Appendix 1

Catch limits for western North Pacific sei, Bryde's and common minke whales calculated in line with the IWC's Revised Management Procedure (RMP)

Japan's RMP Team

EXECUTIVE SUMMARY

Background

Japan has announced its withdrawal from the International Convention for the Regulation of Whaling (ICRW), which comes into effect on 30 June 2019. Japan also announced the start of commercial whaling from July 2019 within Japan's territorial sea and Exclusive Economic Zone (EEZ).

Catch limits for western North Pacific sei, Bryde's and common minke whales have been calculated in line with the IWC's Revised Management Procedure (RMP), based on the Norwegian Catch Limit Algorithm (CLA) computer code and for a tuning level of 0.6.

The application of the CLA was based on the best and latest scientific information on stock structure, which is essential to define management areas and estimate abundance. Discussions on these topics at the International Whaling Commission's Scientific Committee (IWC SC) were duly considered.

Management areas and abundance

For sei whales, a single management area was defined for the North Pacific after considering the scientific evidence, which strongly suggests that a single stock is distributed in this ocean basin. This management area coincides with the areas covered by recent sighting surveys. The latest estimate of abundance of the stock, based on JARPNII and IWC POWER surveys, is 34,718 animals.

For Bryde's whales, after taking account of the best information on stock structure, two management areas were defined. The latest estimate of abundance, based on Japanese dedicated sighting, JARPNII and IWC-POWER surveys, is 34,473 animals.

For common minke whales, after taking account of the best information on stock structure, a single management area was defined on the Pacific side of Japan and including the Okhotsk Sea. The latest estimate of abundance, based on Japanese dedicated sighting and JARPNII surveys, is 20,513 animals.

Catch limits

Based on the CLA, catch limits for sei, Bryde's and common minke whales were calculated as 174, 187 and 180 respectively. In the case of complex stock structure scenarios, catch limits calculated by the CLA were examined for their robustness to some uncertainties (by the so called *Implementation Simulation Trials* process). In the case of the Bryde's whales, the catch limit was robust to alternative catch series, alternative additional variance values and different stock boundaries. In the case of the common minke whales, the catch limit was robust to alternative catch series, different g(0) estimates and alternative stock mixing proportions in sub-area 12.

Japan's implementation of the RMP variant above will continue to be based on the best available science; hence, the catch limits will be revised from time to time to take account of the latest scientific information.

CONTENTS

1. INTRODUCTION

In a statement dated 26 December 2018, Japan announced its withdrawal from the International Convention for the Regulation of Whaling (ICRW), which comes into effect on 30 June 2019. In the same statement, Japan also announced the start of commercial whaling from July 2019 within Japan's territorial sea and Exclusive Economic Zone (EEZ).

The statement stressed that commercial whaling will be conducted within the catch limits calculated in accordance with the method adopted by the International Whaling Commission (IWC), so as to avoid any negative impact on the health of cetacean resources i.e. along the lines of the Revised Management Procedure (RMP) (see explanation of the RMP in section 2).

Based on the scientific information available, Japan specified that the baleen whale species to be targeted by commercial whaling are the North Pacific sei (*Balaenoptera borealis*), Bryde's (*B. brydei*[1]) and common minke (*B. acutorostrata*) whales. A group of domestic specialists drawn from several research institutions in Japan has been working on the application of an approach along the lines of the RMP for calculating catch limits for the stocks of these species.

The objective of this document is to report the results of catch limit calculations in line with the RMP by this Japanese group, together with an explanation of the data and analytical procedures used in the process, for review by external specialists.

2. THE RMP

2.1 Brief history of the development of the RMP in the IWC

In 1982, the International Whaling Commission (IWC) adopted catch limits of zero for commercial whaling (commonly referred to as the moratorium). The primary rationale offered was the argued absence of a sound scientific basis for setting safe catch limits. Specifically, paragraph 10 (e) of the Schedule of the ICRW stated the following: 'Notwithstanding the other provisions of paragraph 10, catch limits for the killing for commercial purposes of whales from all stocks for the 1986 coastal and the 1985/86 pelagic seasons and thereafter shall be zero. This provision will be kept under review, based upon the best scientific advice, and by 1990 at the latest the Commission will undertake a comprehensive assessment of the effects of this decision on whale stocks and consider modifications of this provision and the establishment of other catch limits.'

As part of the comprehensive assessment mentioned in paragraph 10 (e), the IWC Scientific Committee (IWC SC) began the process of developing a procedure for setting safe catch limits for commercial whaling for baleen whales (Donovan, 1989). The procedure developed by the IWC SC in 1992 was called the Revised Management Procedure (RMP). Its agreed management objectives were:

i) Stability of catch limits which would be desirable for the orderly development of the whaling industry;
ii) Acceptable risk that a stock not to be depleted (at a certain level of probability) below some chosen level (e.g. fraction of carrying capacity), so that the risk of extinction is not seriously increased by exploitation;
iii) Making possible the highest possible continuing yield from the stock (IWC, 1992).

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[1] The taxonomy of Bryde's whales is still unresolved. Some authors recognize two species, the smaller one *B. edeni* (Eden's whale) and a larger one *B. brydei* (Bryde's whale). Other authors assign these species a sub-specific status: *B. edeni edeni* and *B. edeni brydei*. The smaller one inhabits primarily coastal and continental shelf waters of the Northern Indian Ocean and the western Pacific Ocean (inshore form), while the larger one inhabits tropical and warm temperature waters worldwide (offshore form). The present document refers to the larger, offshore form Bryde's whale.

The IWC (i.e. the Commission) adopted the RMP in 1994.

2.2 Main characteristics of the RMP

The core component of the RMP is the Catch Limit Algorithm (CLA), which is a feedback control algorithm that sets baleen whale harvest levels to meet the objectives above, on the basis of catch histories and a time series of estimates of absolute abundance derived from sighting surveys. It was developed over a six-year period by the IWC SC, who took particular care to ensure its robustness to a very wide range of conceivable scientific uncertainties (e.g. the effect of environmental change) using simulation testing. The RMP has a built-in safety threshold, i.e. zero catch if the population size is estimated to be below 54% of carrying capacity.

The term ‘continuing yield’ in objective number iii) above refers to the mean (maximum) yearly harvest in the long term, i.e. when the exploited stock has reached a stationary state (Aldrin *et al*., 2008). The CLA has previously been tuned to a specified final depletion after 100 years of management, based on simulations from a population model with maximum sustainable yield (MSY) at 1% of the mature component of the stock. With regard to the tuning procedure, median depletion after 100 years is set to 60%, 66% or 72% of carrying capacity, one of which could be eventually chosen by relevant managers.

The RMP, or CLA to be precise, is a generic method for calculating safe catch limits that could be applied to any baleen whale population on its feeding grounds given perfect knowledge of stock structure (Punt and Donovan, 2007). While the robustness of catch limit calculated by the CLA is thoroughly examined as mentioned above, if the whale population concerned shows more complex behaviour, the robustness of the CLA has to be re-checked taking into account such specific situations. In an IWC context, before recommending that the RMP be applied to a species in a region (generally part of an ocean basin), simulation trials are developed and run to capture the uncertainties deemed to be the most important for that stock complex/region. This process, referred to as ‘*Implementation*’, focuses primarily on uncertainties about stock structure, in particular temporal and spatial variation in the mixing of stocks in areas where whaling is to take place (Punt and Donovan, 2007).

3. JAPANESE CONCEPT FOR THE IMPLEMENTATION OF THE RMP ON WESTERN NORTH PACIFIC BALEEN WHALES

The IWC SC conducted RMP *Implementation/Implementation reviews* in 2007 and 2019 for western North Pacific Bryde’s whales and in 2013 for western North Pacific common minke whales. To reflect a wide range of views within the IWC SC, the scenarios/hypotheses considered in those *Implementation/Implementation reviews* are diverse. Some of the scenarios and hypotheses are supported by actual data, while some others are closer to speculation without specific supporting scientific evidence.

The Japanese implementation of a procedure in line with the RMP is based on the best and latest available scientific information (mainly related to stock structure and abundance for the three species mentioned above). Therefore, even though the discussion at the IWC SC has been duly considered, there are cases where the Japanese implementation of the RMP is based only on hypotheses/scenarios considered by the IWC SC which are reasonably supported by actual scientific data.

Japan’s implementation of RMP will continue to be based on best available science; hence the catch limits will be revised from time to time to reflect the latest scientific information.

Japan’s catch limits were calculated based on the Norwegian code for the CLA (Aldrin and Huseby, 2007; Aldrin *et al*., 2008), though for a tuning level of 0.6 as is also used by Norway for its calculations of catch limits for common minke whales in the North East Atlantic. Input files as well the CLA R program were checked by an independent specialist.

4. WESTERN NORTH PACIFIC SEI WHALE

4.1 Stock structure and definition of management areas

4.1.1 Review of genetic studies

Genetic analyses on stock structure of North Pacific sei whales have been conducted based on the comprehensive data set collected by the Institute of Cetacean Research (ICR). Genetic samples are from three different sources: past commercial whaling, IWC-POWER surveys and JARPNII surveys (Table 1 and Figure 1). Different genetic studies, conducted based on both mitochondrial DNA (mtDNA) control region sequences and microsatellite DNA, provided no indications of genetic inhomogeneity among temporal and spatial strata, suggesting that the pelagic area of the North Pacific is occupied by a single stock (Kanda *et al*., 2009; 2013; 2015a; Pastene *et al*., 2016a; 2016b).

The most recent study was presented in Tamura *et al*. (2019) (Appendix 7) and is described in more detail here. Table 1 shows details of the sampling and Figure 1 shows the geographical distribution of the genetic samples. These samples were collected in summer from approximately 143°E to 137°W, and between 35°N and 50°N. No genetic samples are available for areas west of 143°E and east of 137°W, nor for areas north of 50°N.

Table 1. Number and period of collection of genetic samples analyzed of North Pacific sei whales, by area, source and genetic marker. Parent-offspring and re-sampled animals are excluded from the numbers in this table.

Sub-area	Commercial whaling (1972-1973)		JARPNII (2002-2016)		POWER (2010-2016)		Total	
	mtDNA	msDNA	mtDNA	msDNA	mtDNA	msDNA	mtDNA	msDNA
Western			30	30			30	30
Central	175	177	1322	1323	3	3	1500	1503
Eastern	128	121			75	75	203	196
Total	303	298	1352	1353	78	78	1733	1729

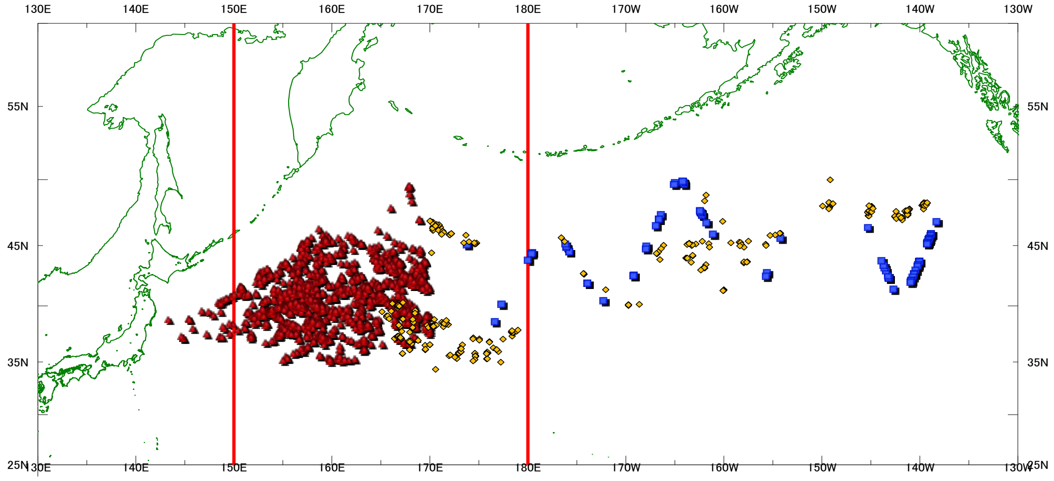

Figure 1. Geographical distribution of genetic samples for North Pacific sei whales. Red: JARPNII surveys (catches); Yellow: past commercial whaling; Blue: IWC POWER surveys (biopsies).

DNA extraction, mtDNA sequencing and microsatellite genotyping

Total genomic DNA was extracted from 0.05g of skin tissue, preserved in 99% ethanol at room temperature or stored frozen at -20°C, using the standard phenol-chloroform method (Sambrook *et al*., 1989) or using Gentra Puregene kits (QIAGEN). Extracted DNA was stored in TE buffer (10 mM Tris-HCl, 1 mM EDTA, pH 8.0).

Approximately 500 base pairs of a partial control region were amplified by the polymerase chain reaction (PCR) using a set of primers MT4 (Árnason *et al*., 1993) and Dlp 5R (5'-CCA TCG AGA TGT CTT ATT TAA GGG GAA C-3'). PCR was performed with an initial denaturation step at 95°C for 5 minutes, followed by 30 cycles of 30 seconds at 94°C, 30 seconds at 50°C and 30 seconds at 72°C, with a final extension step at 72°C for 10 minutes. PCR products were purified using MicroSpin S-400HR columns (Pharmacia Biotech). Cycle sequencing was performed using the BigDye terminator cycle sequence Kit (Applied Biosystems) and the PCR primers, following the protocols given by the manufacturer. The cycle sequencing products were purified using AutoSeq G-50 spin Columns (Pharmacia Biotech). The labeled sequencing fragments from tissue samples collected until 2004, during 2005–2010, and from 2011 were resolved using an ABI PRISM 377, ABI PRISM 3100 and ABI3500 Genetic Analyzers (Applied Biosystems), respectively.

All individuals were genotyped at a total of seventeen microsatellite loci: EV1, EV14, EV21, EV94, EV104 (Valsecchi and Amos, 1996), GT011 (Bérubé *et al*., 1998), GT23, GT211, GT271, GT310, GT575 (Bérubé *et al*., 2000), GATA28, GATA53, GATA98, GATA417, GGAA520 (Palsbøll *et al*., 1997) and DlrFCB17 (Buchanan *et al*., 1996). Primer sequences and PCR cycling profiles generally followed those of the original authors. The multiplex PCR amplifications were performed in 15μl reaction mixtures containing 10-100ng of DNA, 5 pmole of each primer, 0.625 units of Ex Taq DNA polymerase (Takara Shuzo), 2mM of each dNTP, and 10x reaction buffer containing 20mM MgCl2 (Takara Shuzo), at 94°C for 2 minutes, followed by 30 cycles at 94°C for 20 seconds/54–61°C for 45 seconds/72°C for 1 minutes and a post-cycling extension at 72°C for 10 minutes. PCR products from tissue samples collected until 2013 were run on a 6% polyacrylamide denaturating gel (Long Ranger) with internal size standard (GENESCAN400HD, Applied Biosystems) using BaseStation100 DNA fragment analyzer (Bio-Rad). Although alleles were visualized using Cartographer software specifically designed for the BaseStation, allelic sizes were determined manually in relation to the internal size standard and the sei whale's DNA of known size that were rerun on each gel. The PCR products collected after 2013 were electrophoresed on an ABI 3500 DNA Analyzer (Applied Biosystems), and allele sizes were determined using a 600 LIZ size standard (Applied Biosystems) and GeneMapper v. 4.0 (Applied Biosystems). Microsatellite scores from the latter platform were standardized according to those from the former for each locus.

Data analyses

First searches for parent-offspring pairs and resampled whales in the dataset were conducted based on the microsatellite profiles and mtDNA haplotypes. Three re-sampled whales and three calves sampled with their mothers at the same time/area were found. These six samples were excluded from all subsequent analyses to ensure independence within the dataset. In addition to this, nine samples with mtDNA sequencing errors and thirteen samples with microsatellite genotyping errors at more than six loci were also excluded from each of the mtDNA and microsatellite analyses, respectively.

In order to examine genetic variations and stock structure of this species, three sampling areas, i.e., western (–150°E), central (150°E–180°) and eastern (180°–) areas, (Table 1 and Figure 1) were defined as sample populations, taking into account the discussion on management units for the North Pacific sei whale that took place in the IWC SC (IWC, 2018a). In the statistical analyses, FDR corrections (Benjamini and Hochberg, 1995) were used to adjust the significance level for all multiple comparisons.

Considering a long time series of sample collection of over more than 40 years, genetic variations, i.e., haplotype diversity (h) and nucleotide diversity (π) for mtDNA and number of alleles (A), Hardy Weinberg equilibrium (HWE), expected heterozygosity (HE) and the inbreeding coefficient (FIS) for microsatellites, were preliminarily assessed per year in each of the areas. Additionally, pairwise FST estimates for both markers were calculated between years in each area, and AMOVA analyses were performed with a definition of population groups and populations to be areas and years, respectively. Tests for differences in haplotype and allelic frequencies were also conducted among years in each area. These analyses were conducted only for strata with more than ten individuals.

Genetic variations for mtDNA were investigated using π and h (Nei, 1987) with sample standard deviations being estimated using the program ARLEQUIN v. 3.5.1.2 (Excoffier and Lischer, 2010).

For microsatellite DNA, A and HE for each locus and across loci were estimated using the program ARLEQUIN. The FIS (Weir and Cockerham, 1984) in each locus and across loci was estimated using the R package 'Demerelate' (Kraemer and Gerlach, 2017). The departure from HWE was tested for each locus using the R package 'HWxtest' (Engels, 2009), and a global test across loci combining the observed P-values in each locus by Fisher's method was performed using the R package 'metap' (Dewey, 2018).

Genetic differentiation between areas and structuring was assessed by:

- The conventional pairwise FST for mtDNA and FST-like estimates for microsatellites using 10,000 random permutations of the original dataset in the program ARLEQUIN.
- Tests of mitochondrial haplotype frequency among areas using the Monte Carlo simulation-based chi-square test of independence (Roff and Bentzen, 1989) in R. A probability test implemented in the program GENEPOP (Rousset, 2008) was used to detect any genetic heterogeneity in microsatellite allele frequency among areas.
- Analysis of Molecular Variance (AMOVA) implemented in the program ARLEQUIN for both markers, to examine the hierarchical genetic structure, with a group definition of 'coastal' consisting of the western area and 'pelagic' containing central and eastern areas.
- Bayesian clustering analysis using microsatellite data to infer the most likely number of clusters using STRUCTURE 2.3.4 (Pritchard *et al.*, 2000). The analysis was conducted with ten independent runs for K = 2–3. All runs were performed with 100,000 Markov chain Monte Carlo repetitions and 10,000 burn-in length using the admixture model with correlated allele frequencies. The web-based program STRUCTURE HARVESTER (Earl and vonHoldt, 2012) was used to estimate the mean posterior probability of the data.

