abundance estimate by Akaike weight was calculated for POWER and JARPN II over 16 abundance estimates. The average weighted abundance in the POWER survey area was 9,059 (CV=0.173). The difference from the abundance estimate using the best model is 1.6% of the abundance estimate for the best model (8,919). Table 4 shows abundance estimates and weight used for calculation. The average weighted abundance in the JARPN II survey area was 19,573 (CV=0.193). The difference from the abundance estimate using the best model is 0.2% of the abundance estimate for the best model (19,528). Table 5 shows abundance estimates and weight used for calculation.

Table 4

Abundance estimate in POWER 2013-15 survey areas for each detection functions examined in SC/M17/RMP02 with weight (w_i).

Model	Covariates	P	CV(P)	AIC	Δ AIC	w_i
HR	S+B+Y	9,052	0.207	245.31	6.95	0.01
	S+B	8,961	0.209	243.24	4.89	0.02
	S+Y	8,994	0.199	244.26	5.90	0.01
	B+Y	8,771	0.191	245.51	7.16	0.01
	S	8,985	0.207	241.35	2.99	0.06
	B	8,731	0.197	242.62	4.26	0.03
	Y	8,737	0.190	243.69	5.33	0.02
	None	8,719	0.195	240.62	2.26	0.08
HN	S+B+Y	9,511	0.187	242.36	4.01	0.03
	S+B	9,328	0.183	240.60	2.24	0.08
	S+Y	9,455	0.181	242.26	3.91	0.04
	B+Y	8,993	0.174	242.57	4.21	0.03
	S	9,331	0.181	238.79	0.43	0.20
	B	8,913	0.173	240.18	1.83	0.10
	Y	9,013	0.170	241.99	3.64	0.04
	None	8,919	0.171	238.36	0.00	0.25

Table 5

Abundance estimates in JARPN II 2008, 2012 and 2014 survey areas for the detection functions examined in SC/M17/RMP02 with weight (w_i).

Model	Covariates	P	CV(P)	AIC	Δ AIC	w_i
HR	S+B+Y	20,404	0.229	1,005.18	4.15	0.08
	S+B	19,818	0.221	1,011.56	10.53	0.00
	S+Y	19,690	0.227	1,006.17	5.14	0.05
	B+Y	23,850	0.250	1,015.72	14.70	0.00
	S	19,149	0.215	1,016.43	15.40	0.00
	B	23,082	0.241	1,019.73	18.70	0.00
	Y	22,438	0.247	1,016.91	15.88	0.00
	None	21,427	0.214	1,024.26	23.23	0.00
HN	S+B+Y	19,528	0.225	1,001.03	0.00	0.67
	S+B	19,115	0.219	1,009.14	8.11	0.01
	S+Y	19,284	0.224	1,003.70	2.67	0.18
	B+Y	21,526	0.238	1,012.41	11.38	0.00
	S	18,637	0.217	1,016.94	15.91	0.00
	B	20,836	0.231	1,017.29	16.26	0.00
	Y	21,151	0.238	1,013.43	12.41	0.00
	None	20,089	0.228	1,022.38	21.35	0.00

Response to recommendations on TAG report.

Preliminary analysis of $g(0)$ is planned to be conducted based on IO data in POWER 2015 and 2016 using MRDS (Mark Recapture Distance Sampling) engine in program DISTANCE (Thomas *et al.*, 2010) following the recommendation in the TAG report (IWC, 2017), hopefully, by next IWC/SC meeting. TAG agreed that the unidentified large baleen whale sightings were very probably Bryde's whales; this option should be considered in the analyses of the sightings data (IWC, 2017). Given this, an abundance estimation will be conducted treating 'unidentified whales' as Bryde's whale as a sensitivity analysis by next IWC/SC meeting.

REFERENCES

- International Whaling Commission. 2017. Report of the Meeting of the IWC-POWER Technical Advisory Group (TAG), 7-9 October 2015, Tokyo, Japan. *J. Cetacean Res. Manage. (Suppl.)* 18:459-76.
- Thomas, L., Buckland, S.T., Rexstad, E.A., Laake, J.L., Strindberg, S., Hedley, S.L., Bishop, J.R.B., Marques, T.A. and Burnham, K.P. 2010. Distance software design and analysis of distance sampling surveys for estimating population size. *J. Appl. Ecol.* 47: 5-14.

Annex H

Future Survey Plans and Proposed Management Variants

Future survey plans

Japan plans to cover sub-areas 1W, 1E and 2 by a multi-year sighting survey every 6 years (considering the cycle of *Implementation Reviews*). However, because the main area which Japan wishes to operate for whaling is sub-area 1 (especially 1W), Japan will cover only sub-areas 1W and 1E if surveys in sub-area 2 would not be conducted; this would be in circumstances where any ‘acceptable’ variants excluding sub-area 2 from the *Small Area* or *Combination*

Area outperform those including sub-area 2 as a part of a *Combination Area*.

Management variants

Japan considers the management variants outlined in Table 1 (the same as in the *Implementation*) as appropriate in terms of current knowledge of stock structure and for a more organisationally convenient whaling operation.

Table 1
Management variants considered in the 2007 *Implementation*.

