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Review

GENETICALLY IDENTIFIED J-STOCK COMMON MINKE WHALES: AN OVERVIEW OF THEIR BIOLOGICAL AND ECOLOGICAL FEATURES IN WATERS AROUND JAPAN

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Abstract

This paper presents and overview of the biological and ecological features of the J-stock common minke whale (*Balaenoptera acutorostrata scammoni*) in waters around Japan based on analyses of genetically identified individuals. Reviewed information included spatial/temporal distribution, morphology, morphometrics, reproductive characteristics, feeding ecology, environmental pollutants, and ecological markers. Except for feeding ecology and environmental pollutants, these features (e.g., spatial/temporal distribution, morphology such as flipper and fluke color pattern and ecological markers such as cookie cutter shark scars) confirm the biological and ecological uniqueness of the J-stock within the North Pacific common minke whale. Our analysis also confirms the existence of distinct genetically, biologically and ecologically independent stocks with characteristics so far not identified in any other baleen whales in the Western North Pacific, and corroborates the view that the minke whale J-stock should be managed independently.

Key words: North Pacific, common minke whale, stock assignment, morphology, feeding ecology, pollutants, ecological markers, reproductive parameters, J-stock.

Introduction

Biological stocks can be defined as a group of same-species organisms that are genetically self-sustaining and live isolated geographically or temporally during reproduction. The use of the term usually implies that a particular population is more or less isolated from other stocks of the same species. In the western North Pacific, at least two biological stocks of common minke whales (*Balaenoptera acutorostrata scammoni)* are known to exist: the Okhotsk Sea-West Pacific (O-stock) and the Sea of Japan-Yellow Sea-East China Sea (J-stock) (Omura and Sakiura, 1956; Ohsumi, 1977; 1983). The two stocks have been differentiated primarily through morphological and reproductive characteristics (Omura and Sakiura, 1956; Ohsumi, 1977; Kato, 1992; Kato *et al.*, 1992), as well as genetics (Wada and Numachi, 1991 for allozymes; Goto and Pastene, 1997 for mitochondrial DNA (mtDNA); and Kanda *et al.*, 2009a; Kanda *et al.*, 2009b for microsatellite DNA (msDNA)), with the differences reported suggesting their reproductive isolation. Kato (1992) estimated the breeding periods of both stocks from seasonal distribution of fetus body length. He proposed that the 'autumn breeding stock' distributes in the Yellow Sea, the East China Sea and the Sea of Japan and the 'winter breeding stock' distributes off the Pacific coast of northern Japan, with both stocks mixing in the southern Okhotsk Sea in early summer. Kato *et al.* (1992) examined the regional differences in minke whale flipper color patterns and found that they differed between the Sea of Japan and other areas (Okhotsk Sea and off the Pacific coast of northern Japan).

Following these studies, the International Whaling Commission (IWC) proposed and adopted some boundaries for these stocks between the Sea of Japan-Yellow Sea-East China Sea and the Okhotsk Sea-West Pacific (Donovan, 1991).

Various genetic studies have shown that both stocks mix with each other spatially and temporally in the southern part of the Okhotsk Sea (northern Hokkaido) (Wada, 1991; Pastene *et al.*, 1998) and on the Pacific side of Japan (Pastene *et al.*, 2016a). Since the publication of those studies, a substantial number of genetic samples of western North Pacific common minke whales became available, and modern and more powerful genetic markers have been applied in recent years to these samples. The application of such markers to both the previous samples as well as the new samples has enabled finer studies on stock structure of this species in this ocean basin (Pastene *et al.*, 2016a; b).

From 2009, msDNA has been used in genetic analyses of individual assignment to stocks (Kanda *et al.*, 2009a), for example, by using the program STRUCTURE (Pritchard *et al.*, 2000). This approach has allowed several biological and ecological aspects of J- and O-stock common minke whales to be studied separately.

The objective of this paper is to present an overview of the biological and ecological information (e.g., spatial/temporal distribution, morphology, morphometrics, reproductive characteristics, feeding ecology, environmental pollutants and ecological markers) so far accumulated for the J-stock common minke whales derived from analyses of genetically identified individuals with the aim of contributing to the better understanding and management of this stock.

Individual Assignment to Stocks Based on Microsatellite DNA Analyses

Microsatellite DNA

MsDNA became a popular genetic marker for many aspects of molecular ecology, in particular for intraspecific studies, because of its high mutation rate and polymorphisms compared to other markers (Estoup *et al.*, 2002). MsDNA consist of short tandem repeats of mono-, di-, tri-, or tetra-nucleotide repeats, e.g., (AT)n and (GATA)n, which are assumed to be randomly distributed throughout the genomes (Goldstein and Schlotterer, 1999). MsDNA show length variation that results from insertion and/or deletion of the repeat units, which is detected using PCR and separation of the products on capillary gel in the automated sequencer. Since allele sizes differ by as little as one base pair, it is required to have adequate and consistent standards to score the alleles.