Results

Details of the results are shown in Appendix 7 of Tamura *et al.* (2019). The main results may be summarized as follows:

- For both markers and for each area, tests failed to reveal any significant yearly heterogeneity in the areas investigated.
- The h and π values were very similar among areas, ranging from 0.908 in the western area to 0.927 in the eastern area, and from 0.789 in the western area to 0.803 in the central area, respectively. The HE at each locus and across loci were not largely different among areas, and the estimates across loci ranged from 0.632 in the western area to 0.639 in the eastern area. Significant deviations from HWE were not evident for any loci and across loci in each area after FDR correction, which is consistent with the insignificant FIS estimates obtained.
- Pairwise FST-like estimates for microsatellites failed to find any significant genetic differentiations between areas, which was consistent with the results of pairwise conventional FST estimates for mtDNA. Heterogeneity tests also showed no significant differences in mtDNA haplotype and microsatellite allelic frequencies among areas.
- AMOVA analysis showed that most of the genetic variations occurred within areas for both markers, which suggests a possible high gene flow across the survey area.
- The clustering patterns for each K estimated by the program STRUCTURE also did not suggest a distinct genetic structuring of this species.

The three genetic analyses for both markers, i.e., pairwise FST estimates, heterogeneity tests and AMOVA analysis, failed to find any significant genetic differentiations among areas. This was consistent with the results of STRUCTURE analysis using the microsatellite DNA data. These findings imply that there is a single stock of sei whales in the pelagic region investigated (Figure 1).

4.1.2 Review of non-genetic studies

Kanda *et al*. (2015b) reviewed the non-genetic information on stock structure of sei whales in the North Pacific. Five of eight Discovery-type marks recaptured in coastal Japanese waters between 1959 and 1975 moved from the far offshore waters, such as the south of Aleutian archipelago. These showed direct evidence of the interchange of animals between the North Pacific pelagic and Japanese coastal waters. Whales marked in lower latitudinal breeding areas at the same time in winter were recaptured throughout the longitudinal range concerned in the high latitudinal waters of the North Pacific including Japanese coast in summer.

Kanda *et al*. (2015b) showed that a gap in catch positions from about 150°E to 160°E does not reflect a break in whale distribution as it is a consequence of the manner in which commercial whaling was regulated. Sighting data from JARPNII fills this gap. Sighting positions from JARPNII and IWC-POWER show that sei whales are distributed continuously across the North Pacific. This is further confirmed by the results of spatial modeling (Murase *et al*., 2014).

The non-genetic information reviewed by Kanda *et al*. (2015b) is consistent with the hypothesis of a single stock in the North Pacific.

Mizroch *et al*. (2015) reviewed Discovery-type marks, seasonality and sighting data and suggested that the data are consistent with a hypothesis of five stocks in the North Pacific: Pelagic, Japanese coastal, Aleutian Islands/Gulf of Alaska, Eastern North Pacific migratory and Southern North American (California coastal). The proposed ‘Pelagic’ stock corresponds approximately to the area covered by the genetic analyses (see Figure 1).

4.1.3 Hypotheses on stock structure

For assessment purposes, the IWC SC decided to proceed with two hypotheses on stock structure:

Hypothesis 1: a single stock in entire North Pacific; and
Hypothesis 2: a five-stock hypothesis: Japan coastal; North Pacific Pelagic; Aleutian/Gulf of Alaska; northeast Pacific migratory; and California coastal.

In 2016 the IWC SC Subcommittee on *In-depth Assessments* considered that the evidence for the proposed five-stock hypothesis was weak, being based mainly on circumstantial considerations such as differential recovery in abundance in the different regions, with only limited support from marking data. Furthermore, it noted that the lack of genetic samples from four of the five putative stocks was a major information gap (IWC, 2017a).

Genetic analyses of samples from JARPNII taken west and east of 150°E (which is the primary putative boundary between the pelagic stock and a putative western coastal stock) show no significant differences, suggesting that sei whales in the pelagic area belong to the same stock as whales near to Japan (see Appendix 7 of Tamura *et al*., 2019).

Based on the information on stock structure reviewed above it can be concluded that the hypothesis of a single stock of sei whales in the North Pacific (Hypothesis 1) carries strong support while the evidence for Hypothesis 2 is extremely weak and hence should be considered to have only very low plausibility. Therefore, only Hypothesis 1 has been considered in the catch limit calculations.

4.1.4 *Definition of management areas*

The management area was defined based on Hypothesis 1 above. A single *Small Area*[2] was specified for the North Pacific, which coincides with the areas covered by the sighting surveys (the part in blue in Figure 2).

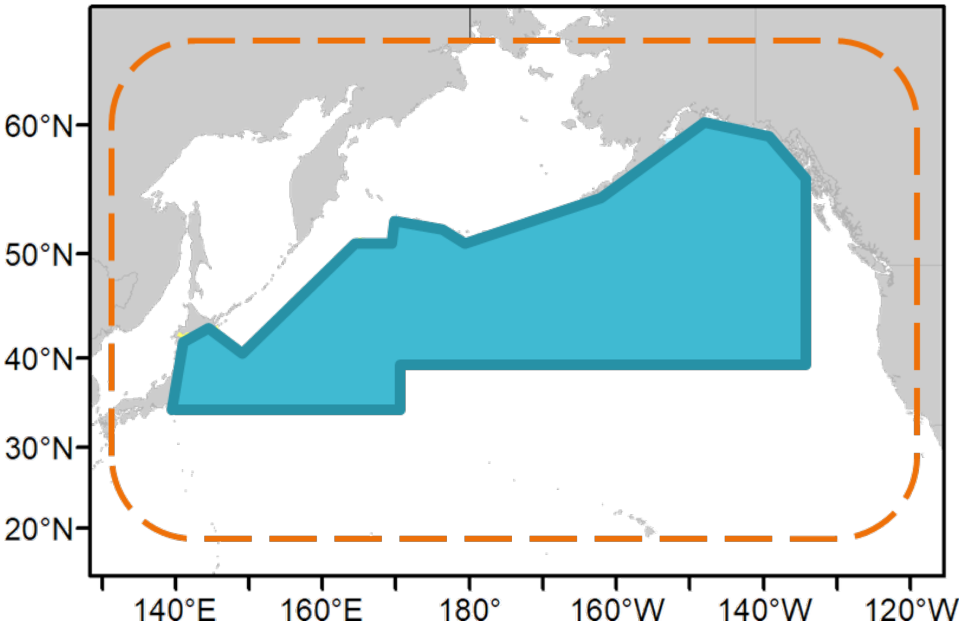

Figure 2. Specification of a *Small Area* for North Pacific sei whale (in blue).

Abundance estimates were computed for this *Small Area*; however the catch history was computed for the whole North Pacific, which reflects a conservative approach.

4.2 Abundance estimates

Abundance estimates were obtained from sighting data collected during systematic sighting surveys using the Line Transect Method. Surveys have been conducted in a systematic manner over time and in general follow the survey design guidelines of the IWC SC, as does their analysis (IWC, 2012a). Sighting data used for the abundance estimates of sei whales come from two sources: JARPNII surveys and IWC-POWER surveys.

4.2.1 *Data*

JARPNII sighting survey were conducted in 2008, 2009, 2011 and 2012 (Tamura *et al*., 2009; Bando *et al*., 2010; Tamura *et al*., 2012; Bando *et al*., 2013). All these surveys apart from that in 2008 were conducted in May-June. The survey in 2008 was conducted July-August. The IWC-POWER sighting surveys were conducted during 2010-2012 (IWC, 2012b; 2013; 2014a). All these surveys were conducted in July-August.

The abundance estimates used for the application of the CLA were based on the surveys conducted in July-August, i.e. the 2008 JARPNII survey and the 2010-2012 IWC-POWER surveys. Figure 3 shows the track-lines and the geographical distribution of the sei whale primary sightings for these surveys.

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[2] Catch limits are calculated by applying the CLA to '*Small Areas*', which are disjoint areas small enough to contain whales from only one biological stock, or be such that if whales from different biological stocks are present in a *Small Area*, catching operations would not be able to harvest them in proportions substantially different to their proportions in that *Small Area*. See more details on RMP terminology and definitions in IWC (2012c).

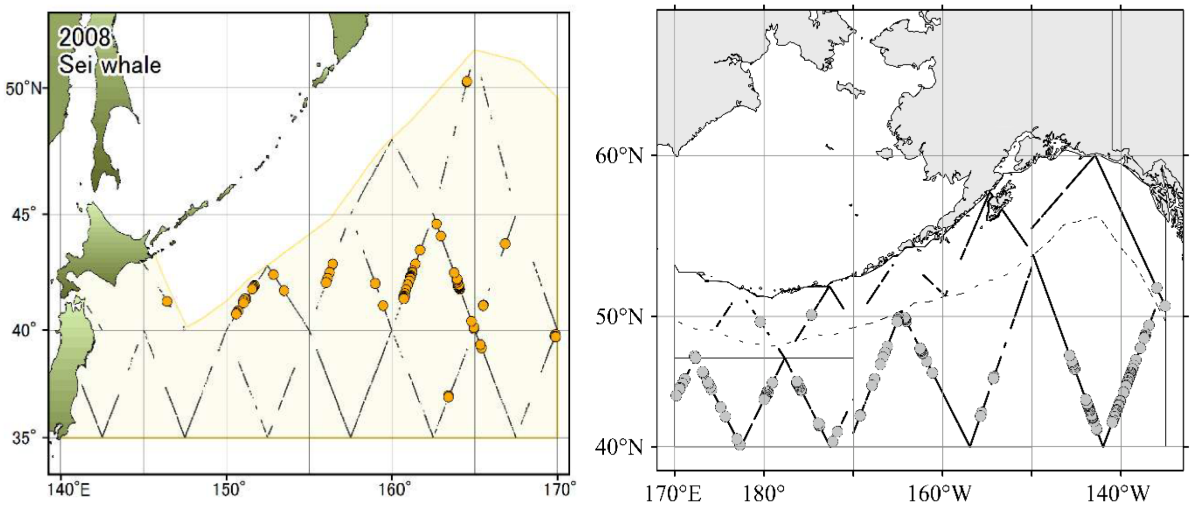


Figure 3. Surveyed track-lines and position of primary sightings of sei whales for the JARPNII survey conducted in 2008 (left), and IWC-POWER surveys conducted over 2010-12 (right). All these surveys were conducted in July-August.

4.2.2 Analytical procedures

Details of the analytical procedures used to calculate abundance estimates are given in Hakamada and Matsuoka (2016) for the JARPNII survey data and in Hakamada *et al*. (2017) for the IWC-POWER survey data.

Basically, the distance sampling method is applied to estimate abundance. Abundance and its CV have been estimated based on a Horvitz-Thompson-like estimator. The computations were conducted truncating the detections at 3.0 n.miles perpendicular distance for this species as is conventional, and the probability to detect this species on the track line was assumed to be 1 (g(0)=1). Hazard Rate and Half-normal models were considered as candidate models for the detection function. In order to consider the effect of covariates such as Beaufort state, school size and year on estimated detection functions, the MCDS (Multiple Covariates Distance Sampling) engine in the DISTANCE program was used. The best model was selected as the case for which the AIC value was smallest. However, if the difference in AIC for the fiotted detection functions was not substantially different among the models, the weighted average (using Akaike weights) was estimated (Buckland *et al*., 1997; Burnham and Anderson, 2002).

4.2.3 Results

Results of the abundance estimates are shown in detail in Hakamada and Matsuoka (2016) and Hakamada *et al.* (2017) for the JARPNII and IWC-POWER surveys, respectively. Table 2 below summarizes those results.

Table 2. Abundance estimates for North Pacific sei whales based on two data sources, IWC-POWER (for the central and eastern North Pacific) and JARPNII (for the western North Pacific).

	Year	*P*	CV(*P*)
POWER	2011	29,632	0.242
JARPNII	2008	5,086	0.378
Total	2010	34,718	0.214

4.3 Catch history

The catch series used for sei whales corresponds to the whole North Pacific. Table 3 reproduces this North Pacific sei whale catch series, as used during the *in-depth assessment* of North Pacific sei whales by the IWC SC. Details are given in Appendix 7 of IWC (2019b).

Table 3. Catch history for North Pacific sei whale (IWC, 2019).

Year	North Pacific	Year	North Pacific	Year	North Pacific
1906	16	1935	297	1964	3611
1907	43	1936	264	1965	3188
1908	101	1937	322	1966	3699
1909	58	1938	393	1967	5046
1910	105	1939	485	1968	4954
1911	217	1940	323	1969	4784
1912	155	1941	496	1970	3816
1913	239	1942	235	1971	2731
1914	202	1943	325	1972	2311
1915	557	1944	683	1973	1856
1916	320	1945	62	1974	1280
1917	545	1946	447	1975	508
1918	725	1947	431	2001	1
1919	983	1948	547	2002	40
1920	482	1949	760	2003	50
1921	385	1950	351	2004	100
1922	189	1951	465	2005	100
1923	471	1952	823	2006	101
1924	634	1953	748	2007	100
1925	447	1954	982	2008	100
1926	484	1955	708	2009	101
1927	436	1956	1027	2010	100
1928	255	1957	839	2011	96
1929	377	1958	1248	2012	100
1930	437	1959	1513	2013	100
1931	286	1960	832	2014	90
1932	264	1961	771	2015	91
1933	266	1962	1821	2016	90
1934	222	1963	2440	2017	134

4.4 Catch limit

The CLA was applied to the *Small Area* specified (Figure 2), which coincides with the geographical sectors covered by the sighting surveys. Abundance estimates are computed for the *Small Area* but the catch history is computed for the whole the North Pacific, which is a conservative approach. Table 4 shows the results of the catch limits computed using the CLA for the tuning level of 0.6. Adjustment for differences in sex ratio is required because females represent a larger proportion than males in the previous catches for this species.

Table 4. Catch limit for North Pacific sei whale based on the CLA with a tuning level of 0.6, adjusted for differences in sex ratio.

Tuning level	Catch limit	Catch limit adjusted for sex ratio
0.6	202	174

4.5 Testing for uncertainties (*ISTs*)

Since the North Pacific sei whales are considered to comprise a single stock, the situation corresponds to that for which the original CLA was developed by the IWC SC. Hence no *ISTs* need be considered for this species (the robustness of the output has already tested and verified through the simulation process used for adopting the original CLA).

4.6 Whaling operations and future surveys

Whaling is proposed to be conducted in the EEZ of the Pacific side of Japan based on the catch limit adjusted for sex ratio listed in Table 4, with whaling taking place during all months of the year. Future sighting surveys in sub-areas 7, 8 and 9 will be in line with those planned for common minke whales (see section 6.5.4). Plans for sighting surveys in the central and eastern North Pacific are being considered as well. Collection of biological data and samples from harvested whales will be conducted for monitoring the stock.

5. WESTERN NORTH PACIFIC BRYDE'S WHALE

5.1 Stock structure and definition of management areas

The IWC SC conducted RMP *Implementation Reviews* of the western North Pacific Bryde's whale which concluded in 2007 and 2019. Figure 4 show the sub-areas used during these *Implementations*.

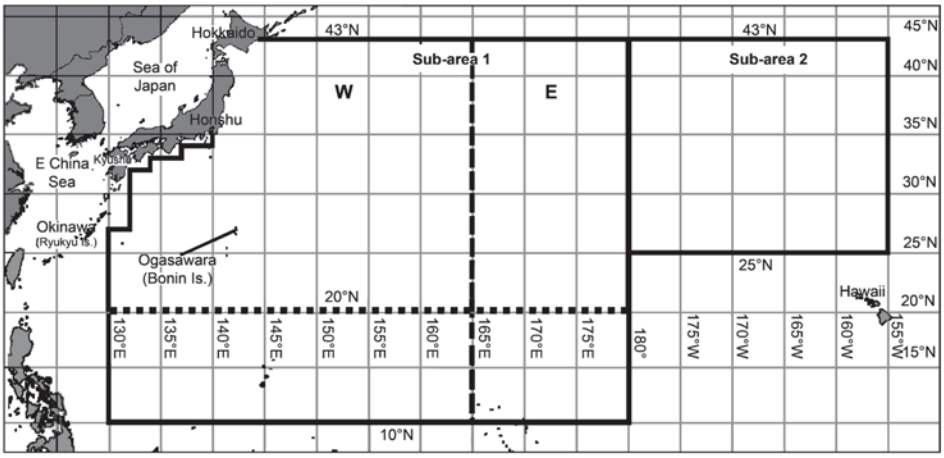


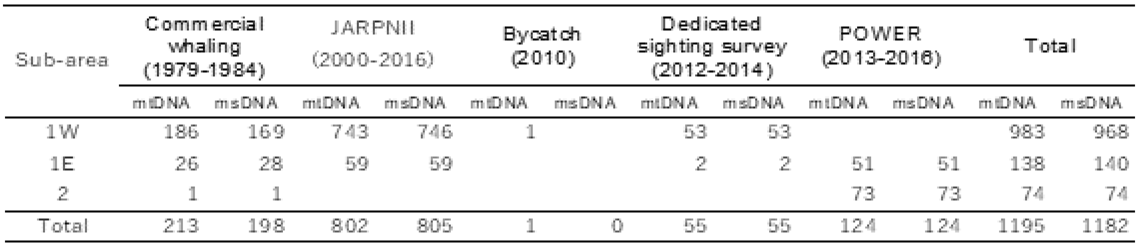
Figure 4. Definition of sub-areas used during the RMP *Implementations* for the North Pacific Bryde's whale by the IWC SC (IWC, 2008; 2018b).

5.1.1 Review of genetic studies

Genetic analyses on the stock structure of North Pacific Bryde's whale have been conducted based on the comprehensive data set held by the Institute of Cetacean Research (ICR). Genetic samples are from five different sources: past commercial samples, IWC-POWER surveys, JARPNII surveys, Japanese dedicated surveys and by-catch (Table 5 and Figure 5). Initial genetic studies based on mitochondrial DNA (mtDNA) and microsatellite DNA focused on samples from sub-area 1. These studies failed to find significant genetic heterogeneity within this sub-area (Pastene *et al.*, 1997; Kanda *et al.*, 2007). Genetic analyses conducted since 2016 have been based on a larger number of samples from both sub-areas 1 and 2, and these studies revealed significant genetic heterogeneity in those sub-areas, which has been associated with additional stock structure (Pastene *et al.*, 2016b; 20016c; Taguchi *et al.*, 2017).