Variant	Description
Variant 1	Sub-areas 1W, 1E and 2 are <i>Small Areas</i> .
Variant 2	Sub-area 2 is taken to be a <i>Small Area</i> and the complete sub-area 1 is treated as a <i>Small Area</i> .
Variant 3	Sub-area 2 is taken as a <i>Small Area</i> and sub-area 1 is a <i>Combination Area</i> . Sub-areas 1W and 1E are <i>Small Areas</i> , with catch-cascading applied.
Variant 4	Sub-areas 1 and 2 (combined) are a <i>Combination Area</i> , and sub-areas 1W, 1E and 2 are <i>Small Areas</i> , with catch-cascading applied.

Annex I

Estimation of Age-at-Maturity for Female Bryde’s Whales

T. Kitakado, S. Inoue and T. Bando

A maturity ogive is estimated for female Bryde’s whales using age-maturity data sampled during JARPN II (see Table 1). The following general formula (Eqn 1) used in Punt (2008) was assumed:

$$y_a \sim \text{Bin}(N_a, p_a), \quad p_a = \left[\frac{\alpha}{1 + \exp[-(a - a_{50}) / \delta]} \right]^\beta \quad (\text{Eqn.1})$$

where:

- p_a is the proportion of animals of age a which are mature;
- a_{50} is the age-at-50%-maturity (if $\alpha=\beta=1$);
- δ is the parameter determines the width of the maturity ogive;
- α is asymptotic fraction of animals which are mature; and
- β is a shape parameter.

Four variant models of the general formula (see Table 2) were used and compared via AIC. The results of maximum likelihood estimation showed that the simplest model is best in terms of AIC though, as shown in Fig. 1, there are negligible differences among models.

The estimated age-at-50%-maturity was about 6 years old in the previous analysis by Punt (2008), while that is around 8.6 in this analysis. This difference might be partly due to difference in the sample size and partly due to the difference in the age-reader (see discussion under Items 3.1.2 and 3.5 of this report).

Table 1

Data employed in the last *Implementation* (JARPNI 2000-03) and this *Implementation Review* (JARPNI 2000-14). Ages greater than 30 were excluded.

Age	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	All
Last Implementation																																
Immature	1	1	1	2	4		2	2	1												1											
Mature						1	2	2	4	4	6	6	3	4	3	1	6	2	3		3	1	2				1			3		72
This Implementation Review																																
Immature		1	4	1	6	10	12	7	3	2	1																					
Mature								1	1	2	10	8	10	14	9	7	11	9	14	12	8	10	7	5	9	3	10	6	8	2	6	229

Table 2

Comparison of the four variant models.

Model	Ass.	a50	δ	α	β	No. of parameters	-Loglike	AIC	Age-at-50%-maturity
Last Implementation									
1	$\alpha=\beta=1$	5.93	2.07	1	1	2	21.04	-	5.93 (0.89)
2	$\beta=1$	6.21	0.915	0.978	1	3	15.66	-	6.21 (0.55)
3	$\alpha=1$	-23.40	2.33	1	212031	3	19.64	-	5.99 (N/A)
4		-7.42	1.25	0.999	30066	4	15.62	-	5.90 (0.51)
This Implementation Review									
1	$\alpha=\beta=1$	8.65	0.598	1	1	2	12.16	28.33	8.65 (0.32)
2	$\beta=1$	8.65	0.598	1.000	1	3	12.16	30.33	8.65 (0.32)
3	$\alpha=1$	8.72	0.579	1	0.935	3	12.15	30.29	8.72 (N/A)
4		9.44	0.378	1.000	0.421	4	12.03	32.06	8.89 (0.55)

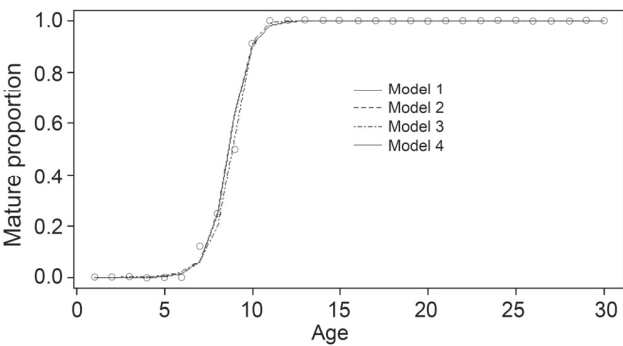


Fig. 1. Fits of the four models to the age-maturity data.

REFERENCE

Punt, A.E. 2008. Report of the Scientific Committee. Annex D. Report of the sub-committee on the revised management procedure. Appendix 4. The specifications for the *Implementation Simulation Trials* for western North Pacific Bryde’s whales (final). Adjunct 3. Estimation of age-at-maturity for female Bryde’s whales. *J. Cetacean Res. Manage. (Suppl.)* 10:114.

Annex J

Specifications for the *Implementation Simulation Trials* for Western North Pacific Bryde's Whales

A. Basic concepts and stock-structure

The trials detailed below consider the implications of alternative variants of the RMP for Bryde's whales in sub-areas 1 and 2 of the western North Pacific (Fig. 1). Sub-area 1 is further sub-divided into sub-areas 1W and 1E at 165°E. The trials model two stocks (Stocks 1 and 2) and explore alternative placements of the boundary between them. The sub-areas are further divided into smaller 'Component areas' (see Fig. 1 and Table 1) to enable these alternatives to be tested.