Laboratory work of microsatellite DNA

Details of the laboratory procedures for msDNA analysis were described by Pastene and Goto (2016) and Taguchi *et al.* (2023). A summary is provided as follows.

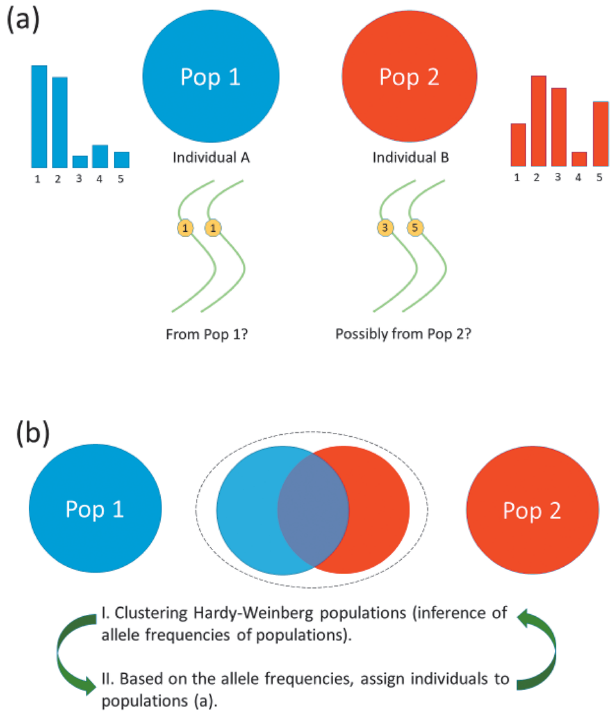
MsDNA polymorphisms were analyzed using 16 loci: EV1, EV14, EV21, EV37, EV94, (Valsecchi and Amos, 1996), GT23, GT195, GT211, GT310, GT509, GT575 (Bérubé *et al.*, 2000), GATA28, GATA98, GATA417, TAA31 (Palsbøll *et al.*, 1997), DlrFCB14 (Buchanan *et al.*, 1996). EV1, EV14, EV21 were developed from sperm whale, EV37, EV94, GT23, GT310, GT575, GATA28, GATA98, GATA417, TAA31 from humpback whale, and DlrFCB14 from beluga whale. All GT, EV and DlrFCB primers are dinucleotide repeats, TAA31 trinucleotide repeats, and all GATA primers tetranucleotide repeats. Primer sequences and PCR profiles followed those of the original authors with slight modifications.

PCR amplifications were performed in 15 μL reaction mixtures containing 10–100 ng of DNA, 5 pmole of each primer, 0.625 units of Ex Taq DNA polymerase (Takara Shuzo), and 2 mM of each dNTP, and 10x reaction buffer containing 20 mM $MgCl_2$ (Takara Shuzo). PCR amplifications followed the manufacturer's instructions for the use of Ex Taq DNA polymerase (Takara Shuzo). Amplified products with internal size standard (GENESCAN400HD, Applied Biosystems Japan) were run on a 6% polyacrylamide denaturing gel (Long Ranger^{TM}) using a BaseStation TM100 DNA fragment analyzer (Bio-Rad) or were electrophoresed on an Applied Biosystems 3500 Genetic Analyzer. Allele sizes were determined using a 600 LIZ size standard and GeneMapper v. 5.0 (ABI).

Data analysis for assignment of individuals to stock

Pastene *et al.* (2016a) and Taguchi *et al.* (2017) described the analytical procedures for stock assignment based on msDNA, and a summary is provided below.

The Bayesian clustering approach was implemented with the microsatellite data in the program STRUCTURE version 2.0 (Pritchard *et al.*, 2000) to determine the most likely number of genetically distinct stocks present in the samples. The program is a model-based clustering method for inferring stock structure (K is the number of stocks in the model) using multilocus genotype data with and without information on sampling locations. STRUCTURE allowed for the analyses of the samples without choosing sample units that did not necessarily correspond to real biological stock boundaries. A conceptual diagram of individual assignment under STRUCTURE is shown in Fig. 1. In a case of allele frequency at single loci (bar plot in this figure) in each source population being available (Fig. 1(a)), it is highly possible that individual A originates from population 1 since it has two alleles that are major in population 1. In contrast, individual B is likely to come from population 2 since it has two alleles that are minor in population 1. Another case is individual assignment with no allele frequency in each source population (Fig. 1(b)). Here, genotypes at multiple loci in each individual allow the estimation of an allele frequency for source population and an assignment probability in each individual by repeating the following steps: (I) estimation of allele frequency from tentative clustering in Hardy-Weinberg equilibrium, and (II) individual assignment based on the tentative allele frequency according to the concept of Fig. 1(a).