The most recent study is presented in Tamura *et al.* (2019) (Appendix 6), which is described in more details below. Table 5 gives details of the sampling and Figure 5 shows the geographical distribution of the genetic samples.

Table 5. Number and period of collection of genetic samples analyzed of North Pacific Bryde's whale, by area, source and genetic marker. Parent-offspring and re-sampled whales are excluded from the numbers in this table.



Sub-area	Commercial whaling (1979-1984)		JARPNII (2000-2016)		Bycatch (2010)		Dedicated sighting survey (2012-2014)		POWER (2013-2016)		Total	
	mtDNA	msDNA	mtDNA	msDNA	mtDNA	msDNA	mtDNA	msDNA	mtDNA	msDNA	mtDNA	msDNA
1W	186	169	743	746	1		53	53			983	968
1E	26	28	59	59			2	2	51	51	138	140
2	1	1							73	73	74	74
Total	213	198	802	805	1	0	55	55	124	124	1195	1182

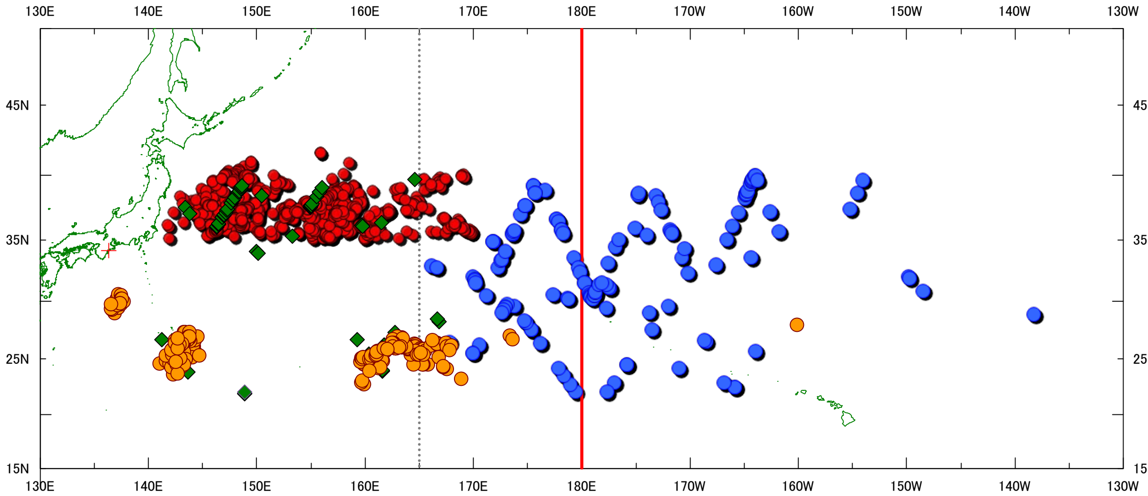


Figure 5. Geographical distribution of genetic samples for North Pacific Bryde's whale. Red: JARPNII surveys (catches); Green: dedicated sighting surveys (biopsy); Blue: IWC POWER surveys (biopsy); Yellow: past commercial whaling; Red cross: bycatch.

DNA extraction, mtDNA sequencing and microsatellite genotyping was as in the case of sei whales. The set of 17 microsatellites used in the case of the Bryde's whale was the following: EV1, EV14, EV21, EV94, EV104 (Valsecchi and Amos, 1996), GT011 (Bérubé *et al*., 1998), GT23, GT310, GT575 (Bérubé *et al*., 2000), GATA28, GATA53, GATA98, GATA417, GGAA520, TAA31 (Palsbøll *et al*., 1997), and DlrFCB14 and DlrFCB17 (Buchanan *et al*., 1996).

Data analysis

First searches for parent-offspring pairs and resampled whales in the dataset were conducted based on the microsatellite profiles and mtDNA haplotypes. Four re-sampled whales and 21 calves sampled with their mothers at the same time/area, were found. These 25 samples were excluded from all subsequent analyses to ensure independence within the dataset.

In order to examine genetic variations and stock structure for this species, three sub-areas, i.e., sub-areas 1W (–165°E), 1E (165°E–180°) and 2 (180°–) (Table 5 and Figures 4-5) were treated as potentially distinct populations based on the *Implementation Review* for the North Pacific Bryde's whale in 2017 (IWC, 2018b). In the statistical analyses, FDR corrections (Benjamini and Hochberg, 1995) were made to adjust the significance level for all multiple comparisons.

Considering the long time series of sample collection of over 37 years and the seasonal migration of this species, genetic variations, i.e., AR, HWE, HE and FIS for microsatellite and h and π for mtDNA, in each area were preliminary estimated in terms of the temporal strata reflected by three periods, i.e., until the 1980s, the 2000s and the 2010s, and for two seasons, i.e., April-June and July-October. Additionally, pairwise FST estimates for both markers were calculated among the strata in each area, and AMOVA analyses were performed with the definition of groups and populations to be in terms of these periods and seasons, respectively. Possible differences in allelic and haplotype frequencies were also checked by testing among the strata in each area. Those analyses were conducted only for strata with more than ten individuals.

Genetic variation for mtDNA was investigated by examining π and h using the program ARLEQUIN v. 3.5.1.2 (Excoffier and Lischer, 2010).

Genetic variations for microsatellite DNA were investigated by the allelic richness (AR) and inbreeding coefficient (FIS; Weir and Cockerham, 1984) per locus and across loci in each sub-area using the R package 'diveRsity' (Keenan *et al*., 2013), and their 95% confidence limits were calculated from 10,000 bootstrap replicates. The expected heterozygosity (HE) for each locus and across loci was estimated using the program ARLEQUIN v. 3.5.1.2 (Excoffier and Lischer, 2010). The possibility of departure from Hardy-Weinberg equilibrium (HWE) was tested using the GENEPOP 4.2 (Rousset, 2008).

Genetic differentiation between areas and structuring was evaluated by:

- The conventional pairwise FST for mtDNA and FST-like estimates for microsatellites using 10,000 random permutations of the original dataset in the program ARLEQUIN.
- Tests of mitochondrial haplotype frequency among areas using the Monte Carlo simulation-based chi-square test of independence (Roff and Bentzen, 1989) in R. A probability test implemented in the program GENEPOP (Rousset, 2008) was used to detect the genetic heterogeneity in microsatellite allele frequency among areas.
- An Analysis of Molecular Variance (AMOVA) to examine the hierarchical genetic differentiation among areas. In this analysis, statistical significance of the pairwise FST estimates and heterogeneity tests were used to divide the survey area into two sub-area groups: Group 1 including sub-areas 1W and 1E and Group 2 containing sub-area 2.
- A Bayesian clustering analysis using microsatellite data to infer the most likely number of clusters using STRUCTURE 2.3.4 (Pritchard *et al*., 2000). The analysis was conducted with ten independent runs for K= 1–3. All runs were performed with 100,000 Markov chain Monte Carlo repetitions and a 10,000 burn-in length using the admixture model with correlated allele frequencies. The web-based program STRUCTURE HARVESTER (Earl and vonHoldt, 2012) was used to estimate the mean posterior probability of the data.
- A Discriminant Analysis of Principal Component (DAPC; Jombart *et al*., 2010) to identify and describe clusters of genetically related individuals, using *a priori* geographical group assignments based on the sampling area and microsatellite data at K = 3, i.e., sub-areas 1W, 1E and 2, in the R package 'adegenet'.
- Genetic variations along a longitudinal cline using genetic statistics, i.e., first and second principal components (PCs) of the DAPC, FIS, and h (calculated for 2.5° longitudinal intervals and plotted as moving averages over 5° intervals).

Results

Details of the results are shown in Appendix 6 of Tamura *et al*. (2019). The main results are summarized below.

- Tests failed to detect any significant temporal (period and season) genetic heterogeneity in all sub-areas.
- Significant deviations from HWE were not observed for any loci or sub-areas. AR and HE at each locus were not largely different among sub-areas, ranging from 6.63 to 7.07 (average over loci for AR) and from 0.677 to 0.689 (average over loci for HE). Although FIS estimates for over all loci in sub-area 2 were lower than in sub-area 1E, the 95% confidence intervals for both estimates contained zero, suggesting that the FIS values were not different from zero. The h and π values were similar among sub-areas, ranging from 0.82 to 0.89 and from 0.009 to 0.013 respectively.
- Pairwise FST estimates for microsatellites suggested significant differentiation of Bryde's whales not only between areas 1W and 2, but also between areas 1E and 2, and pairwise conventional FST estimates for mtDNA statistically supported a genetic difference between areas 1W and 2. Heterogeneity tests for all pairs of sub-areas showed significant differences in microsatellite allele and mitochondrial haplotype frequencies between sub-areas 1W and 2, and between sub-areas 1E and 2. However, the tests failed to reveal significant differences between sub-areas 1W and 1E.
- AMOVA analyses for both markers showed high genetic variation within sub-areas and low genetic differentiation between sub-areas as well as among sub-area groups, which suggested high genetic diversity in each sub-area and a possible gene flow across the sub-areas examined.

- The clustering patterns in each K estimated by the program STRUCTURE did not indicate a distinct genetic structuring for this species.
- The DAPC analysis showed that a few separations of sub-area 2 from 1W and 1E were evident along the first discriminant function axis, but substantial overlap among geographical clusters remained.
- Moving averages for three quantities, i.e., PC 1 from the DAPC analysis, FIS and h, for four statistics gradually changed along a longitudinal cline, which showed the positive PC, and the lower FIS and higher h in sub-area 2 than 1W, with a boundary somewhere in area 1E.

All analyses conducted showed no evidence of genetic differentiation between sub-areas 1W and 1E, which was consistent with results of previous studies (Wada and Numachi, 1991; Wada, 1996; Pastene *et al*., 1997; Kanda *et al*., 2007) which had suggested a lack of genetic differentiation within sub-area 1. However, significant differences were found between sub-areas 1 and 2, with larger differences between sub-areas 1W and 2.

Based on the results above it is postulated that weakly differentiated stocks occur in these sub-areas, with one stock occurring in sub-area 1 and the other in sub-area 2 with possible mixing in sub-area 1E.

5.1.2 Review of non-genetic studies

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 at the end of 1987 season. A total of 537 whales were effectively marked by the Japanese marking programme during the years 1972 to 1985. Whale marking programmes took place from January to November in latitudes 1°S to 45°N, while whaling operated from April to October in latitudes 22°N to 43°N. A total of 52 marked whales (including one whale marked by the USSR) had been recaptured by the end of 1987. Twelve whales marked between January and March in the western tropical Pacific were recaptured between April-July off the Pacific coast of Japan (2 whales), off the Bonin Islands (3) and in the pelagic grounds (7). Three whales marked in the same season (January to March) in the higher latitudes around 25°N were recaptured in later months at almost the same latitudes. The data suggest that Bryde's whales summering in the whaling grounds, winter over a wide latitudinal range (1°S to 25°N). The study did not find evidence for more than one stock of Bryde's whales in the western North Pacific whaling grounds (mainly sub-area 1).

Murase *et al*. (2016) reported the movement 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 recorded for 13 days 4 hours 57 minutes from 13 to 26 July 2006. The other whale was recorded for 20 days 5 hours 5 minutes from 24 July to 13 August 2008. It has been documented that the subarctic-subtropical transition area (around 40°N) is one of the feeding areas for Bryde's whales in summer. However, the results of this study revealed that some Bryde's whales move from the subarctic-subtropical transition area to the sub-tropical area even in summer. This study provided the first information about continuous movement of Bryde's whales in the offshore western North Pacific in summer.

Results of these marking studies do not contradict the results of genetic studies.

5.1.3 Hypotheses concerning stock structure

From the information on stock structure reviewed above, two stock structure hypotheses (called 'Hypothesis 2' and 'Hypothesis 5', respectively) for the central and western North Pacific have been considered highly plausible by the IWC SC *Implementation Review* in 2019.

Hypothesis 2: one stock (west stock) distributes in sub-area 1 and the other stock (east stock) distributes in sub-area 2 with no spatial mixing;

Hypothesis 5: as in 1 above but both stocks mix in sub-area 1E, where there is a preponderance of the west stock.

Japan consider that these two IWC SC hypotheses are supported by sound science; therefore both hypotheses are considered below in the definition of management areas.

5.1.4 Definition of management areas

Based on the two stock structure hypotheses above, the following management areas were defined: i) 1W+1E (Figure 4) is a *Small Area*, and ii) sub-area 1 is a *Combination Area*[3]. Abundance estimates and catch history were computed according to these definitions for *Small Areas*.

It should be noted that both inshore and offshore forms of Bryde's whales occur in the western North Pacific. However, the distribution of the inshore form is restricted to coastal waters inside the Kuroshio Current, and this region is not included in the *Small Areas* defined above. The inshore form of this species is not subject to commercial whaling. The *Small Areas* so defined relate to the larger, offshore form of Bryde's whales, which is distributed outside the Kuroshio Current (see Figure 4).

5.2 Abundance estimates

Abundance estimates were based on sighting data collected during systematic sighting surveys designed for application of the Line Transect analysis Method. Surveys have been conducted in a systematic manner through the years and in general follow the survey design and analytical procedure guidelines of the IWC SC (IWC, 2012a). Sighting data used for the abundance estimates of Bryde's whales come from three sources: Japanese dedicated sighting surveys, JARPNII surveys and IWC-POWER surveys.

5.2.1 Data used

Abundance estimates were based on sighting data collected during Japanese sighting surveys in two periods (1988-1995 and 1998-2002) (Shimada and Miyashita, 1997; 1999; Shimada, 2004; Shimada et al., 2008); JARPNII sighting surveys (2008, 2012 and 2014) (Tamura *et al*., 2009; Matsuoka *et al*., 2013; 2015b); and IWC-POWER sighting surveys (2013-2016) (Matsuoka *et al*., 2014; 2015a; 2016).

The abundance estimates for the purpose of the application of the CLA were based on the surveys conducted in July-September.

Figures 6 and 7 shows the track-lines and the geographical distribution of the Bryde's whale primary sightings on Japanese sighting surveys for two periods. Figure 8 shows the track-lines and the geographical distribution of the Bryde's whale primary sightings during the JARPNII and IWC-POWER surveys combined.

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[3] Catch limits are calculated by applying the CLA to '*Small Areas*' or, where appropriate, to *Combination Areas* (disjoint unions of *Small Areas*) when *Catch-cascading* (process by which a catch limit calculated for a *Combination Area* is distributed among the *Small Areas* that make up the *Combination Areas* in proportion to the calculated relative abundance in those *Small Areas*) is used. See more details on RMP terminology and definitions in IWC (2012c).

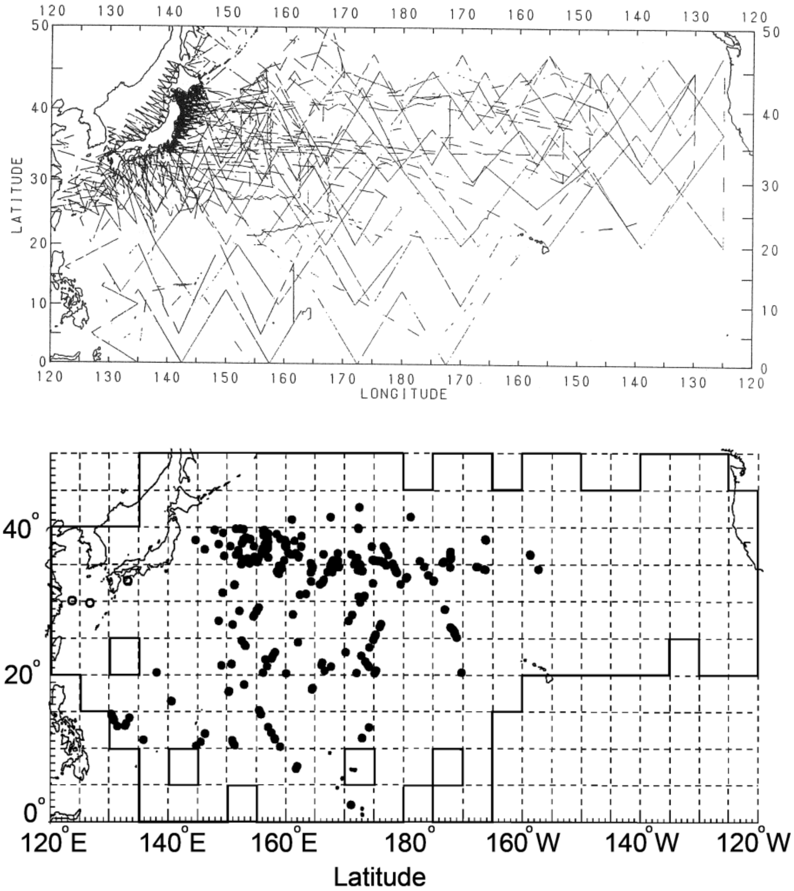


Figure 6. Track-lines (above) and positions of primary sightings (below) of Bryde's whales in August and September during surveys over 1988-95 (Shimada and Miyashita, 1996).

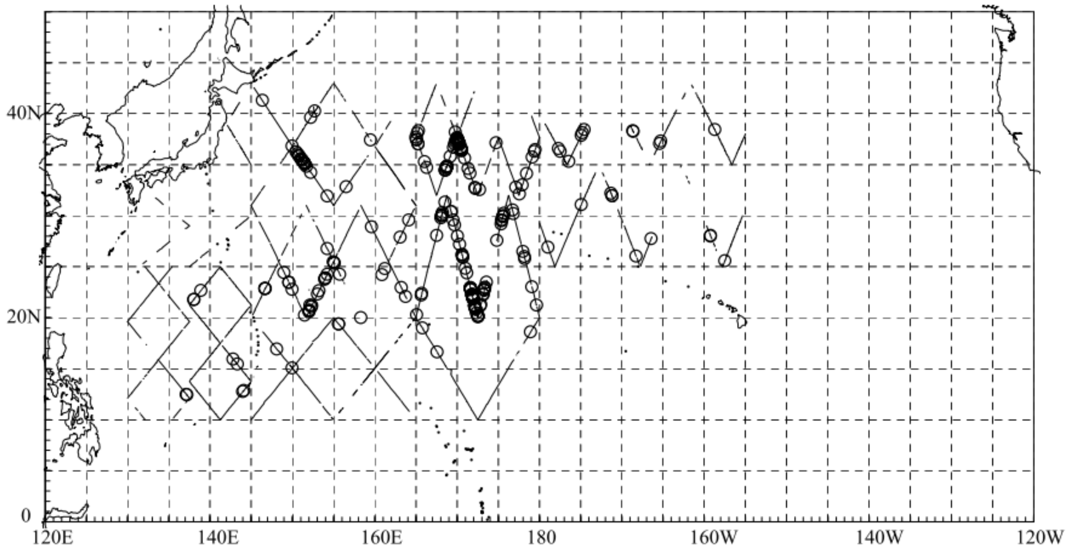


Figure 7. Track-lines and position of primary sighting of Bryde's whales in August and September during surveys over 1998-2002 (Shimada *et al*., 2008).