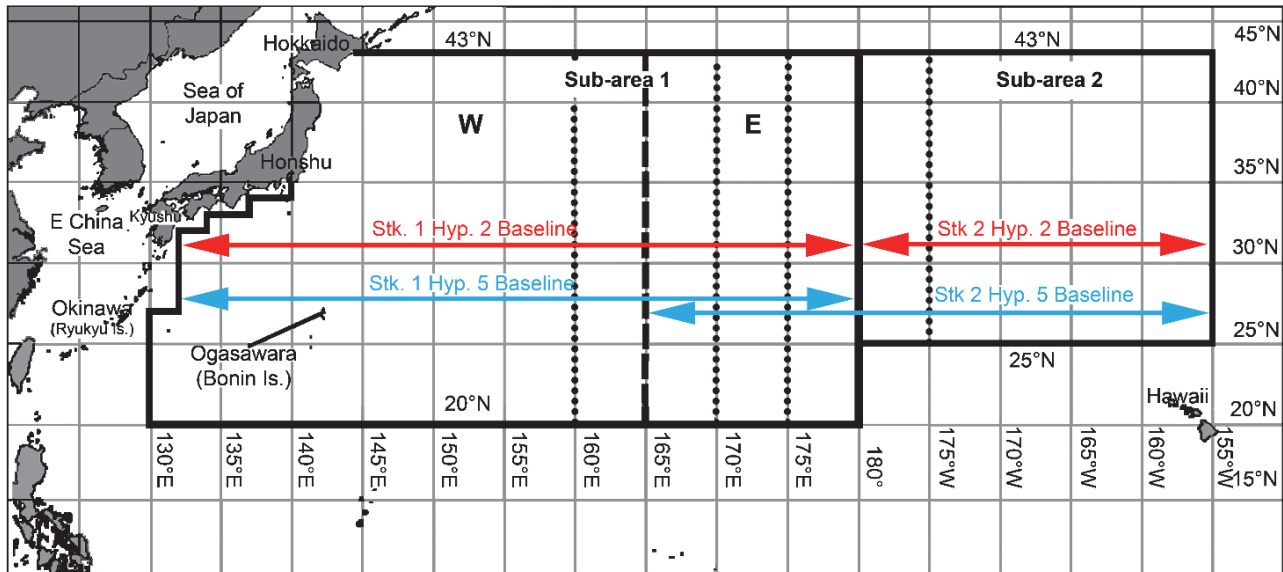


Fig. 1. Map of the western North Pacific showing the sub-areas defined for the western North Pacific Bryde's whales. The ranges of the stocks for Hypotheses 2 and 5 (baselines) are also shown. The boundary between the 1W and 1E sub-areas at 165°E, indicated by a dashed line, is a management boundary (used by the RMP). The dotted lines at 160°E, 170°E, 175°E and 175°W denote the boundaries between 'Component areas' and are used for trials in which the true boundary between the stocks differs from the boundary on which the RMP is based. The staggered border to the South of Japan is used to ensure that no catches of the inshore form occur. The southern boundary of sub-area 1 was revised from the 10° line used in the 2008 trials, in order to avoid the breeding grounds.

There are two general hypotheses regarding stock structure¹:

- (1) Stock structure hypothesis 2. There are two stocks of Bryde's whales in sub-areas 1 and 2. One stock is found in sub-area 1 and the other is found in sub-area 2. The trials investigate sensitivity to the position of the boundary between the stocks.
- (2) Stock structure hypothesis 5. There are two stocks of Bryde's whales in sub-areas 1 and 2. One stock is found in sub-area 1W and the other is found in sub-area 2. Sub-area 1E is a region of mixing. The trials explore various assumptions regarding the regions of mixing.

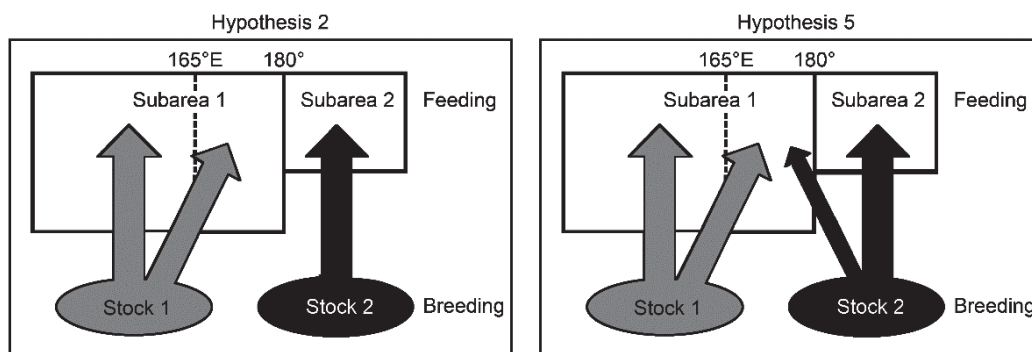


Fig. 2. The two hypotheses considered in the *Implementation Simulation Trials*.

¹Note that stock structure hypotheses 1, 3 and 4 developed in the previous *Implementation* are not carried forward here; for consistency the hypothesis numbers have not been changed.