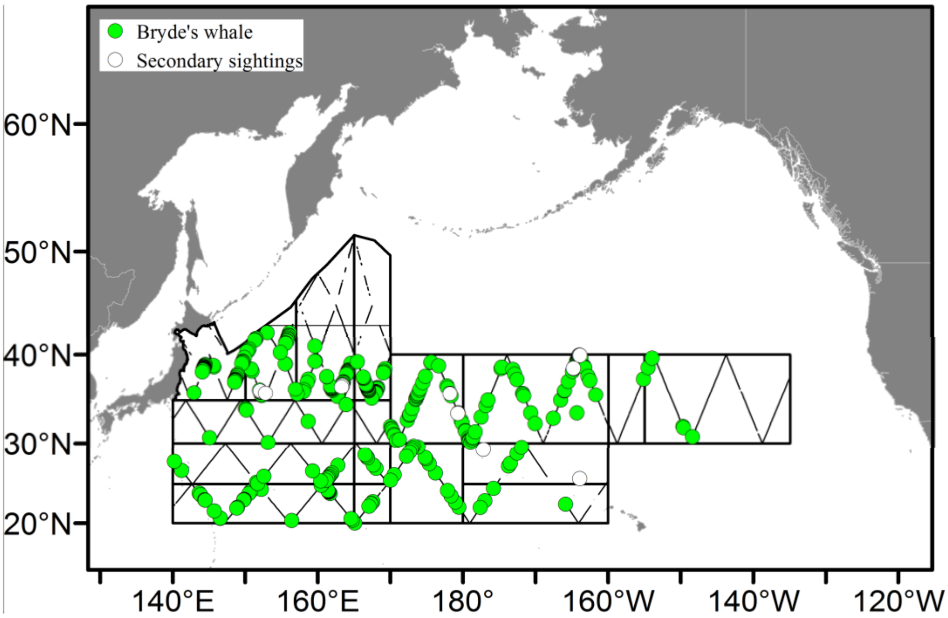


Figure 8. Track-lines and position of primary and secondary sighting of Bryde's whales in July-September in 2008, 2012, 2013, 2014 and 2015 (JARPNII and IWC-POWER data combined).

There are three series of abundance estimates used with the following time stamps (IWC, 2018b):

1. The original series used in the 2007 *Implementation* that took place during 1988-96 and was time stamped at 1995.
2. A series agreed to by the SC (IWC, 2009) for use in the *CLA* which took place over 1998-2002 (Kitakado *et al*., 2008) and was time stamped at 2000.
3. A new series using data collected during 2008-2015 (Hakamada *et al*., 2017) which was time stamped at 2011.

5.2.2 Analytical procedures including g (0) estimates

Details of the analytical procedures are given in Shimada and Miyashita (1997), Kitakado *et al*. (2007) and Kitakado *et al*. (2008) for the Japanese sighting surveys', and in Hakamada *et al*. (2017) for the JARPNII-IWC-POWER surveys' data. For g(0)-corrected abundance estimates, details are given in Hakamada *et al*. (2018).

Basically, the distance sampling method was applied to estimate abundance. Abundance and its CV were estimated based on a Horvitz-Thompson like estimator. The detections were truncated at 3.0 n.miles for this species according to convention, and the probability to detect this species on the track line g(0) was not assumed to be 1 (see below). Hazard Rate and Half-normal models were considered as candidates for the detection function. In order to take account of the effect of covariates such as Beaufort state, school size and year on the detection functions estimated, the MCDS (Multiple Covariates Distance Sampling) engine in the DISTANCE program was used. The best model was selected in cases where the AIC value was clearly the lowest. However, if the difference in AIC for the detection functions fitted was not substantially different among the models, the weighted average using Akaike weights was calculated (Buckland *et al*., 1997; Burnham and Anderson, 2002).

g(0) estimate

To obtain this estimate, IO mode data collected during the 2015 and 2016 IWC-POWER surveys were used (Hakamada *et al*., 2018). Mark-Recapture (MR) and the distance sampling (DS) models (Hazard rate and Half normal detection functions were considered) were used in combination (MRDS). MRDS methods are described in Laake and Borchers (2004) and Burt *et al*. (2014). The analyses were conducted using the library MRDS in R-DISTANCE (Thomas *et al*., 2010). Hakamada *et al*. (2018)

assumed that the only covariate that needs to be considered in both (MR, DS) models is Beaufort Sea state. Further, following suggestions from the Intersessional workshop on the North Pacific Bryde's whale *Implementation Review*, a weighted harmonic mean of the g(0) estimates under good (g(0)= 0.899 (SE: 0.255)) and bad (g(0)= 0.543 (SE:0.208)) Beaufort sea state was calculated for each sub-area (see Table 6 of Hakamada *et al*., 2018).

Additional variance estimation

The issue of the process error or additional variance arises from the fact that the estimated sampling variances for the abundance estimates do not account for all the variability of these estimates, especially due to inter-annual changes in distribution of the whale population in the areas surveyed. If the additional variance is ignored, the uncertainty of abundance estimates will tend to be underestimated. An estimate of the extent of the process error, expressed as an additional CV, was estimated in the manner detailed in Hakamada *et al*. (2017).

5.2.3 Results

Results for these abundance estimates are shown in detail in several studies (Kitakado *et al*., 2007; Kitakado *et al*., 2008; Hakamada *et al*., 2017). These estimates took account of information on additional variance obtained previously. The *g*(0)-corrected abundance estimates in Hakamada *et al*. (2018) are summarized in Table 6.

Table 6. Abundance estimates for North Pacific Bryde's whales, based on sighting data obtained during JARPNII and IWC POWER surveys, by IWC SC sub-area.

Year	Sub-area	g(0)-corrected	
		P	CV(*P*)
1995	1W	12,149	0.550
	1E	15,695	0.558
2000	1W	6,894	0.598
	1E	19,200	0.676
2011	1W	25,158	0.524
	1E	9,315	0.483

5.3 Catch history

Catch series used for the CLA calculations correspond to the 'best' series used in the IWC SC *Implementation Review* for the western North Pacific Bryde's whale (IWC, 2020) (Table 7).

Table 7. Catch history for the North Pacific Bryde’s whale, by sub-area (IWC, 2020).

Year	Sub-area 1 W	Sub-area 1 E	Sub-area 1	Year	Sub-area 1 W	Sub-area 1 E	Sub-area 1
1906	13	0	13	1961	167	0	167
1907	35	0	35	1962	504	0	504
1908	81	0	81	1963	210	0	210
1909	47	0	47	1964	68	0	68
1910	55	0	55	1965	8	2	10
1911	156	0	156	1966	55	3	58
1912	81	0	81	1967	45	0	45
1913	124	0	124	1968	171	3	174
1914	56	0	56	1969	89	16	105
1915	169	0	169	1970	73	11	84
1916	105	0	105	1971	217	284	501
1917	181	0	181	1972	84	63	147
1918	148	0	148	1973	592	51	643
1919	161	0	161	1974	709	306	1015
1920	92	0	92	1975	701	296	997
1921	89	0	89	1976	851	577	1428
1922	81	0	81	1977	787	150	937
1923	75	0	75	1978	490	293	783
1924	111	0	111	1979	1240	39	1279
1925	118	0	118	1980	755	0	755
1926	134	0	134	1981	485	0	485
1927	118	0	118	1982	482	0	482
1928	80	0	80	1983	545	0	545
1929	63	0	63	1984	528	0	528
1930	62	0	62	1985	357	0	357
1931	135	0	135	1986	317	0	317
1932	104	0	104	1987	317	0	317
1933	88	0	88	1988	0	0	0
1934	99	0	99	1989	0	0	0
1935	96	0	96	1990	0	0	0
1936	88	0	88	1991	0	0	0
1937	126	0	126	1992	0	0	0
1938	159	0	159	1993	0	0	0
1939	193	0	193	1994	0	0	0
1940	105	0	105	1995	0	0	0
1941	145	0	145	1996	0	0	0
1942	21	0	21	1997	0	0	0
1943	30	0	30	1998	1	0	1
1944	74	0	74	1999	0	0	0
1945	12	0	12	2000	43	0	43
1946	126	0	126	2001	50	0	50
1947	111	0	111	2002	50	0	50
1948	133	0	133	2003	50	0	50
1949	198	0	198	2004	44	7	51
1950	273	0	273	2005	50	0	50
1951	307	0	307	2006	38	13	51
1952	491	0	491	2007	48	2	50
1953	61	0	61	2008	50	0	50
1954	75	0	75	2009	35	15	50
1955	94	0	94	2010	36	14	50
1956	24	0	24	2011	46	4	50
1957	39	0	39	2012	31	3	34
1958	254	0	254	2013	28	0	28
1959	263	0	263	2014	25	0	25
1960	404	0	404	2015	25	0	25
				2016	26	0	26

5.4 Catch limit

Table 8 shows the results of the CLA applied to the management areas defined above i): sub-areas 1W+1E are a *Small Area*; and ii): sub-area 1 is a *Combination Area* with 1W and 1E each *Small Areas* and *Catch Cascading* applying.

As explained above, this catch limit applies to the larger, pelagic Bryde's whales, which is distributed outside the Kuroshio Current where whaling operation will be conducted. An adjustment for sex ratio was not required because the actual sex ratio in the catch of Bryde's whales is almost 50:50.

Table 8. Catch limits for the North Pacific Bryde's whale based on the CLA with a tuning level of 0.6, under two management options.

Tuning level	Option i	Option ii	
	SA1	SA1W	SA1E
0.6	187	100	87

5.5 Testing for the consequences of uncertainty (*ISTs*)

5.5.1 Trials scenario

For testing the consequences of the uncertainty associated with some basic information such as the stock hypotheses, stock boundaries and value of MSYR for the performance of the CLA, a total of 14 simulation trials listed in Table 9 was conducted. These trials were basically the same as those examined in the 2019 IWC SC *Implementation Review* for this population with the same numbering convention, but the CLA tuning level of 0.6 was used instead of 0.72.

We denote trial scenario using the format as BRnn-r (nn is the trial number and r is MSYR value assumed). The trials BR01 (stock hypothesis 2) and BR02 (stock hypothesis 5) were treated as baseline trials (see Figure 9 for explanation of these hypotheses). Trials BR03 (alternative numbers of the historical catches), BR04 (alternative value of the additional variance for abundance estimates), and BR05-07 (alternative boundary between stocks) were conducted for testing the consequences of uncertainties. All trials were conducted for both MSYR 1% (1+) and 4% (mature) (BRnn-1 or BRnn-4), and the results are treated as of Medium Weight (or plausibility) when deciding acceptability of the variants.

Table 9. List of candidate trials considered for domestic *ISTs* for the western North Pacific Bryde's whale, selected from the list of trials in the associated IWC SC *Implementation Review* (IWC, 2020).

Trial number	Stock hypotheses	*MSYR*[*1]	Additional variance	Catch series	Western Boundary of stock 2	Eastern Boundary of stock 1	Description	Trial weight
BR01-1	2	1%	Baseline	Baseline	180°	180°	Baseline stock scenario 2	M
BR01-4	2	4%	Baseline	Baseline	180°	180°	Baseline stock scenario 2	M
BR02-1	5	1%	Baseline	Baseline	165°E	180°	Baseline stock scenario 5	M
BR02-4	5	4%	Baseline	Baseline	165°E	180°	Baseline stock scenario 5	M
BR03-1	5	1%	Baseline	High	165°E	180°	Stock scenario 5 with high catches	M
BR03-4	5	4%	Baseline	High	165°E	180°	Stock scenario 5 with high catches	M
BR04-1	5	1%	Upper CI	Baseline	165°E	180°	Stock scenario 5 with higher additional variance	M
BR04-4	5	4%	Upper CI	Baseline	165°E	180°	Stock scenario 5 with higher additional variance	M
BR05-1	2	1%	Baseline	Baseline	175°E	175°E	Stock scenario 2 with alternative boundary[2]	M
BR05-4	2	4%	Baseline	Baseline	175°E	175°E	Stock scenario 2 with alternative boundary[2]	M
BR06-1	5	1%	Baseline	Baseline	160°E	175°E	Stock scenario 5 with alternative boundary[*2]	M
BR06-4	5	4%	Baseline	Baseline	160°E	175°E	Stock scenario 5 with alternative boundary[2]	M
BR07-1	5	1%	Baseline	Baseline	170°E	175°W	Stock scenario 5 with alternative boundary[2]	M
BR07-4	5	4%	Baseline	Baseline	170°E	175°W	Stock scenario 5 with alternative boundary[2]	M

[1]: *MSYR* 1% is related to 1+ component and 4% is related to mature component.
[2]: Based on alternative mixing proportion data.

5.5.2 Data and assumptions

The assumptions used in these simulation trials are almost the same as those used in the *Implementation Review* of this population by the IWC SC (IWC, 2020).

There are two sub-areas 1 and 2. Sub-area 1 is divided into sub-areas 1W and 1E by the 165°E longitude line (Figure 9).

There are two general hypotheses regarding stock structure for the Bryde's whales (see also section 5.1.3):

(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 robustness 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.

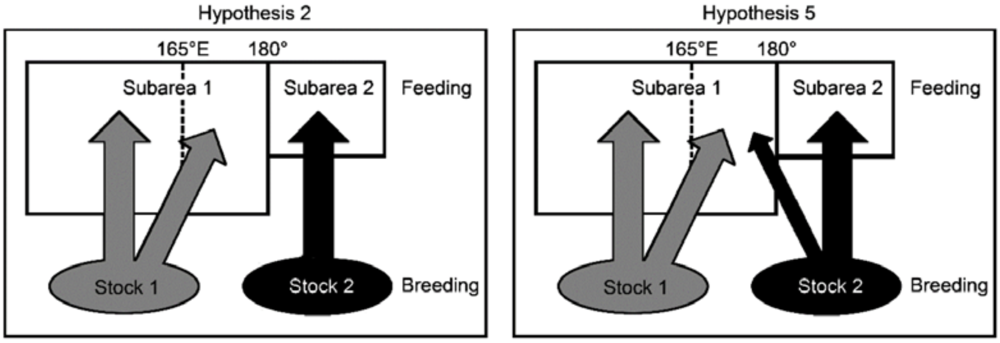


Figure 9. The two stock structure hypotheses considered in the IWC *Implementation Review* (IWC, 2020).

Sensitivity of the western boundary of stock 2 and eastern boundary of stock 1 was considered (Trials BR05, BR06 and BR07). The longitudinal distributions of stocks 1 and 2 in these three trials are illustrated in Figure 10.

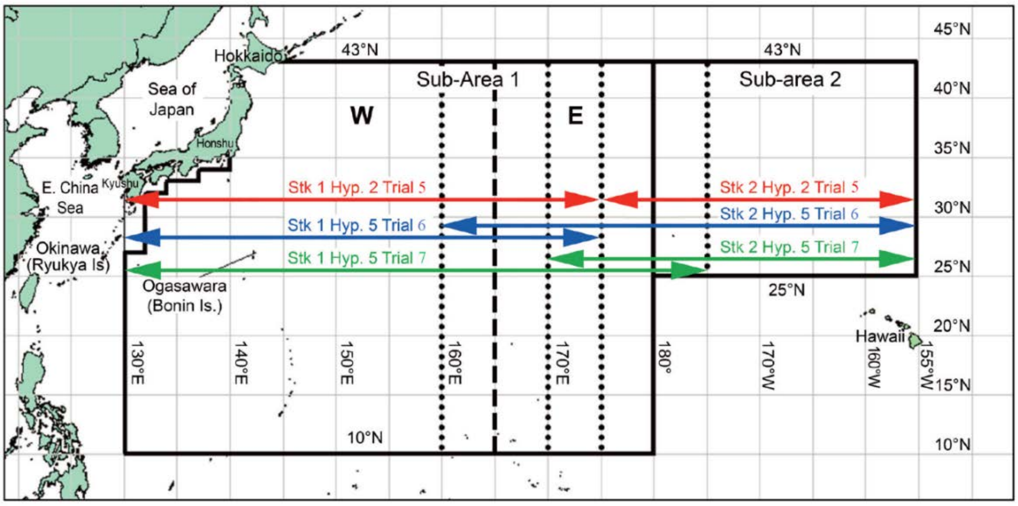


Figure 10. Alternative stocks boundaries examined in the IWC *Implementation Review* (IWC, 2020).

The alternative historical catch used in BR03 is shown in Table 10. This trial assumes that commercial catch in the period 1906-1985 is more than that recorded in Table 7 (the best series). The historical catch series from 1986 is the same as in the best series (baseline scenario).

An additional CV value of 0.737 is assumed for trial BR04, whereas 0.335 is assumed for the baseline trials.

Table 10. Catch history for the North Pacific Bryde’s whale assumed in trial BR03, by sub-area (IWC, 2020).