B. Basic dynamics

The dynamics of the animals in stock j are governed by equation B.1:

$$N_{t+1,a}^{g,j} = \begin{cases} 0.5 b_{t+1}^j & \text{if } a=0 \\ (N_{t,a-1}^{g,j} - C_{t,a-1}^{g,j}) \tilde{S}_{a-1} & \text{if } 1 \leq a < x \\ (N_{t,x}^{g,j} - C_{t,x}^{g,j}) \tilde{S}_x + (N_{t,x-1}^{g,j} - C_{t,x-1}^{g,j}) \tilde{S}_{x-1} & \text{if } a = x \end{cases} \quad (\text{B.1})$$

where

- $N_{t,a}^{g,j}$ is the number of animals of gender g and age a in stock j at the start of year t ;
- $C_{t,a}^{g,j}$ is the catch (in number) of animals of gender g and age a in stock j during year t (whaling is assumed to take place in a pulse at the start of each year);
- b_t^j is the number of calves born to females from stock j at the start of year t ;
- $\tilde{S}_a$ is the survival rate = e^{-M_a} where M_a is the instantaneous rate of natural mortality (assumed to be independent of stock, time, and gender); and
- x is the maximum age (treated as a plus-group);

Note that $t=0$, the year for which catch limits might first be set, corresponds to 2017.

C. Births

For most trials (including the baseline trials), density-dependence is assumed to act on the female component of the 'mature' population. The convention of referring to the mature population is used here, although this actually refers to animals that have reached the age of first parturition.

$$b_t^j = B^j N_t^{f,j} \{1 + A^j (1 - (N_t^{f,j} / K^{f,j})^{z^j})\} \quad (\text{C.1})$$

where

- B^j is the average number of births (of both sexes) per year for a mature female in stock j in the pristine population;
- A^j is the resilience parameter for stock j ;
- z^j is the degree of compensation for stock j ;
- $N_t^{f,j}$ is the number of 'mature' females in stock j at the start of year t :

$$N_t^{f,j} = \sum_{a=a_m}^x N_{t,a}^{f,j} \quad (\text{C.2})$$

a_m is the age-at-first-parturition; and

$K^{f,j}$ is the number of mature females in stock j in the pristine (pre-exploitation written as $t=-\infty$) population:

$$K^{f,j} = \sum_{a=a_m}^x N_{-\infty,a}^{f,j} \quad (\text{C.3})$$

The values of the parameters A^j and z^j for each stock are calculated from the values for $MSYL^j$ and $MSYR^j$ (Punt, 1999). Their calculation assumes harvesting equal proportions of males and females.

D. Catches

It is assumed that whales are homogeneously distributed across a Component-area. The catch limit for a Component-area is therefore allocated to stocks by gender and age relative to their true density within that Component-area and a mixing matrix V (that is independent of year, gender and age in these trials), i.e.:

$$C_{t,a}^{g,j} = \sum_k F_t^{g,k} V^{j,k} S_{t,a}^k N_{t,a}^{g,j} \quad (\text{D.1})$$

$$F_t^{g,k} = \frac{C_t^{g,k}}{\sum_{j'} V^{j',k} \sum_{a'} S_{t,a'}^k N_{t,a'}^{g,j'}} \quad (\text{D.2})$$

where

- $F_t^{g,k}$ is the exploitation rate in Component-area k on recruited animals of gender g during year t ;
- $S_{t,a}^k$ is the selectivity on animals of age a in Component-area k during year t ;
- $C_t^{g,k}$ is the catch of animals of gender g in Component-area k during year t ; and
- $V^{j,k}$ is the fraction of animals in stock j that is in Component-area k during year t .

The historical (pre-2017) catches by Component-area and year are set to one of three series (see IWC, 2008) which will be updated to include catches since 2006); or, in the future, are determined using the RMP. There are no incidental catches. The sex ratio for future catches is assumed to be 50:50.

E1. Mixing

The entries in the mixing matrix V are selected to model the distribution of each stock at the time when the catch is removed. Mixing is deterministic. Table 1 lists the mixing matrices for each of the stock structure hypotheses.

Table 1
The catch mixing matrices. The γ s indicate that the entry concerned is to be estimated during the conditioning process.
The shaded areas show the areas in which the stocks mix.

Stock structure hypothesis	Component Area	Sub-Area						
		1W		1E			2	
		1Wa 130-160°E	1Wb 160-165°E	1Ea 165-170°E	1Eb 170-175°E	1Ec 175°E-180°	2a 180°-175°W	2b 175-155°W
2. Baseline.	Stock 1	4	1	γ_1	γ_1	γ_1	0	0
	Stock 2	0	0	0	0	0	1	4
2. Trial 6	Stock 1	4	1	γ_1	γ_1	0	0	0
	Stock 2	0	0	0	0	Y	1	4
5. Baseline	Stock 1	4	1	γ_1	γ_1	γ_1	0	0
	Stock 2	0	0	γ_2	γ_2	γ_2	1	4
5. Trials 7	Stock 1	1	γ_3	γ_3	γ_3	0	0	0
	Stock 2	0	γ_4	γ_4	γ_4	Y	1	4
5. Trials 8	Stock 1	4	1	1	$Y\gamma_5$	$Y\gamma_5$	γ_5	0
	Stock 2	0	0	0	$Y\gamma_6$	$Y\gamma_6$	γ_6	1

Notes

The 4:1 ratios used in sub-area 1W are calculated from the ratio of the areas of sub-areas 1Wa and 1Wb, but ignoring the area to the South of Japan between 130-140°E as very few Bryde's whales are seen there.

Y is calculated using the ratio of the number of degrees of latitude covered by the two areas 1Ec and 2a, i.e. $Y=23/18$.

For Hypothesis 2, the number of Stock 1 whales in sub-area 1W and 1E is estimated during conditioning using the relative abundance in the two sub-areas. In Trial 6, the boundary between the two stocks changes from 180° to 175°E.

For Hypothesis 5, the density of each stock is assumed to be uniform across the mixing area band.

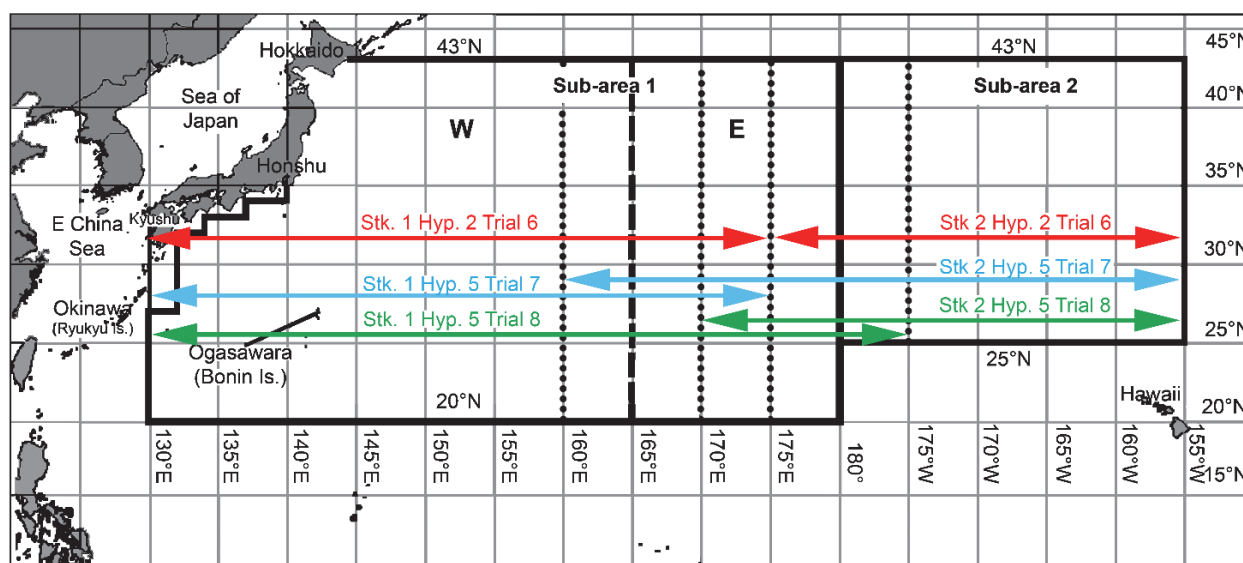


Fig. 3. The ranges of the stocks tested in Trials 6, 7 and 8.

E2. Boundary

In the baseline trials, the boundary between sub-areas 1W and 1E and between 1E and 2 used when modelling the true population dynamics is the same as that used when applying the RMP and is at 165°E and 180°, respectively. However, a different boundary is used for some of the trials based on stock structure hypothesis 5 that assumes mixing between stocks 1 and 2 in an inter-mediate area. This inter-mediate area corresponds to Sub-area 1E for the baseline hypothesis 5. In Trial 7 the boundaries between the true stock and stock-mixing areas are 5° further west than for the baseline, while in Trial 8 the boundaries are 5° further east (Fig. 3).

The management boundaries are fixed at 165°E and 180° for all trials.

F. Generation of data

The actual historical estimates of absolute abundance (and their associated CVs) provided to the RMP are listed in Table 2. Future surveys are assumed to cover each of sub-areas 1W, 1E and 2 in their entirety in a single survey. This is a slight simplification of reality; the entire area will actually be covered in four years (see Table 3 for the proposed survey plan), but the westernmost part of sub-area 1W contains very few Bryde's whales so the two surveys in sub-area 1W are treated as one for the purposes of trials. The trials assume that it takes two years for the results of a sighting survey to become available to be used by the management procedure, i.e. a survey conducted in 2020 could first be used for setting the catch limit in 2022.

The future estimates of abundance for a survey area E are generated using the formula:

$$\hat{P} = P Y w / \mu = P^* \beta^2 Y w \quad (\text{F.1})$$

where

Y is a lognormal random variable $Y = e^\varepsilon$ where $\varepsilon \sim N(0; \sigma_\varepsilon^2)$ and $\sigma_\varepsilon^2 = \ln(\alpha^2 + 1)$;

w is a Poisson random variable with $E(w) = \text{var}(w) = \mu = (P / P^*) / \beta^2$, Y and w are independent;

P is the current total (1+) population size in survey area E :

$$P = P_t^E = \sum_{k \in E} \sum_j V_t^{j,k} \sum_g \sum_{a \geq 1} N_{t,a}^{g,j} \quad (\text{F.2})$$

and

P^* is the reference population level, and is equal to the expected total (1+) population size in the survey area prior to the commencement of exploitation in the area being surveyed (where the expectation is taken with respect to inter-annual variation in the mixing matrix).