Year	Sub-area 1 W	Sub-area 1 E	Sub-area 1		Year	Sub-area 1 W	Sub-area 1 E	Sub-area 1
1906	20	0	20		1946	264	0	264
1907	52	0	52		1947	179	0	179
1908	124	0	124		1948	259	0	259
1909	72	0	72		1949	321	0	321
1910	76	0	76		1950	321	0	321
1911	237	0	237		1951	335	0	335
1912	136	0	136		1952	580	0	580
1913	209	0	209		1953	129	0	129
1914	119	0	119		1954	157	0	157
1915	362	0	362		1955	94	0	94
1916	220	0	220		1956	24	0	24
1917	266	0	266		1957	39	0	39
1918	250	0	250		1958	254	0	254
1919	245	0	245		1959	263	0	263
1920	179	0	179		1960	404	0	404
1921	165	0	165		1961	167	0	167
1922	150	0	150		1962	504	0	504
1923	160	0	160		1963	210	0	210
1924	234	0	234		1964	68	0	68
1925	208	0	208		1965	8	2	10
1926	257	0	257		1966	55	2	57
1927	219	0	219		1967	45	0	45
1928	148	0	148		1968	171	4	175
1929	110	0	110		1969	89	16	105
1930	134	0	134		1970	73	11	84
1931	212	0	212		1971	216	285	501
1932	147	0	147		1972	84	63	147
1933	176	0	176		1973	592	51	643
1934	138	0	138		1974	709	306	1015
1935	128	0	128		1975	701	296	997
1936	186	0	186		1976	851	577	1428
1937	245	0	245		1977	787	150	937
1938	270	0	270		1978	622	293	915
1939	388	0	388		1979	1306	39	1345
1940	224	0	224		1980	755	0	755
1941	323	0	323		1981	622	0	622
1942	51	0	51		1982	709	0	709
1943	95	0	95		1983	623	0	623
1944	250	0	250		1984	804	0	804
1945	26	0	26		1985	606	0	606

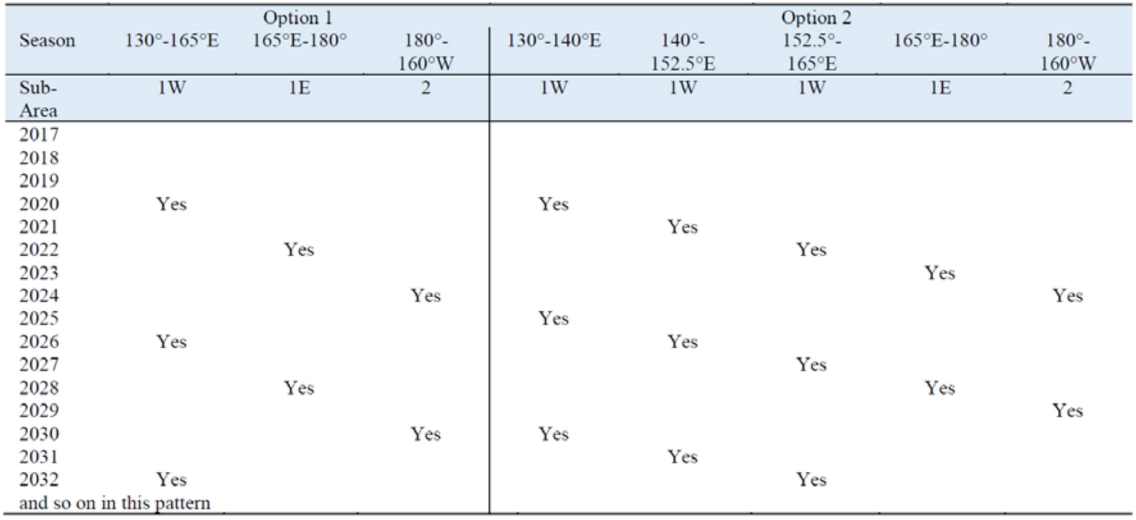
5.5.3 Conditioning

The results of conditioning, kindly provided by the IWC Secretariat, were used to run the trials. Data to be fitted were abundance estimates by sub-area and stock mixing proportion data for cases when aa mixing area was assumed. The details of the conditioning process are provided in IWC (2020).

5.5.4 Future surveys

There are two plans assumed in the trials to cover the survey area north of 20ºN (Table 11). It is assumed that the same pattern will be repeated every six years. Under option 2 in Table 11, the additional CV in sub-area 1W is assumed to increase to 0.767 in the baseline trial, and to 1.516 in trial BR04.

Table 11. The future sighting survey pattern assumed in the trials conducted. All surveys are conducted in July-August (following IWC, 2020)



	Option 1			Option 2				
Season	130°-165°E	165°E-180°	180°-160°W	130°-140°E	140°-152.5°E	152.5°-165°E	165°E-180°	180°-160°W
Sub-Area	1W	1E	2	1W	1W	1W	1E	2
2017								
2018								
2019								
2020	Yes			Yes				
2021					Yes			
2022		Yes				Yes		
2023							Yes	
2024			Yes					Yes
2025				Yes				
2026	Yes				Yes			
2027						Yes		
2028		Yes					Yes	
2029								Yes
2030			Yes	Yes				
2031					Yes			
2032	Yes					Yes		
and so on in this pattern								

5.5.5 Management variants

Whaling is assumed to be conducted in sub-area 1W within Japan’s EEZ during all months of the year. There are two management variants, V1 and V2, which correspond to Options i and ii of the CLA implementations considered, respectively (section 5.4).

V1: Sub-area 1 is a *Small Area*. Catches are taken from sub-area 1W.
V2: Sub-area 1 is a *Combination Area*. Sub-areas 1W and 1E are *Small Areas* with *Catch Cascading* applying. Catches are not taken from sub-area 1E.

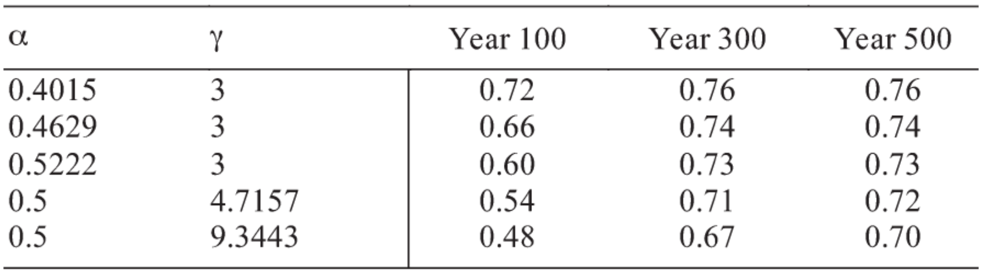
The management variant of no commercial catches (V00) is also considered for comparison purposes. Combinations of the two variants above and the two future survey plans are regarded as four management variants. Conservation performances among the management variants were compared.

5.5.6 Conservation performance

The conservation performance for each trial and variant was examined using the IWC SC’s guidelines to determine whether each combination of variant and trial is classified as ‘acceptable’, ‘borderline’ or ‘unacceptable’. There are two conservation performance statistics for each of the two stocks. They are the final depletion and the minimum depletion ratio (the minimum over each of the 100-year projections of a trial of the ratio of the population size to that when there are only incidental catches) (IWC, 2012c).

To construct thresholds of the acceptability, equivalent single stock trials were conducted for *MSYR*(1+)=1%. Details are provided in IWC (2012c). The tuning levels of 0.6 and 0.48 were used because the catch limit calculation is based on the 0.6 tuning level as in the case of the North Atlantic fin whales (NAMMCO, 2017). Tuning parameters to provide tuning levels of 0.6 and 0.48 after 100 years were those obtained by Aldrin *et al.* (2008) (Table 12).

Table 12. Median depletion for combinations of tuning parameters (Aldrin *et al*., 2008). α is the probability and γ is slope parameter of the catch control law of the CLA.



α	γ	Year 100	Year 300	Year 500
0.4015	3	0.72	0.76	0.76
0.4629	3	0.66	0.74	0.74
0.5222	3	0.60	0.73	0.73
0.5	4.7157	0.54	0.71	0.72
0.5	9.3443	0.48	0.67	0.70

In order to decide acceptability of the variants, the questions listed below were examined, following the procedure set out in IWC (2012c):

Q1: Is the performance ‘acceptable’ on all trials? If yes, the variant is acceptable, otherwise go to Q2.
Q2: Are there any ‘unacceptable’ performance for at least one ‘high’ weight trial? If yes, the variant is ‘unacceptable’, otherwise go to Q3.
Q3: Do the only problems relate to ‘borderline’ performance on medium trials? If yes, go to Q4, otherwise the variant is not acceptable.
Q4: Are results ‘acceptable’ through detailed evaluation of results. If yes, the variant is acceptable, otherwise the variant is not acceptable.

Table 13 shows the results for this conservation performance. All variants except for the V1 with the 2_20 survey plan were ‘acceptable’, because there were no trials that failed to achieve ‘acceptable’ performance (answer of Q1 is yes). There is no ‘unacceptable’ performance for the variant V1 with 2_20 (answer of Q2 is no and Q3 is yes). The variant V1 with 2_20 had some medium trials with ‘borderline’ performance, but after a detailed evaluation of the results (the performance plot for all these trials showed results close to ‘acceptable’ levels), this variant could also be determined to be ‘acceptable’ (answer of Q4 is yes).

In conclusion, all the combinations of the variants (V1 and V2) and future survey plans (1_20 and 2_20) examined were evaluated to be acceptable.

Table 13. Summary of acceptability of trials and variants for MSYR(1+)=1%.

Variant	Future survey	Borderline Trials	Unacceptable Trials	Recommendation
V1	1_20	None	None	Acceptable
V1	2_20	BR01-1, BR02-1, BR03-1, BR05-1, BR06-1, BR07-1	None	Acceptable
V2	1_20	None	None	Acceptable
V2	2_20	None	None	Acceptable

5.6 Whaling operations and future surveys

Since all the combinations of variants and trials are ‘acceptable’, it is considered that Japan consider adopting Option i (or V1), which gives larger catch limit without causing conservation problems. All the whales would then be taken in sub-area 1W within Japan’s EEZ and there would be no temporal restrictions. Future sighting surveys for updating abundance estimates and the CLA would be conducted in line with the options indicated in section 5.5.4. Collection of biological data and samples from harvested whales would be conducted for monitoring the exploited stock and improving the specification of scenarios to be considered in future trials.

6. WESTERN NORTH PACIFIC COMMON MINKE WHALE

6.1 Stock structure and definition of management areas

Studies on stock structure of western North Pacific common minke whale in the context of management have been conducted since 1993. Different stock structure hypotheses have been proposed during the RMP *Implementation Reviews* but the IWC SC was unable to agree on the relative plausibility of the three hypotheses discussed in the last *Implementation Review* in 2013. These three hypotheses were Hypothesis A: Two stocks (J and O) in the Yellow Sea, Sea of Japan, Pacific Side of Japan and Sea of Okhotsk Sea; Hypothesis B: same as in Hypothesis A but a different stock (Y) occurs in the Yellow Sea; and Hypothesis C: Five stock hypothesis (Y, Jw, Je, Ow and Oe). Most of the studies on stock structure presented to the JARPNII final review workshop in 2016 were focused to evaluate the plausibility of Hypothesis C, in particular the occurrence of a putative coastal O stock (Ow).

Results of the most comprehensive studies on stock structure at that time were presented during the JARPNII final review workshop (IWC, 2017b). The genetic and non-genetic analyses presented followed previous recommendations by the IWC SC related to the relevant analyses. A summary of these studies is presented below.

More recently (2018) the IWC SC started a new *Implementation Review* and new genetic analyses were conducted and then discussed. These analyses and the emerging hypotheses are also summarized below.

Figure 11 shows the sub-areas used during the *Implementation Reviews* of the western North Pacific common minke whale conducted by the IWC SC.

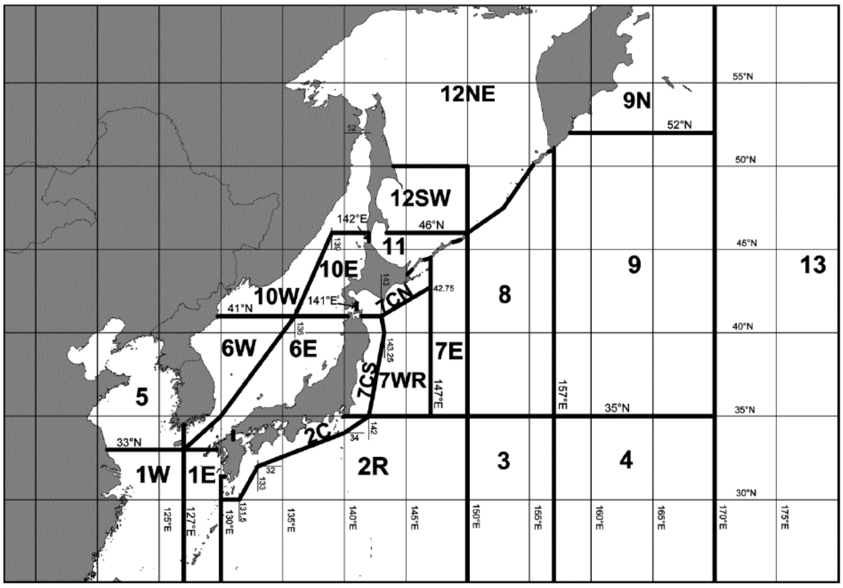


Figure 11. The 22 sub-areas used during the IWC SC *Implementation Reviews* of the western North Pacific common minke whale (IWC, 2014b).

6.1.1 Review of the genetic studies

Genetic samples are from two main sources: JARPN/JARPNII surveys (coastal and offshore) and bycatches (Table 14 and Figure 12). These genetic samples have been used in many analytical studies on stock structure, which are summarized below.

Table 14. Number and period of collection of genetic samples from the western North Pacific common minke whale, by area, source and genetic marker.

Sub-area	JARPN/JARPNII Offshore (1994-2013)		JARPN/JARPNII Coastal (2002-2016)		Bycatch (2001-2016)		Total	
	mtDNA	msDNA	mtDNA	msDNA	mtDNA	msDNA	mtDNA	msDNA
1E					76	76	76	76
2C					372	372	372	372
6E					1002	1002	1002	1002
7CN	321	321	728	728	167	167	1216	1216
7CS	135	135	549	549	279	279	963	963
7WR	89	89					89	89
7E	49	49					49	49
8	251	252					251	252
9	541	541					541	541
10E					18	18	18	18
11	80	80			49	49	129	129
Total	1466	1467	1277	1277	1963	1963	4706	4707

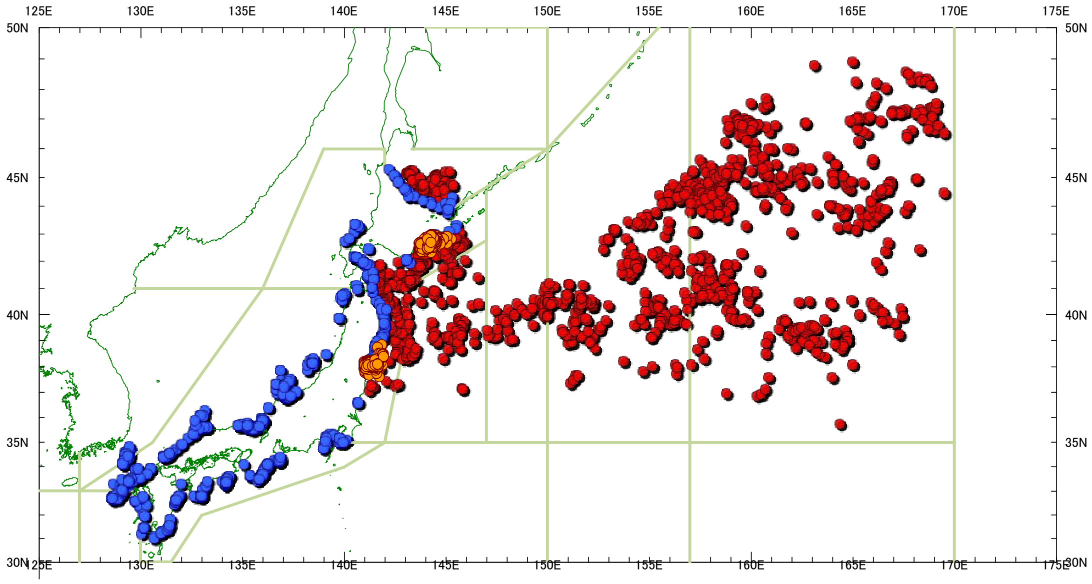


Figure 12. Geographical distribution of genetic samples from the western North Pacific common minke whale. Red: JARPN/JARPNII offshore surveys (catches); Orange: JARPN/JARPNII coastal surveys (catches); Blue: bycatches.

<u>Studies presented to the final JARPNII review</u>

Pastene *et al*. (2016d) examined a total of 4,275 western North Pacific common minke whales with a set of 16 microsatellite DNA loci and used the program STRUCTURE to assign individuals to either the J or the O stock. The pertinent information in this paper for discussion in the Stock Definition Working Group (SDWG) related to the individuals which were unassigned in the STRUCTURE analyses. A simple simulation exercise showed that the number of unassigned individuals decreased with the increase in the number of microsatellite loci used, and that they were widely distributed geographically. The authors concluded that the unassigned individuals are not related to any additional stock structure. Based on these results, the authors considered that only the animals assigned to the O-stock with assignment probability greater than 90% should be used to investigate additional structure within the O-stock, using alternative analytical approaches.

Pastene *et al*. (2016e) examined the genetic population structure of 'O' stock of common minke whales in the western North Pacific based on mitochondrial DNA control region sequencing (487bp) and microsatellite DNA (16 loci). Samples used in the tests of homogeneity were obtained during the surveys conducted during JARPN and JARPNII in sub-areas on the Pacific side of Japan between 1994 and 2014 (n= 2,071 for microsatellite; n=2,070 for mtDNA). Whales were assigned to the 'O' stock by an analysis using STRUCTURE, which was presented in Pastene *et al*. (2016d). Tests based on both genetic markers and different groupings of the samples showed no evidence of sub-structure in the 'O' stock of common minke whale in the Pacific side of Japan. A simulation exercise showed that the statistical power of the homogeneity test was high. In addition, a Discriminant Analysis of Principal Components (DAPC), based on the total samples used in Pastene *et al*. (2016d), showed clear differentiation between J and O stock whales but no evidence of sub-structure within the O stock samples. Consequently, the results of this study suggested a low plausibility for the hypothesis of sub-division of the O stock common minke whale into Ow and Oe components (as in Hypothesis C).

Analyses conducted after the JARPNII final review

Tiedemann *et al*. (2017) used a dataset of complete genotypes at 16 microsatellite loci, accompanied with mtDNA and biological information, for 4,554 North Pacific common minke whales to infer Parent-Offspring (P-O) relationships, using a Maximum-Likelihood approach. The relationship between False Discovery Rate (FDR) and Power (P) was evaluated by simulation. Of 145 inferred P-O pairs at an estimated FDR of 0.1, 141 were further evaluated by typing 10 additional microsatellite loci. 75 were confirmed (among them 26 Mother-Fetus pairs), while 66 pairs were ranked as "False Positives", yielding an overall observed FDR (FDRO) of 0.468. The FDRO was substantially reduced when the J and O individuals were analysed separately. While observed and estimated values for Power were of the same order of magnitude, the observed FDR was always substantially higher than the estimated FDR. This was attributed to the fact that FDRE was estimated via simulation, implicitly assuming a single panmictic population, an assumption clearly not met in the present data set. This interpretation is corroborated by the reduced FDRO when the groups of individuals from each stock were analysed separately. The dataset with 26 microsatellites clearly outperformed (in terms of statistical power) the 16 microsatellite data sets. At FDRE=0.001, Power was at or close to 100% (PE=0.989 and PO=1.000) and the observed False Discovery Rate was FDRO=0.128. Among the validated P-O pairs, O stock pairs were statistically significantly overrepresented, while pairs between J and O stock individuals were absent. Specimens not assigned to either the J or the O stock (i.e. "unassigned") exhibited a stronger affinity to the O stock. The J stock seems to appear on both sides of Japan closer to the coast, while the O stock occurs mostly east of Japan, both close to the coast and far offshore. This analysis provided no evidence for further stock structure in the area covered by this data set. This study demonstrated that a modest increase in the number of loci investigated (here, from 16 to 26 microsatellite loci) may already substantially improve kinship inference under Maximum Likelihood. It further addressed recommendations made at both the JARPNII final review and the 2016 IWC Scientific Committee meeting regarding kinship analysis for North Pacific common minke whales.

Taguchi *et al*. (2019a) showed the results of Discriminant Analysis of Principal Component (DAPC) and Spatial Analysis of Principal Component (sPCA) conducted using microsatellite data (16 loci) to investigate stock structure in the western North Pacific common minke whale. The analyses were performed especially to assess the plausibility of the stock structure proposed under Hypothesis C of the previous RMP *Implementation Review* for the western North Pacific common minke whale. The DAPC was performed by forcing *K* to a different numbers of clusters that simulated putative stocks under Hypothesis C (O_W, O_E, J_W and J_E). The spatial distribution of clusters was compared with the geographical distribution of the putative stocks as specified in the mixing matrices of Hypothesis C. Under this rational, the DAPC analyses were performed forcing $K = 2$: assuming only O and J stocks; $K = 3$: assuming O_W, O_E and J stocks or O, J_W and J_E stocks; and $K = 4$: assuming O_W, O_E, J_W and J_E stocks. The DAPC analyses at $K = 2$ clearly showed two clusters, with distributions corresponding to the known distributions of the J and O stocks. The analysis for $K = 3$ subdivided the O stock cluster into two sub-clusters, and the analyses at $K = 4$ subdivided the O and J stock clusters into two sub-clusters each. The spatial distribution patterns for clusters under $K = 3$ and $K = 4$ were not consistent with the hypothesized distribution pattern of the putative stocks under Hypothesis C. Furthermore, the mtDNA conventional F_{ST} analysis showed no significant differences among the O stock sub-clusters and among the J stock sub-clusters, suggesting that the additional clusters were an artifact. Additionally, the temporal distribution patterns of each sub-cluster were examined based on the idea that different stocks should show different frequency of occurrence reflecting independent population dynamics. This analysis suggested temporal differences only, which were associated with the known pattern of distribution of the J and O stocks. Taking all the results from the DAPC into account, it is likely both that the O_w or J_E stocks do not exist, but also that multiple stocks with overlapping geographic ranges do not exist either. Results from the sPCA analyses were consistent with those from the DAPC analyses. In summary, this DAPC and sPCA study provided no evidence of the existence of additional stocks to the O and J stocks, bso that these analyses provided no support for Hypothesis C of the previous RMP *Implementation Review* for western North Pacific common minke whale.

Goto *et al*. (2019) updated the genetic analyses on parent-offspring (P-O) pairs identified amongst western North Pacific common minke whales. The analyses were based on a maximum likelihood approach described in the original study (Tiedemann *et al*., 2017), which examined 4,554 whales including fetus samples (n=53). This update is based on the analysis of new samples collected in 2016 by JARPNII and bycatches (n=206), for which complete genotypes at 16 microsatellite loci, mtDNA control region sequences and biological information were available. The analyses revealed four new P-O pairs from the J stock. The total number of P-O pairs identified so far is 40 for the O stock and 13 for the J stock. In the case of the O stock, several of the P-O pairs linked across coastal and offshore sub-areas, while that some of the J stock pairs linked the Sea of Japan and the Pacific side of Japan, which is inconsistent with the specifications of the Hypothesis C of the previous *Implementation Review* for the western North Pacific common minke whale.

de Jong and Hoelzel (2019) applied spatially explicit population structure analyses that provide greater power than the program STRUCTURE. The data were analysed as a total dataset (not based on any assignment by STRUCTURE), and included temporal subdivision to assess possible seasonal changes in patterns of connectivity. The analysis compared a subset of samples genotyped at 26 loci with the same samples at 16 loci, and determined that the larger sample size available for the 16-locus dataset provided greater power than the increased number of loci for the smaller sample set, so that further analyses were conducted based on 16 loci. The authors ran Geneland, TESS and BAPS, and found the first to be the most informative. Additional analyses were conducted to test the inference from Geneland that suggested four putative populations in the dataset. Results of this study provided the basis for proposing a new stock structure hypothesis (Hypothesis E, see item 6.1.3).

Responses to the study by de Jong and Hoelzel (2019) were presented by Goto *et al*. (2019) and Taguchi *et al*. (2019b). After examining all genetic and non-genetic evidence, they concluded that the additional genetic coastal clusters in de Jong and Hoelzel (2019) could be much better explained by mixing of the J and O stocks in coastal areas of Japan than by additional stock structure.

6.1.2 Review of the non-genetic studies

Bando and Hakamada (2016) conducted a morphometric analysis to examine the stock structure of western North Pacific common minke whales by using external measurement data collected from 1994 to 2014 during the JARPN and JARPNII surveys. External measurements of mature males were first compared between O and J stock animals, as assigned by the microsatellite DNA analysis. Following this, only assigned O stock animals were compared among sub-areas. The analytical procedures used were the Analysis of Covariance (ANCOVA) and Discriminant Analysis (DA). Significant differences were detected between O and J stock whales. J stock animals had a longer head region compared to O stock animals. No significant differences were detected in O stock animals among sub-areas. The results of the present morphometric analyses provided no evidence for sub-structuring of the O stock into Ow and Oe components, as is implemented in one of the hypotheses used in the RMP *Implementation*, as common minke whales from coastal and offshore sub-areas did not differ in their morphometric characters.

Kitakado and Maeda (2016) used the catch-at-age data for common minke whales in the western North Pacific, as provided by the JARPN/JARPNII program, to refine existing RMP *Implementation Simulation Trials* (*ISTs*) in a simple way. Their aim was to investigate the relative plausibility of the single- and two (Ow and Oe) stock hypotheses for the O whales in the Pacific side of Japan. While the single stock scenario seemed consistent with these age data, it was difficult to reconcile the two stock hypothesis with these data because of the relative absence of particularly younger whales in a supposedly separate discrete Oe stock.

Taguchi *et al*. (2019b) reviewed the non-genetic information in the context of the additional genetic clusters presented by de Jong and Hoelzel (2019). They concluded that the non-genetic evidence strongly supports the view that these clusters represent mixing assemblages of the J and O stocks, rather than reflecting additional stock structure in the coastal areas.

Most of the analyses in the documents summarized above were in response to recommendations made during the 2009 JARPNII mid-term review, and most of them point to a single O stock distributed from the Japanese coast to approximately 170°E, and a single J stock, with a complex pattern of mixing in the Japanese coastal areas.

6.1.3 Hypotheses on stock structure

During the 2019 *Implementation Review*, the IWC SC agreed that the previous stock structure Hypothesis C was not supported by the scientific evidence, and consequently would not be considered further. The IWC SC also then agreed on three stock structure hypotheses: A and B of the previous *Implementation Review*, and a new hypothesis called E which was based on a single study (de Jong and Hoelzel, 2019).

> Hypothesis A: there is a single J stock distributed in sub-areas 1W, 1E, 2C, 5, 6W, 6E, 7CS, 7CN, 10W, 10E, 11 and 12SW, and a single O stock in sub-areas 2C, 2R, 3, 4, 7CS, 7CN, 7WR, 7E, 8, 9, 9N, 10E, 11, 12SW, 12NE and 13 (referred to as Hypothesis A as in 2013);
>
> Hypothesis B: as for hypothesis A, but there is a third stock (Y) that resides in sub-area 1W, 5 and 6W and overlaps with J stock in the southern part of sub-area 6W (referred to as Hypothesis B as in 2013); and
>
> Hypothesis E: there are four stocks, referred to Y, J, P, and O, two of which (Y and J) occur to the west of Japan, and three of which (J, P, and O) are found to the east of Japan and in the Okhotsk Sea. Stock P (earlier termed “purple”) is a coastal stock.

The IWC SC assigned high plausibility to Hypotheses A and B above. It was unable to assign plausibility to Hypothesis E, needing first to await additional genetic and demographic analyses (IWC, 2020). It should be noted that the occurrence of Y stock (Hypotheses B and E) has no management implication for the Pacific side of Japan. Furthermore, it should be noted that there is no agreement as to the existence of a putative P stock in coastal waters of Japan (Hypothesis E). Taguchi *et al*. (2019b) showed that the additional genetic clusters indicated by Geneland (that provided the basis for

Hypothesis E) may be explained by a mixture of O and J stocks without the need to postulate additional stock structure in coastal waters.

Based on the information reviewed above, the conclusion has been drawn that the most plausible hypothesis based on the available scientific data concerning stock structure in the Sea of Japan and Pacific side of Japan, as well as in the Okhotsk Sea, is that of two stocks, the J and O stocks, which mix spatially and temporally. It should be emphasized that this hypothesis was accorded high plausibility by the IWC SC in 2019.

Mixing of the J and O stocks occurs in coastal areas on the Pacific side of Japan, as well as in the Okhotsk Sea, and there mainly in the southern part of the northern coast of Hokkaido. There is no mixing of the J and O stocks in offshore areas on the Pacific side of Japan.

6.1.4 Specification of management areas

As a first step in the specification of *Small Areas*, four aggregations of sub-areas were considered (Figure 13):

A: sub-areas 7CS and 7CN combined (where mixing of J and O stocks occurs)
B: sub-areas 7WR, 7E, 8 and 9 combined (only O stock present)
C: sub-area 11 in the southern part of the Okhotsk Sea (where mixing of J and O stocks occurs)
D: sub-area 12 in the central and northern part of the Okhotsk Sea (where mixing of J and O stocks occurs)

It was decided to specify A+B+C+D as a *Small Area*, and consequently the abundance estimate and catch history were computed for this *Small Area*. It was assumed that the abundance in this *Small Area* reflects O stock whales only. However, other more conservative options assuming different proportions of this stock in the aggregations of sub-areas were also considered. All historical catches in this *Small Area* were attributed to the O stock, which constitutes a conservative decision from the perspective of the O stock.

There is scientific evidence based on length compositions of common minke whale that that O stock migrates to the Okhotsk Sea (D) through sub-areas 7, 8 and 9 (A and B) in summer (Hatanaka and Miyashita, 1997).

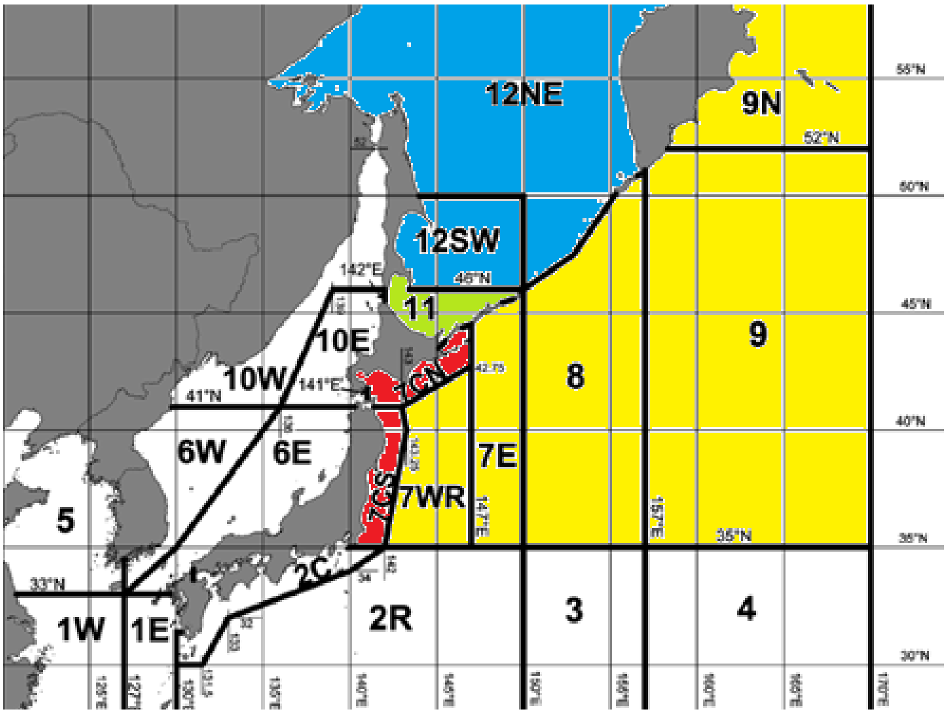


Figure 13. Four aggregations of sub-areas: A (red): 7CS+7CN; B (yellow): 7WR+7E+8+9; C (green): 11; and D (blue): 12SW+12NE.

Table 15 shows the proportions of whales from the O stock in various sub-area aggregations which were considered for the more conservative options mentioned above. These proportions are based on genetic data for the J and O stocks available for the sub-area aggregations A, B and C. Yoshida *et al.* (2010; 2011) reports the only recent genetic information available for aggregation sub-area D. They analyzed eight biopsy samples taken from sub-areas 12NE (7) and 12SW (1). All animals in sub-area 12NE were identified as O stock while only a single minke whale from 12SW was identified as J stock. Although this sample size is small, the study suggests that most of the common minke whales in 12NE are O stock whales. The more conservative options S3 and S4 in Table 10 consider smaller proportions of this stock in 12NE.

Table 15. Four alternative options (S1-S4) for the proportions of whales present in various aggregations of sub-areas that belong to the O stock.

Aggregated sub-areas	S0	S1	S2	S3	S4
A (7CS, 7CN)	100	80	80	80	80
B (7WR, 7E, 8, 9)	100	100	100	100	100
C (11)	100	80	80	70	60
D (12SW)	100	80	90	70	60
D (12NE)	100	100	100	90	75

6.2 Abundance estimates

Abundance estimates were based on sighting data collected during systematic sighting surveys, which were analysed using the Line Transect Method. Surveys have been conducted in a systematic manner through the years, and in general followed the survey design and analytical procedure guidelines of the IWC SC (IWC, 2012a). Sighting data used for the abundance estimates of common minke whales come from two sources: Japanese dedicated sighting surveys and JARPNII surveys.

6.2.1 Data

Abundance estimates in the Pacific side of Japan are based on sighting data collected during the JARPNII surveys in 2002-2004 (Fujise *et al*., 2003; Tamura *et al*., 2004; Tamura *et al*., 2005), and Japanese sighting surveys conducted in 1990, 1991 and 1992 (Miyashita and Shimada, 1994). Abundance estimates in the Sea of Okhotsk are based on sighting surveys conducted in sub-areas 11 and 12 in 1990, 1992, 2000 and 2003 (Buckland *et al*., 1992; Miyashita *et al*., 2000; Miyashita and Okamura, 2011). IO mode data were collected from a series of sighting surveys conducted for stock assessment of common minke whales (Miyashita, 2007; 2008; Miyashita *et al*., 2009). These data were used for the estimation of g(0).

The abundance estimates for the purpose of the application of the CLA were based on surveys which were conducted mainly during the summer season.

Figure 14 shows the track-lines and the geographical distribution of common minke whale primary sightings on JARPNII surveys over 2002 to 2004. Figure 15 shows this same information for Japanese sighting surveys in 1991 and 1992, while Figure 16 does this for four surveys in the Sea of Okhotsk that took place over the period from 1990 to 2003.

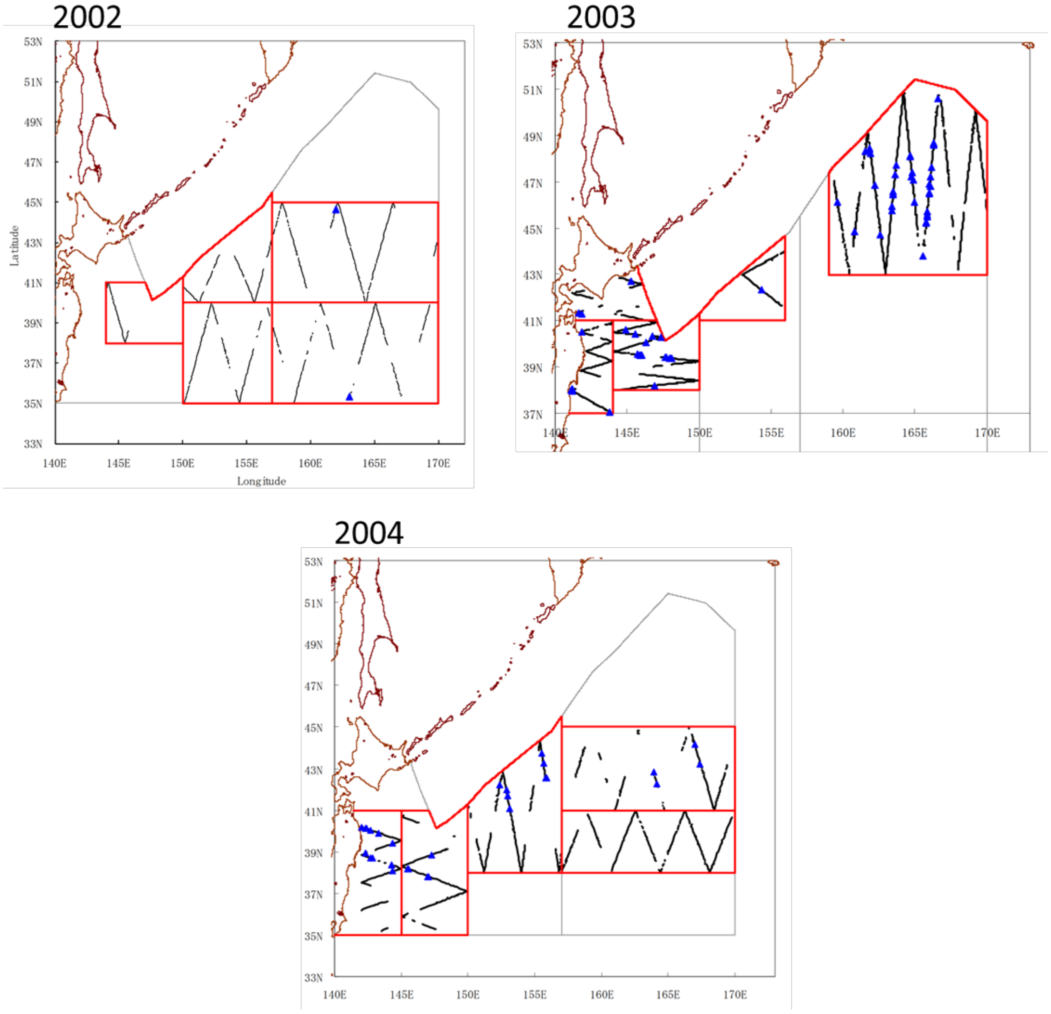


Figure 14. Track-lines and primary sighting positions of common minke whales for the JARPNII surveys in 2002 (June-August), 2003 (May-September) and 2004 (May-July) (Hakamada and Kitakado, 2010).