Note that under the approximation $CV^2(ab) \cong CV^2(a) + CV^2(b)$, $E(\hat{P}) \cong P$ and $CV^2(\hat{P}) \cong \alpha^2 + \beta^2 P^* / P$.

For consistency with the first stage screening trials for a single stock (IWC, 1991, p.109; IWC 1994, pp.85-6), the ratio $\alpha^2 : \beta^2 = 0.12 : 0.025$, so that:

$$CV^2(\hat{P}) = \tau(0.12 + 0.025 P^* / P) \quad (\text{F.3})$$

The value of τ is calculated from the survey sampling CV's of earlier surveys in survey-area E . If $\overline{CV^2}$ is the average value of CV^2 estimated for each of these surveys, and $\bar{P}$ is the average value of the total (1+) population sizes in area E in the years of these surveys, then:

$$\tau = \overline{CV^2} / (0.12 + 0.025 P^* / \bar{P}) \quad (\text{F.4})$$

Note therefore that:

$$\alpha^2 = 0.12\tau \quad \beta^2 = 0.025\tau \quad (\text{F.5})$$

The above equations apply in the absence of additional variance. In these trials, an additional variance CV_{add} is incorporated by making the following adjustment:

$$\sigma_\varepsilon^2 = \ln(1 + \alpha^2 + CV_{add}^2) \quad (\text{F.6})$$

$CV_{add} = 0.335$ in the baseline trials (SC/67a/RMP04).

An estimate of the CV is generated for each sighting survey estimate of abundance $\hat{P}$:

$$CV(\hat{P})_{est}^2 = \sigma^2 \chi^2 / n \quad (\text{F.7})$$

where

$\sigma^2 = \ln(1 + \alpha^2 + \beta^2 P^* / \hat{P})$, and

χ^2 is a random number from a Chi-square distribution with n degrees of freedom (where $n=10$ as used for the North Pacific minke whale *Implementation Trials*; IWC, 2004).

Table 2
The estimates of abundance and their sampling errors.

Sub-area	Year	Estimate	Sampling CV
1W	1995	5,110	0.192
	2000	4,222	0.317
	2011	15,422	0.289
1E	1995	7,246	0.479
	2000	9,251	0.295
	2011	6,716	0.216
2	1995	2,262	0.300
	2000	3,711	0.337
	2014	4,161	0.264

Table 3

Sighting survey plan (the results from surveys in the westernmost part of sub-area 1W are combined in the trials - see section F).

Season	Sector			
	130°-145°E	145°-165°E	165°E-180°	180°-160°W
Sub-Area	1W		1E	2
2017				Yes
2018		Yes		
2019			Yes	
2020	Yes			
2021				Yes
2022		Yes		
2023			Yes	
2024	Yes			
2025				Yes
2026		Yes		
2027			Yes	
2028	Yes			
2029				Yes
2030		Yes		
2031			Yes	
2032	Yes			
and so on in this pattern				

Table 4

The values for the biological and technological parameters that are fixed.

Parameter	Value
Plus group age, x	15 yrs
Natural mortality, M	0.08yr^{-1}
Age-at-first-parturition, a_m	9 years (see Annex I of this report: calculated as 8.6)
Selectivity (historical)	
Sub-area 1W:	Knife-edged at age 5 (IWC, 2000; 2005b)
Sub-areas 1E and 2:	Knife-edged at age 9 (IWC, 2000; 2005b)
Selectivity (future)	Knife-edged at age 5 (IWC, 2007, p.415)
Maximum Sustainable Yield Level, $MSYL$	0.6 in terms of mature female component of the population

G. Parameters and conditioning

The values for the biological and technological parameters are listed in Table 4. In relation to selectivity, historically a 35ft (10.7m) legal minimum size limit applied to coastal whaling and a 40ft (12m) limit applied to pelagic operations. These size limits correspond to ages of five and nine years respectively (Ohsumi, 1977). The size limits are implemented by making selectivity depend on sub-area. Historically, pelagic whaling occurred in sub-areas 1E and 2, and coastal whaling in sub-area 1W. Therefore, selectivity is assumed to be knife-edged at age five for sub-area 1W, while selectivity for sub-areas 1E and 2 is assumed to be knife-edged at age nine. All future catches are assumed have a knife-edged selectivity at age five (hence the t -subscript on S in Equations D.1 and D.2).

The ‘free’ parameters of the above model are the initial (pre-exploitation) sizes of each of the stocks and the values that determine the mixing matrices. The process used to select the values for these ‘free’ parameters is known as conditioning. The conditioning process involves first generating 100 sets of ‘target’ data, detailed in steps (a) and (b) below, and then fitting the population model to each (in the spirit of a bootstrap). The number of animals in Component-area k at the start of year t is calculated starting with guessed values of the initial population sizes and projecting the operating model forward to 2017 to obtain values of abundance by stock and mixing proportions for comparison with the generated data.

(a) The ‘target’ values for the historical abundance by survey-area are generated using the formula:

$$P_t^E = O_t^E \exp[\mu_t^E - (\sigma_t^E)^2 / 2]; \mu_t^E \sim N[0; (\sigma_t^E)^2] \quad (\text{G.1})$$

where

P_t^E is the abundance for survey-area E in year t ;

O_t^E is the actual survey estimate for survey-area E in year t (Table 4); and

σ_t^E is the CV of O_t^E .