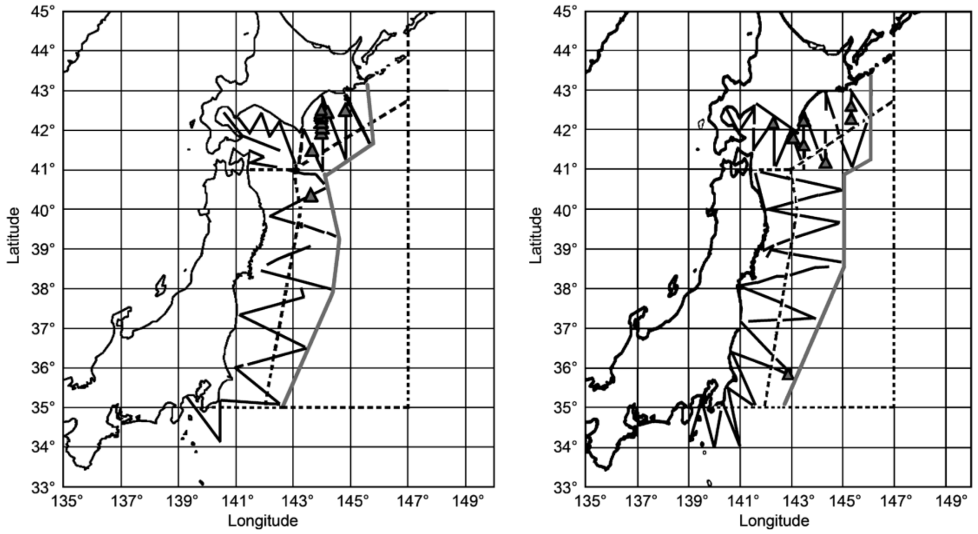


Figure 15. Track-lines and primary sighting positions (triangles) of common minke whales for the Japanese sighting surveys in 1991 (left) and 1992 (right) (Butterworth and Miyashita, 2014). Surveys were conducted in August-September.

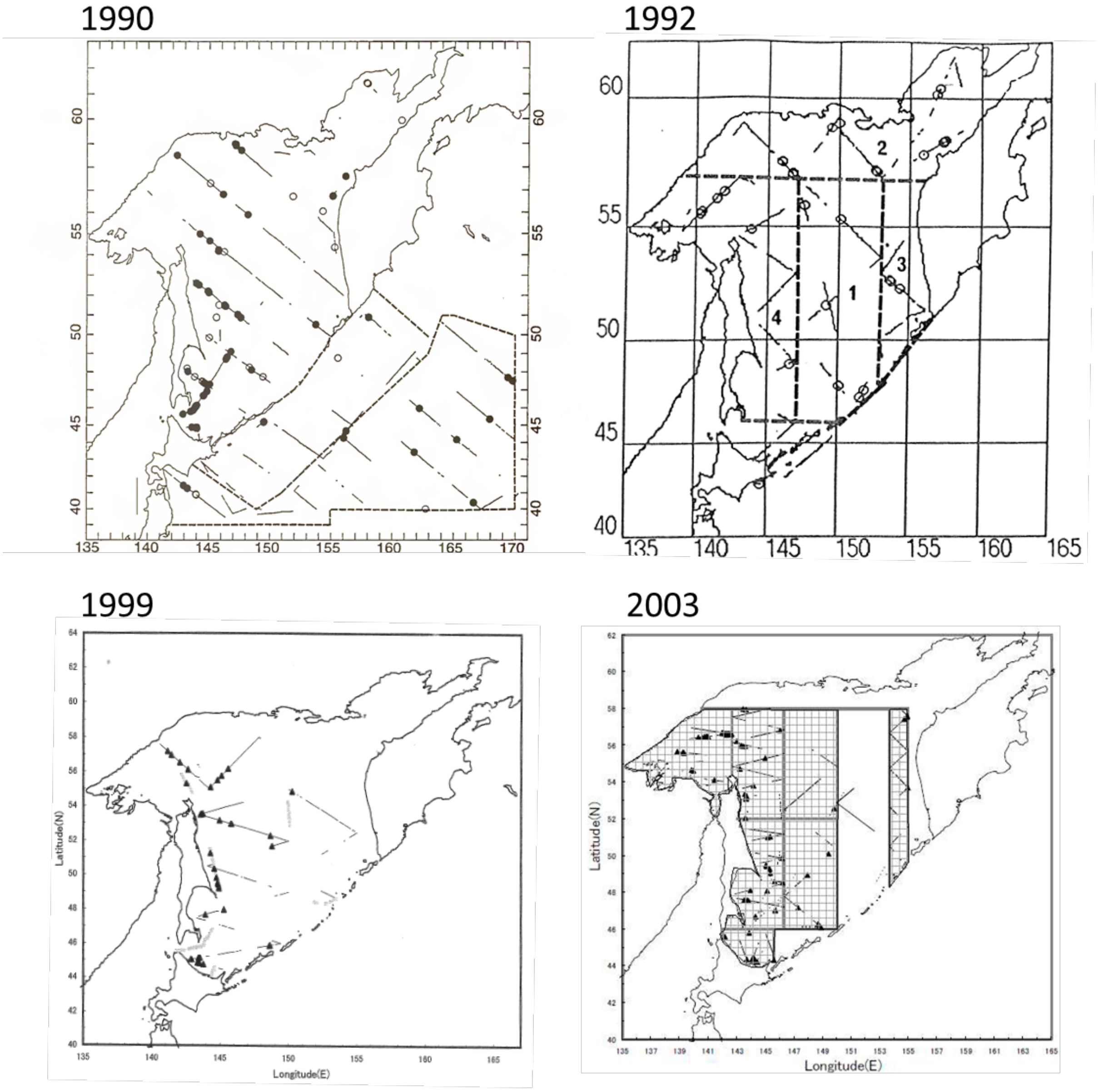


Figure 16. Track-lines and primary sighting positions for common minke whales for the surveys in 1990 (top left; Buckland *et al*., 1992; solid circles indicate primary sightings), 1992 (top right; Miyashita and Shimada, 1994; open circles indicate primary sightings), 1999 (bottom left; Miyashita *et al*., 2000) and 2003 (bottom right; Miyashita and Okamura, 2011).

6.2.2 Analytical procedures including g (0) estimates

Details of the analytical procedures applied to obtain abundance estimates are given in Buckland *et al*. (1992), Miyashita and Shimada (1994), Miyashita *et al*. (2000), Miyashita and Okamura (2011) and Butterworth and Miyashita (2014) for the Japanese sighting surveys, and in Hakamada and Kitakado (2010) for the JARPNII surveys.

Basically, the distance sampling method was applied to estimate abundance. Abundance and its CV were estimated based on a Horvitz-Thompson like estimator. The detections were truncated at 1.5 n.miles perpendicular distance for this species according to the standard convention, and the probability to detect this species on the track-line, g(0), was set at 0.798 (see below). Hazard Rate and Half-normal models were considered as candidate models for the detection function. In order to consider the effect of covariates such as Beaufort state, school size and year on estimated detection functions, the MCDS

(Multiple Covariates Distance Sampling) engine in the DISTANCE program was used. The best model was selected as the case for which the AIC value was smallest. Furthermore, if the difference in AIC amongst detection functions was not substantially different, the weighted average using Akaike weight was calculated (Buckland *et al*., 1997; Burnham and Anderson, 2002).

g(0) estimates

The latest estimate of g(0) for Top barrel and Upper bridge combined is 0.798. This was obtained by applying the OK method (Okamura and Kitakado, 2009), and using the IO passing mode sighting survey data from 2003, 2005, 2006 and 2007 in sub-areas 10, 11 and12 (Okamura *et al*., 2010). A hazard probability model was used for the estimation of esw (the effective strip width). The analysis assumed that there was no need to consider school size effects in the estimation model because minke whales schools in Russian and Japanese waters nearly all consist of single animals.

6.2.3 Results

Detailed results for abundance estimates of North Pacific common minke whales are available in IWC (2014b) and in the documents referenced above.

Table 16 provides a summary of these abundance estimates for the different sub-areas. In cases where more than one abundance estimate is available for the same sub-area, the abundance estimates are averaged using inverse variance weighting. Abundance estimates for the *Small Area* (A+B+C+D) are obtained from the sum over abundance estimates by sub-area taking into account of the estimate of g(0)=0.798 with SE=0.134 (Okamura *et al*., 2010). Table 17 shows the abundance estimates for this *Small Area* assuming different proportions of the whales present in that *Small Area* that are from the O stock (see above).

Table 16. Abundance estimates for North Pacific common minke whale assuming g(0)= 1, based on sighting surveys during JARPNII and other national surveys, presented by IWC SC sub-area. These data were used in 2013 *Implementation Simulation Trials* (IWC 2014b).

Sub-area	Year	Estimate	CV	Areal Cover	Used	Month
7CS	1991	0	-	100	Y*	
7CS	2004	504	0.291	36.7	Y*	May
7CN	1991	853	0.230		Y*	Aug-Sep
7CN	2003	184	0.805	75.4	NA*	May
7WR	1991	311	0.230		Y*	Aug-Sep
7WR	2003	267	0.700	26.7	Y*	May-Jun
7WR	2004	863	0.648	88.8	Y	May-Jun
7E	1990	791	1.848		N	Aug-Sep
7E	2004	440	0.779	57.1	Y	May-Jun
8	1990	1,057	0.706	62.2	Y	Aug-Sep
8	2002	0	-	65	Y	Jun-Jul
8	2004	1,093	0.576	40.5	Y	Jun
9	1990	8,264	0.396	35.1	Y	Aug-Sep
9	2003	2,546	0.276	33.2	Y	Jul-Sep
11	1990	2,120	0.449	100	Y	Aug-Sep
11	1999	1,456	0.565	100	Y	Aug-Sep
11	2003	882	0.820	33.9	Y*	Aug-Sep
12SW	1990	5,244	0.806	100	Y*	Aug-Sep
12SW	2003	3,401	0.409	100	Y*	Aug-Sep
12NE	1990	10,397	0.364	100	Y*	Aug-Sep
12NE	1992	11,544	0.380	89.4	Y*	Aug-Sep
12NE	1999	5,088	0.377	63.8	Y*	Aug-Sep
12NE	2003	13,067	0.287	46	Y*	Aug-Sep

*: indicates that further analysis needs to be considered for an estimate to become acceptable for use in a real application of the RMP.

Table 17. Abundance estimates for the O stock of common minke whale under several assumptions for the proportion of whales present in *Small Area* (A+B+C+D) which are from that stock.

Year	A+B+C+D									
	S0		S1		S2		S3		S4	
	Estimate	CV	Estimate	CV	Estimate	CV	Estimate	CV	Estimate	CV
1991	37,001	0.273	34,941	0.267	35,598	0.271	32,654	0.267	29,685	0.269
2003	20,513	0.227	19,205	0.226	19,631	0.227	17,792	0.225	15,956	0.223

6.3 Catch history and other removals

The historical catch series used for the CLA (Table 18) corresponds to the ‘best’ series used during the *Implementation Review* of western North Pacific common minke whale by the IWC SC. Details concerning these data can be found in Appendix 2 of IWC (2014b). The series shown in Table 18 has been updated to 2017 from that shown in IWC (2014b).

Table 18. Catch history for North Pacific common minke whale for the *Small Area* (A+B+C+D).

Year	A+B+C+D	Year	A+B+C+D	Year	A+B+C+D
1930	13	1959	281	1988	0
1931	14	1960	257	1989	0
1932	22	1961	333	1990	0
1933	23	1962	239	1991	0
1934	32	1963	220	1992	0
1935	33	1964	289	1993	0
1936	24	1965	312	1994	21
1937	58	1966	360	1995	100
1938	68	1967	270	1996	77
1939	69	1968	225	1997	100
1940	79	1969	202	1998	100
1941	58	1970	310	1999	100
1942	68	1971	268	2000	40
1943	102	1972	340	2001	100
1944	79	1973	518	2002	150
1945	69	1974	363	2003	150
1946	97	1975	328	2004	159
1947	125	1976	339	2005	220
1948	169	1977	246	2006	195
1949	132	1978	400	2007	207
1950	201	1979	392	2008	169
1951	231	1980	364	2009	162
1952	291	1981	358	2010	119
1953	234	1982	309	2011	126
1954	274	1983	279	2012	182
1955	374	1984	367	2013	95
1956	455	1985	319	2014	81
1957	357	1986	311	2015	70
1958	516	1987	304	2016	37
				2017	128

The series of bycatches (Table 19) is also that used during the IWC SC *Implementation Review* (IWC, 2014b), again updated to 2017.

Table 19. Incidental catches (bycatches) of western North Pacific common minke whales for A+B+C+D aggregations.

Year	A+B+C+D	Year	A+B+C+D
1946	11.67	1982	37.17
1947	12.83	1983	37.67
1948	13.50	1984	37.83
1949	14.50	1985	38.33
1950	15.83	1986	37.50
1951	16.83	1987	37.50
1952	17.33	1988	36.67
1953	18.17	1989	37.83
1954	19.67	1990	37.01
1955	20.33	1991	36.84
1956	21.34	1992	37.01
1957	21.83	1993	37.00
1958	23.00	1994	35.66
1959	23.66	1995	33.50
1960	24.33	1996	34.66
1961	25.00	1997	34.83
1962	26.00	1998	35.00
1963	27.17	1999	35.00
1964	27.83	2000	35.00
1965	28.83	2001	35.00
1966	29.33	2002	35.00
1967	30.16	2003	36.00
1968	31.33	2004	35.00
1969	31.66	2005	34.00
1970	32.33	2006	35.00
1971	31.84	2007	32.00
1972	32.67	2008	32.83
1973	32.33	2009	32.83
1974	32.00	2010	32.83
1975	31.83	2011	32.67
1976	33.00	2012	32.67
1977	35.49	2013	23.00
1978	36.66	2014	38.00
1979	37.83	2015	38.00
1980	37.17	2016	38.00
1981	37.83	2017	38.00

6.4 Catch limit

The combination of the aggregations of sub-areas A, B, C and D is treated as a *Small Area*. Catch limits for the O stock are calculated for this *Small Area*. Alternative catch limits are calculated for several assumptions for the proportions of whales in this *Small Area* which are from the O stock (S1-S4 above) (Table 20). Adjustments for differences in the sex ratio from 50:50 were not required because, unlike in the case of the sei whale, males represent a larger proportion than females in the actual catches of minke whales.

Table 20. Catch limits for the O stock of common minke whales based on the Norwegian CLA code applied to a *Small Area* (A+B+C+D), under several assumptions for the proportion of whales in this *Small Area* which are from the O stock.

Tuning level	Option S0 (all O stock)	Option S1	Option S2	Option S3	Option S4
0.6	180	168	171	152	129

6.5 Testing for the consequences of uncertainties (*ISTs*)

6.5.1 Trials scenario

For western North Pacific common minke whales, stock Hypothesis A (see section 6.1.3) is considered to have the highest plausibility, so that only this hypothesis has been considered. The mixture proportions of the J and O stocks in the Okhotsk Sea under this hypothesis have been treated as the main uncertainties. Based on Kitakado and Goto (2018), MSYR 4% (mature) and 2% (1+) were treated as the baseline values for the trials. The plausibility of the MSYR 1% (1+) possibility was considered to be low, but corresponding trials were conducted as sensitivity test. In addition, the uncertainties in the past catch records, and the value of g(0) used in abundance estimation were also considered in the trials. Taking all these possibilities into account, a total of 30 simulation trials (Table 21) was conducted for each MP variant.

Trial scenarios are denoted using the format as Ann-r (nn is the trial number and r is MSYR value). The trials A01 are baseline trials, and their specifications are almost the same as those used in the 2014 IWC SC *Implementation Review* of this species (but the CLA tuning level of 0.6 was used instead of 0.72 for tests under these trials). Trials A02 (alternative numbers of the historical catches and bycatches), A03 (assuming g(0)=1 for abundance estimates) and A04-10 (alternative proportions of J and O stock whales in the Okhotsk Sea) were conducted for testing robust to major uncertainties. All trials were conducted for both MSYR 4% (mature) and 2% (1+) (Ann-4 or Ann-2), and the results were treated as medium weight when deciding the acceptability of the variants.

Table 21. List of the trials conducted for western North Pacific common minke whale.

Trial numbers	*MSYR*	Description	Trial weight
A01-1,	1%(1+)	Baseline two stock scenario, *g*(0)=0.8, Chinese bycatch	L*
A01-2	2%(1+)		M
A01-4	4%(mature)		M
A02-1,	1%(1+)	High direct catches and alternative Korean and Japanese bycatches	L*
A02-2	2%(1+)		M
A02-4	4%(mature)		M
A03-1,	1%(1+)	Assume *g*(0)=1	L*
A03-2	2%(1+)		M
A03-4	4%(mature)		M
A04-1	1%(1+)	10% J stock in sub-area 12SW in August (20% in base case)	L*
A04-2	2%(1+)		M
A04-4	4%(mature)		M
A05-1	1%(1+)	30% J stock in sub-area 12SW in August (20% in base case)	L*
A05-2	2%(1+)		M
A05-4	4%(mature)		M
A06-1	1%(1+)	40% J stock in sub-area 12SW in August (20% in base case)	L*
A06-2	2%(1+)		M
A06-4	4%(mature)		M
A07-1	1%(1+)	10% J stock in sub-area 12 in August	L*
A07-2	2%(1+)		M
A07-4	4%(mature)		M
A08-1	1%(1+)	20% J stock in sub-area 12 in August	L*
A08-2	2%(1+)		M
A08-4	4%(mature)		M
A09-1	1%(1+)	30% J stock in sub-area 12 in August	L*
A09-4	4%(mature)		M
A09-2	2%(1+)		M
A10-1	1%(1+)	40% J stock in sub-area 12 in August	L*
A10-4	4%(mature)		M
A10-2	2%(1+)		M

*: The plausibility of MSYR 1% (1+) is considered to be low, but trails were conducted as a sensitivity test.

6.5.2 Data and assumptions

The number of the direct and incidental catches by sub-area were updated from those used in the previous *Implementation Review* conducted by IWC SC (IWC, 2014b). The numbers of the annual catches are shown in Table 18 above (see section 6.3).

Abundance estimates for common minke whales based on the Japanese sighting surveys during 2008-2018 (Hakamada and Matsuoka, 2016; Hakamada *et al.*, 2019; Miyashita 2019) were used in the trials.

An age and sex-structured Pella-Thomlinson model was used to model the population dynamics of the J and O stocks common minke whales. Details of the model are provided in IWC (2014b).

6.5.3 Conditioning

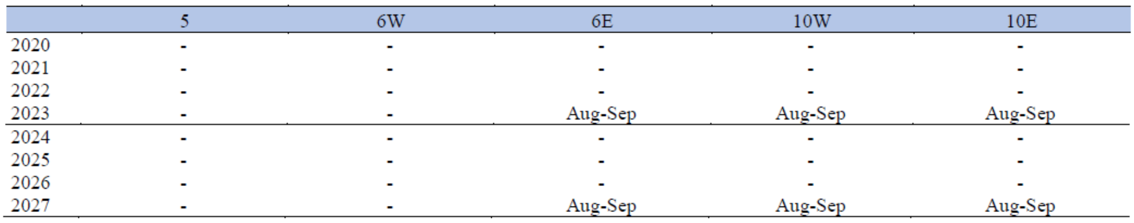
Data used for conditioning involved proportions of whales in various sub-areas that belonged to the J stock, abundance estimates by sub-area and estimated numbers of incidental catches. For the trials A01-4, A02-4 and A03-4, the results of conditioning by the IWC SC were used (IWC, 2014b). In order to improve the fit, three different sets of initial values were used for trials A01, A02, A03, A04 and A05, which are similar to trials conducted in the previous IWC SC *Implementation Review* (IWC, 2014b). A total of five initial sets of values were used for trials A06, A07, A08, A09 and A10, which are new scenarios not previously considered by the IWC SC.

Conditioning plots (including fits to the abundance estimates and bycatch series) were produced and inspected for any unexpected behavior. Based on these plots, the fits were all considered to be satisfactory.

6.5.4 Future survey plan

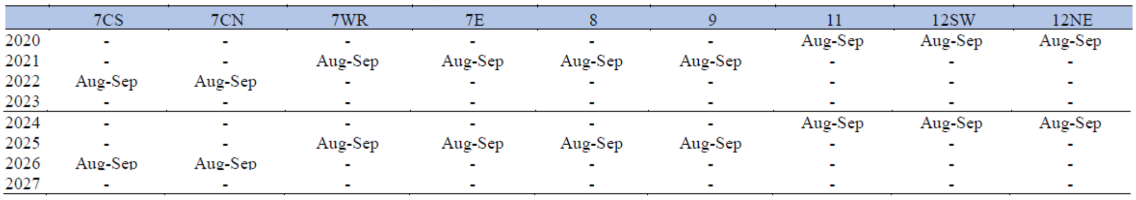
The same future survey plan as in the *Implementation Review* for the common minke whale (IWC, 2019a) was taken to apply. Table 22a and 22b show the assumed future Japanese sighting survey plan during 2020-2028 in the Sea of Japan, and in the North Pacific and Okhotsk Sea. The same pattern is to be repeated every four years.

Table 22a. Future Japanese sighting survey plan assumed for 2020-2028 in sub-areas 5, 6 and 10 (Sea of Japan) (IWC, 2019).



	5	6W	6E	10W	10E
2020	-	-	-	-	-
2021	-	-	-	-	-
2022	-	-	-	-	-
2023	-	-	Aug-Sep	Aug-Sep	Aug-Sep
2024	-	-	-	-	-
2025	-	-	-	-	-
2026	-	-	-	-	-
2027	-	-	Aug-Sep	Aug-Sep	Aug-Sep

Table 22b. Future Japanese sighting survey plan assumed for 2020-2028 in sub-areas 7, 8, 9, 11 and 12 (North Pacific and Okhotsk Sea) (IWC, 2019).



	7CS	7CN	7WR	7E	8	9	11	12SW	12NE
2020	-	-	-	-	-	-	Aug-Sep	Aug-Sep	Aug-Sep
2021	-	-	Aug-Sep	Aug-Sep	Aug-Sep	Aug-Sep	-	-	-
2022	Aug-Sep	Aug-Sep	-	-	-	-	-	-	-
2023	-	-	-	-	-	-	-	-	-
2024	-	-	-	-	-	-	Aug-Sep	Aug-Sep	Aug-Sep
2025	-	-	Aug-Sep	Aug-Sep	Aug-Sep	Aug-Sep	-	-	-
2026	Aug-Sep	Aug-Sep	-	-	-	-	-	-	-
2027	-	-	-	-	-	-	-	-	-

6.5.5 Management variants

Whaling is to be conducted in sub-areas 7CS, 7CN, 7WR and 11 within Japan's EEZ. Catch limits are to be calculated treating sub-areas 7, 8, 9, 11 and 12 as a *Small Area*, with the catches taken from sub-areas 7CS, 7CN, 7WR and 11. There are four factors considered to define the management procedure variants considered (for convenience, the variants examined in the trials are represented by four-digit numbers):

Abundance estimates for using actual CLA.
There are five options to calculate abundance estimates as inputs for the CLA. One is to sum over abundance estimates for sub-areas 7, 8, 9, 11 and 12 (hereafter, this option is termed All O stock or S0). Given that there may be some J stock animals in this aggregation of sub-areas, the assumed proportion in each aggregation sub-area consisting of O stock whales was multiplied by the abundance estimates in order to obtain approximate abundances of the O stock in each sub-area (options S1-S4 in Table 15 and 17).

Whaling: Spatial closure
Two options for spatial closure are considered: i) no whales are to be taken in waters within 10nm from the coast in sub-areas 7CS and 7CN, and ii) no spatial closure. Past studies have shown that the

proportion of of the whales present that are from the J stock is higher within 10 n.miles of the coast than that from further offshore (i.e. more than 10 n.miles away from the coast) (IWC, 2014b).

Whaling: temporal closure
Two options for temporal closure are considered: i) whaling is to be restricted to the period April-October in sub-areas 7CS, 7CN and 7WR, and to the period August to October in sub-area 11, and ii) whaling occurs in all months.

Allocation of catch limit
Alternative allocations of the catch limit to the four coastal sub-areas are investigated. One option is the application of *Catch Cascading*. The other option is assigning catch proportions to the sub-areas as set out in Table 23.

Table 23. Proportions of the catch allocated to sub-areas 7CS, 7CN, 7WR and 11 (%)

	Opt1	Opt2	Opt3	Opt4	Opt5
7CS	40	100	0	0	0
7CN	20	0	100	0	0
7WR	20	0	0	100	0
11	20	0	0	0	100

ID representing the variants.
With a combination of four factors, a total of 120 variants (5 sets of abundance estimates × 2 spatial options × 2 temporal options × 6 catch limit allocations) were examined for the 30 trials listed in Table 24. For convenience, those variants are represented by four-digit numbers (Vxxxx) as shown in that Table.

Table 24. Variant ID for the trials for common minke whales.

Factor		
Abundance for CLA	Thousand's place (Vx***)	0: All O stock, 1: S1, 2: S2, 3: S3, 4: S4
Spatial closure	Hundred's place (V*x**)	0: Closure within 10n.m in 7CS and 7CN, 1: No closure
Temporal closure	Ten's place (V**x*)	0: Restriction of whaling season, 1: No restriction
Catch Allocation	One's place (V***x)	0: Catch cascading, 1: Opt1, 2: Opt2, 3: Opt3, 4: Opt4, 5: Opt5

For example, V0001 means the variant with All O stock abundance option, spatial closure option, temporal restriction option, and catch allocation Opt1. V1011 means the variant with S1 abundance option, spatial closure option, no temporal restriction option, and catch allocation Opt1.

6.5.6 Conservation performance

The conservation performance for each trial and variant was examined using the same method described in section 5.5.6, except that the IWC SC's equivalent single stock trial process was followed for MSYR(1+)=2% and MSYR(mat)=4%. In order to decide on the acceptability of the variants, questions Q1-Q4 listed in the section 5.5.6 for each variant were examined for trials with MSYR(1+)=2% and MSYR(mat)=4%. The results of trials with MSYR(1+)=1% were examined only for sensitivity purposes.

It should be noted that, for the O stock, results were “acceptable” (A) for most of the trials and variants, and “borderline” (B) for the rest. This was the case even with MSYR(1+)=1%. This implies that there is no problem with conservation performance for the O stock under any variant. Where unacceptability occurs, this is a consequence of “unacceptable” performance for the J stock.

Although all 30 trials with 120 variants were conducted, only the results of the trials for variants with S0 (i.e. all O stock option) are shown in Table 25. If the results of the trials are “acceptable” for S0 option, other options used to calculate abundance estimate for the use of CLA (options S1, S2, S3 and S4) will also be “acceptable” because the future catch will be lower than those in the S0 option.

Table 25. Summary of trial results for variant S0 (the all O stock option) which were borderline or showed unacceptable performance.

Variant	Borderline trials	Unacceptable trials	Recommendation
V0000	*A04-1*, *A05-1*, *A06-1*, *A07-1*, *A08-1*, A01-2, A04-2, A05-2, A06-2, A01-4, A04-4, A05-4, A06-4, A07-4	*A01-1*, *A02-1*, *A03-1*, A02-2, A03-2, A02-4, A03-4	Unacceptable
V0001	*A03-1*, A02-4, A03-4	*A02-1*	Acceptable*
V0002	None	None	Acceptable
V0003	None	None	Acceptable
V0004	None	None	Acceptable
V0005	*A09-1*, *A10-1*, A05-2, A06-2, A08-2, A09-2, A08-4, A09-4, A10-4	*A01-1*, *A02-1*, *A03-1*, *A04-1*, *A05-1*, *A06-1*, *A07-1*, *A08-1*, A01-2, A02-2, A03-2, A04-2, A07-2, A01-4, A02-4, A03-4, A04-4, A05-4, A06-4, A07-4	Unacceptable
V0010	*A07-1*, *A08-1*, *A09-1*, *A10-1*, A01-2, A04-2, A05-2, A06-2, A07-2, A08-2, A07-4, A09-4, A10-4	*A01-1*, *A02-1*, *A03-1*, *A04-1*, *A05-1*, *A06-1*, A02-2, A03-2, A01-4, A02-4, A03-4, A04-4, A05-4, A06-4	Unacceptable
V0011	*A03-1*, A02-2, A03-2, A01-4, A02-4, A03-4, A04-4	*A02-1*	Acceptable*
V0012	None	None	Acceptable
V0013	None	None	Acceptable
V0014	None	None	Acceptable
V0015	A09-2, A10-2, A08-4, A10-4	*A01-1*, *A02-1*, *A03-1*, *A04-1*, *A05-1*, *A06-1*, *A07-1*, *A08-1*, *A09-1*, *A10-1*, A01-2, A02-2, A03-2, A04-2, A05-2, A06-2, A07-2, A08-2, A01-4, A02-4, A03-4, A04-4, A05-4, A06-4, A07-4, A09-4	Unacceptable
V0100	*A05-1*, *A06-1*, *A07-1*, *A08-1*, *A09-1*, A01-2, A04-2, A05-2, A06-2, A07-2, A05-4, A06-4, A07-4, A09-4	*A01-1*, *A02-1*, *A03-1*, *A04-1*, A02-2, A03-2, A01-4, A02-4, A03-4, A04-4	Unacceptable
V0101	A05-1, A06-1, A07-1, A08-1, A01-2, A02-2, A03-2, A04-2, A01-4, A04-4, A05-4, A06-4, A07-4	A01-1, A02-1, A03-1, A04-1, A02-4, A03-4	Unacceptable
V0102	*A08-1*, *A09-1*, A01-2, A04-2, A05-2, A06-2, A07-2, A08-2, A05-4, A06-4, A09-4	*A01-1*, *A02-1*, *A03-1*, *A04-1*, *A05-1*, *A06-1*, *A07-1*, A02-2,	Unacceptable

		A03-2, A01-4, A02-4, A03-4, A04-4, A07-4	
V0103	*A03-1*, A02-4, A03-4	None	Acceptable
V0104	None	None	Acceptable
V0105	*A09-1*, *A10-1*, A05-2, A06-2, A08-2, A09-2, A08-4, A09-4, A10-4	*A01-1*, *A02-1*, *A03-1*, *A04-1*, *A05-1*, *A06-1*, *A07-1*, *A08-1*, A01-2, A02-2, A03-2, A04-2, A07-2, A01-4, A02-4, A03-4, A04-4, A05-4, A06-4, A07-4	Unacceptable
V0110	*A08-1*, *A09-1*, *A10-1*, A05-2, A06-2, A07-2, A08-2, A09-4, A10-4	*A01-1*, *A02-1*, *A03-1*, *A04-1*, *A05-1*, *A06-1*, *A07-1*, A01-2, A02-2, A03-2, A04-2, A01-4, A02-4, A03-4, A04-4, A05-4, A06-4, A07-4	Unacceptable
V0111	*A05-1*, *A06-1*, *A07-1*, *A08-1*, A01-2, A04-2, A07-2, A05-4, A06-4, A07-4	*A01-1*, *A02-1*, *A03-1*, *A04-1*, A02-2, A03-2, A01-4, A02-4, A03-4, A04-4	Unacceptable
V0112	*A08-1*, *A09-1*, A01-2, A04-2, A05-2, A06-2, A07-2, A08-2, A05-4, A06-4, A09-4	*A01-1*, *A02-1*, *A03-1*, *A04-1*, *A05-1*, *A06-1*, *A07-1*, A02-2, A03-2, A01-4, A02-4, A03-4, A04-4, A07-4	Unacceptable
V0113	*A03-1*, A02-4, A03-4	None	Acceptable
V0114	None	None	Acceptable
V0115	A09-2, A10-2, A08-4, A10-4	*A01-1*, *A02-1*, *A03-1*, *A04-1*, *A05-1*, *A06-1*, *A07-1*, *A08-1*, *A09-1*, *A10-1*, A01-2, A02-2, A03-2, A04-2, A05-2, A06-2, A07-2, A08-2, A01-4, A02-4, A03-4, A04-4, A05-4, A06-4, A07-4, A09-4	Unacceptable

Trials indicated in *italics* (for MSYR(1+)=1%) are intended as sensitivity checks only, and do not determine the acceptability of variants.

* Only one trial (A02-1) was ‘unacceptable’, for which plausibility was low. This variant was ‘acceptable’ for 26 trials and ‘borderline’ for three trials among the 29 remaining trials. For these reasons, the variant was deemed to be ‘acceptable’.

Regarding spatial closure options, the number of acceptable variants with option i) is more than those with option ii) (Table 25), indicating that spatial closure is an effective management measure for the western North Pacific common minke whale. Therefore, variants with option i) (i.e. no whales will be taken in waters within 10nm from the coast in sub-areas 7CS and 7CN) is to be adopted.

With regard to the temporal option, the number of acceptable variants are similar for option i) and option ii) , indicating that temporal closure is not a useful management measure.

As regards allocation of the catch among the sub-areas 7CS, 7CN, 7WR and 11, catch cascading and option 5 (variant ID with ‘0’ or ‘5’ in the “One’s place” – see Table 24) are unacceptable. As seen in Table 16 in section 6.2.3, catch cascading allocates a higher proportion of the catch to sub-area 11 than catch allocation options 1-4 do. Given that the proportion of the whales in sub-area 11 that are from the J stock is higher than in sub-areas 7CS, 7CN and 7WR, these two options lead to more catch from the J stock than other options, and this is the reason why these options are unacceptable. Options 1, 2, 3 and 4 for catch allocation are acceptable whenever no whales are to be taken in waters within 10nm from the coast in sub-areas 7CS and 7CN (V0001, V0002, V0003, V0004, V0011, V0012, V0013 and V0014). This means a) up to 20% of catch limits can be allocated to sub-area 11, and b) any of the allocation pattern suggested among sub-areas 7CS, 7CN and 7WR is acceptable.

It is notable that, in the case of variants V0001 and V0011 (option 1 in catch allocation with spatial closure), conservation performances are unacceptable in the sensitivity case A02-1 for which MSYR(1+)=1% is assumed. This implies that, notwithstanding that MSYR(1+)=1% is considered an implausible assumption, further research on MSYR is of considerable importance for future studies.

In conclusion, V0001 to V0004, V0011 to V0014, V0103 to V0104, and V0113 to V0114 are ‘acceptable’ for both J and O stocks.

These results indicate that the All O stock option (S0) can be applied for the CLA, and that the resulting catch limit can be allocated in line with options 1, 2, 3 or 4, as long as the spatial restriction (no whales will be taken in waters within 10nm from the coast in sub-areas 7CS and 7CN) is implemented. Temporal restriction is not necessary.

Results for other options for CLA calculation (S1, S2, S3 and S4) were almost the same as for the All O stock option, i.e. the catch limit can be allocated under option 1, 2, 3 or 4, and the spatial option is needed to maintain adequate conservation performance. These options for CLA calculation are not considered further, since the safety of the all O stock option had been confirmed.

6.6 Whaling operations and future surveys

Considering the results of the trials, Japan is to adopt the all O stock option (S0) for the abundance estimate for the CLA. A 10 mile spatial closure is to be introduced on the Pacific side of Japan to decrease the catch of J stock whales. Twenty percent of the catch limit is to be allocated to sub-area 11, while 80% of the catch is to be allocated to the Pacific side of Japan (a block quota for sub-areas 7CS, 7CN and 7WR).

Future sighting surveys for providing further abundance estimates for use in the CLA will be conducted in line with the options shown in section 6.5.4. Collection of biological data and samples from harvested whales will be conducted for monitoring the exploited stock, and improving specification of the scenarios to be considered in future trials.

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