(b) The ‘targets’ for the mixing proportion in the mixing area trials based on stock structure hypothesis 5 are generated from normal distributions (Table 5), truncated at 0 and 1.

Table 5

Estimates and asymptotic standard errors for the mixing proportions between Stocks 1 and 2 in Hypothesis 5 trials.

Area	Average proportion of Stock 1 between 2004-14 (from JARPNII/POWER samples)	Standard error	Proportion of Stock 1 in 1978 (from commercial samples)	Standard error
Baseline: 165°E-180°	1.000	0.114	0.851	0.132
Trial 7: 160°E-175°E	0.900	0.065	0.933	0.057
Trial 8: 170°E-175°W	0.644	0.144	1.000	0.467

Calculation of the likelihood

The likelihood function consists of two components. Equations G.2 and G.3 list the negative of the logarithm of the likelihood for each of these components so the objective function minimised is $L_1 + L_2$, where L_2 only applies for Hypothesis 5. An additional penalty is added to the likelihood if the full historical catch is not removed.

Abundance estimates

$$L_1 = 0.5 \sum_n \frac{1}{(\sigma_n)^2} \ln \left(P_n / \hat{P}_n \right)^2 \quad (\text{G.2})$$

where $\hat{P}_n$ is the model estimate of the 1+ abundance in the same year and survey-area as the n^{th} estimate of abundance P_n (the target abundances).

Mixing proportions

$$L_2 = 0.5 \frac{1}{\sigma_{78}^2} (p_{78} - \hat{p}_{78})^2 + 0.5 \frac{1}{\sigma_{04}^2} (p_{04} - \hat{p}_{04})^2 \quad (\text{G.3})$$

where

$\hat{p}_{78}$ is the model estimate of the proportion of stock 1 animals in the mixing area² in 1978;

$\hat{p}_{04}$ is the average of the model estimate of the proportion of stock 1 animals in the mixing area over 2004 to 2014; and

p_{78} and p_{04} are the ‘target’ mixing proportions from commercial samples in 1978 and JARPNII/POWER survey samples between 2004-2014, respectively, given in Table 5.

H. Trials

The *Implementation Simulation Trials* for the western North Pacific Bryde's whales are listed in Table 6. All of the trials are based on the assumption $g(0)=1$. Table 7 lists the factors used in the trials.

Table 6

The *Implementation Simulation Trials* for the Western North Pacific Bryde's whales.

Trial	Stock structure hypothesis	MSYR ¹	Additional variance	Catch series	1W/1E boundary	1E/2 boundary	Comment
Br1-1	2	1	Baseline	Best	165°E	180°	Baseline stock structure hypothesis 2
Br1-4	2	4	Baseline	Best	165°E	180°	Baseline stock structure hypothesis 2
Br2-1	5	1	Baseline	Best	165°E	180°	Baseline stock structure hypothesis 5
Br2-4	5	4	Baseline	Best	165°E	180°	Baseline stock structure hypothesis 5
Br3-1	5	1	Baseline	Low	165°E	180°	Stock hypothesis 5 with low catches
Br3-4	5	4	Baseline	Low	165°E	180°	Stock hypothesis 5 with low catches
Br4-1	5	1	Baseline	High	165°E	180°	Stock hypothesis 5 with high catches
Br4-4	5	4	Baseline	High	165°E	180°	Stock hypothesis 5 with high catches
Br5-1	5	1	Upper CI	Best	165°E	180°	Stock hypothesis 5 with higher additional variance
Br5-4	5	4	Upper CI	Best	165°E	180°	Stock hypothesis 5 with higher additional variance
Br6-1	2	1	Baseline	Best	165°E	175°E	Stock hypothesis 2 with alternative boundaries ^{1 2}
Br6-4	2	4	Baseline	Best	165°E	175°E	Stock hypothesis 2 with alternative boundaries ^{1 2}
Br7-1	5	1	Baseline	Best	160°E	175°E	Stock hypothesis 5 with alternative boundaries ^{1 2}
Br7-4	5	4	Baseline	Best	160°E	175°E	Stock hypothesis 5 with alternative boundaries ^{1 2}
Br8-1	5	1	Baseline	Best	170°E	175°W	Stock hypothesis 5 with alternative boundaries ^{2 2}
Br8-4	5	4	Baseline	Best	170°E	175°W	Stock hypothesis 5 with alternative boundaries ^{2 2}
Br9-1	?	1	Baseline	Best	165°E	180°	Density dependent M
Br9-4	?	4	Baseline	Best	165°E	180°	Density dependent M

¹MSYR=1% is related to the 1+ component; MSYR =4% is related to mature component. ²Based on alternative mixing proportion data.

²The mixing area is sub-area 1E (165°E-180°E) for the baseline trials, but changes to 160°E-175°E for Trial 7, and 170°E-175°W for Trial 8.

Table 7
Factors considered in the revised trials. The values in **bold** are the baseline values.

Factor	Values considered
Stock structure hypotheses	2, 5
<i>MSYR</i>	<i>MSYR</i>₁₊ = 1%; <i>MSYR</i>_{mat}=4%
Catch series	Low, Best , High
Additional variance	Baseline , Upper 5%ile
1W/1E boundary	160°E, 165°E , 170°E
1E/2 boundary	175°E, 180° , 175°W

I. Management options

In all cases, the boundary between sub-areas 1W and 1E is defined as 165°E and that between sub-areas 1E and 2 at 180° irrespective of the true boundary used to define the structure of the populations in the operating model. The following five management options will be considered.

- V1 Sub-areas 1W, 1E and 2 are *Small Areas* and catch limits are set by *Small Area*.
- V2 Sub-area 2 is taken to be a *Small Area* and the complete sub-area 1 is treated as a *Small Area*. For this management option, all of the future catches in sub-area 1 are taken from sub-area 1W.
- V3 Sub-area 2 is taken to be a *Small Area* and sub-area 1 is taken to be a *Combination area*. Sub-areas 1W and 1E are *Small Areas*, with catch-cascading applied.
- V4 Sub-area 1W is taken to be a *Small Area* and sub-areas 1E and 2 (combined) are taken to be a *Combination Area*. Sub-areas 1E and 2 are *Small Areas*, with catch-cascading applied.
- V5 Sub-areas 1 and 2 (combined) are taken to be a *Combination area*. Sub-areas 1W, 1E and 2 are *Small Areas*, with catch-cascading applied.

The simulated application of the RMP is based on using the ‘best’ catch series (see IWC, 2008).

J. Output statistics

Population-size and continuing catch statistics are produced for each stock and catch-related statistics for each sub-area.

- (1) Total catch (TC) distribution: (a) median; (b) 5th value; (c) 95th value.
- (2) Initial mature female population size (P_{initial}) distribution: (a) median; (b) 5th value; (c) 95th value.
- (3) Final mature female population size (P_{final}) distribution: (a) median; (b) 5th value; (c) 95th value.
- (4) Lowest mature female population size (P_{lowest}) distribution: (a) median; (b) 5th value; (c) 95th value.
- (5) Average catch by sub-area over the first ten years of the 100 year management period: (a) median; (b) 5th value; (c) 95th value.
- (6) Average catch by sub-area over the last ten years of the 100 year management period: (a) median; (b) 5th value; (c) 95th value.

Plots are produced showing following types of outputs for all variants and the no-catch scenarios:

- (a) the median population size trajectories by stock;
- (b) the 5%-ile, median and 95%-ile of the population depletion trajectories by stock from year 2000 to the end of the projection period);
- (c) the median catch trajectories from year 2000 onwards; and
- (d) ten individual population trajectories for each stock.

In addition, plots and tables are produced summarising the application of the procedure for defining ‘acceptable’ - A, ‘borderline’ - B and ‘unacceptable’ - U performance, by comparison with the equivalent single stock trials - see IWC (2005a).

K. References

- International Whaling Commission. 1991. Report of the Sub-committee on Management Procedures, Appendix 4. Report of the *ad hoc* trials subgroup. *Rep. int. Whal. Commn* 41:108-12C.
- International Whaling Commission. 1994. Report of the Scientific Committee, Annex D. Report of the Sub-committee on Management Procedures, Appendix 2. Minimum standards trials. *Rep. int. Whal. Commn* 44:85-8.
- International Whaling Commission. 2000. Report of the Scientific Committee, Annex D. Report of the Sub-Committee on the Revised Management Procedure. *J. Cetacean Res. Manage. (Suppl.)* 2: 79-124.
- International Whaling Commission. 2004. Report of the Scientific Committee, Annex D. Report of the Sub-Committee on the Revised Management Procedure, Appendix 10. North Pacific minke whale *Implementation Simulation Trial* specifications. *J. Cetacean Res. Manage. (Suppl.)* 6: 118-139.
- International Whaling Commission. 2005a. Report of the Scientific Committee, Annex D. Report of the Sub-committee on the Revised Management Procedure, Appendix 2. Requirements and Guidelines for *Implementations*. *J. Cetacean Res. Manage. (Suppl.)* 7: 84-92.
- International Whaling Commission. 2005b. Report of the Workshop on the *pre-Implementation assessment* of western North Pacific Bryde’s whales. *J. Cetacean Res. Manage. (Suppl.)* 8: 337-355.
- International Whaling Commission. 2007. Report of the first intersessional Workshop on the Western North Pacific Bryde’s whale *Implementation*. Report of the First Intersessional Workshop, 25-29 October 2005, Shizuoka, Japan. *J. Cetacean Res. Manage. (Suppl.)* 9:407-27.
- International Whaling Commission. 2008. Report of the Scientific Committee, Annex D. Report of the Sub-Committee on the Revised Management Procedure, Appendix 4. The specifications for the *Implementation Simulation Trials* for Western North Pacific Bryde’s whales (final). Adjunct 1. The catch series used in the trials. *J. Cetacean Res. Manage. (Suppl.)* 10: 112-13.
- Ohsumi, S. 1977. Further assessment of population of Bryde’s whales in the North Pacific. *Rep. int. Whal. Commn* 27:156-60.
- Punt, A.E. 1999. Report of the Scientific Committee, Annex R. A full description of the standard Baleen II model and some variants thereof. *J. Cetacean Res. Manage. (Suppl.)* 1: 267-76.