I. Clustering Hardy-Weinberg populations (inference of allele frequencies of populations).

II. Based on the allele frequencies, assign individuals to populations (a).

Fig. 1. Basic concept of individual assignment. Pop: population. (See "Individual assignment to stocks based on microsatellite DNA analyses" section for explanation).

Posterior probabilities for K were estimated from ten independent runs for each value of K from one to five with genetic information only. These data were calculated based on burn-in period of 10,000 iterations and runs of 100,000 iterations. Individual assignment was then conducted for the most plausible K using the estimated individual proportion of membership probability (90%). The ancestry model used for the simulation was the admixture model, which assumes individuals may have mixed ancestry. The allele frequency model used was the correlated allele frequencies model, which assumes that frequencies in the different stocks are likely to be similar due to migration or shared ancestry.

Unassigned whales are those with less than 90% membership probability in the STRUCTURE analyses. This could be due to lack of power, because when the number of loci used is increased, a larger number of individuals are assigned to either stock. Regarding the unassigned whales in the STRUCTURE analyses, a simple simulation exercise showed that the number of unassigned whales decreased with the increase in the number of microsatellite loci used, and that they were widely distributed geographically (Taguchi *et al.*, 2017). Therefore, it is confirmed that the number of loci used for assignment to the J- or O-stock is one of the factors leading to the unassigned individuals in the STRUCTURE analysis of common minke whale. This is also supported by an earlier study suggesting that, in practice, the accuracy of the assignments depends on the number of loci (Pritchard *et al.*, 2000).

Biological and ecological characterization of the J-stock

Several biological and ecological studies have been conducted on the J-stock common minke whale based on genetically assigned individuals to this stock as described in the above section. Table 1 shows a summary of studies examined in this overview by topic, data sources, number, sampling period and references. Unassigned individuals were excluded from the analyses of these topics, except for spatial/temporal distribution and ecological marker (cookie cutter shark scar) analyses. In this section, a brief summary of the results by study topic is provided.

As shown in Fig. 2(a), the IWC Scientific Committee (IWC SC) has defined sub-areas for the management of the common minke whales in the western North Pacific (IWC, 1994). Relevant sub-areas mentioned in this paper are sub-areas 7, 11, 2 and 6 (Fig. 2(b)). The western part of sub-area 7 (7W) corresponds to the coastal zone of Japan, while sub-areas 11, 2 and 6 correspond to northern Hokkai-

Table 1. Summary of different biological and ecological features studied on the J-stock common minke whales with sample information and key references.

Feature	Samples*	Year obtained	Source**	Reference
Distribution and movement				
Spatial distribution	$n=4{,}275$	1994 to 2014	JARPN/JARPNII; bycatch	Goto *et al.* (2017)
Temporal distribution	$n=2{,}522$	2001 to 2004	JARPNII; bycatch	Goto *et al.* (2017)
Distance from coastal line	$n=986$	1994 to 2007	JARPN/JARPNII; bycatch	Kanda *et al.* (2017)
Morphology and morphometry				
Flipper color pattern	$n=220$	2012 and 2013	JARPNII	Nakamura *et al.* (2016)
Fluke color pattern	$n=164$	2007	JARPNII	Nagatsuka (2008; 2010)
Morphometry	$n=500$	2000 to 2007	JARPN/JARPNII	Hakamada and Bando (2009)
Reproduction				
Conception date	$n=107$	1994 to 2007	JARPN/JARPNII	Bando *et al.* (2010a)
Feeding ecology				
Stomach contents	$n=742$	1996 to 2018	JARPN/JARPNII; NEWREP-NP	Goto *et al.* (2021)
Ecological markers				
Total Hg levels	$n=59$	2012 and 2013	JARPNII	Yasunaga and Fujise (2016)
Cookie cutter shark marks	$n=1{,}037$	2002 to 2007	JARPN/JARPNII	Bando *et al.* (2010b)

**n*: Number of animals used in the analyses.

**JARPN: Japanese Whale Research Program under Special Permit in the western North Pacific. JARPNII: JARPN Phase II; NEWREP-NP: New Scientific Whale Research Program in the western North Pacific.

do, the southern part of the Pacific side of Japan and the Sea of Japan side of Japan, respectively.

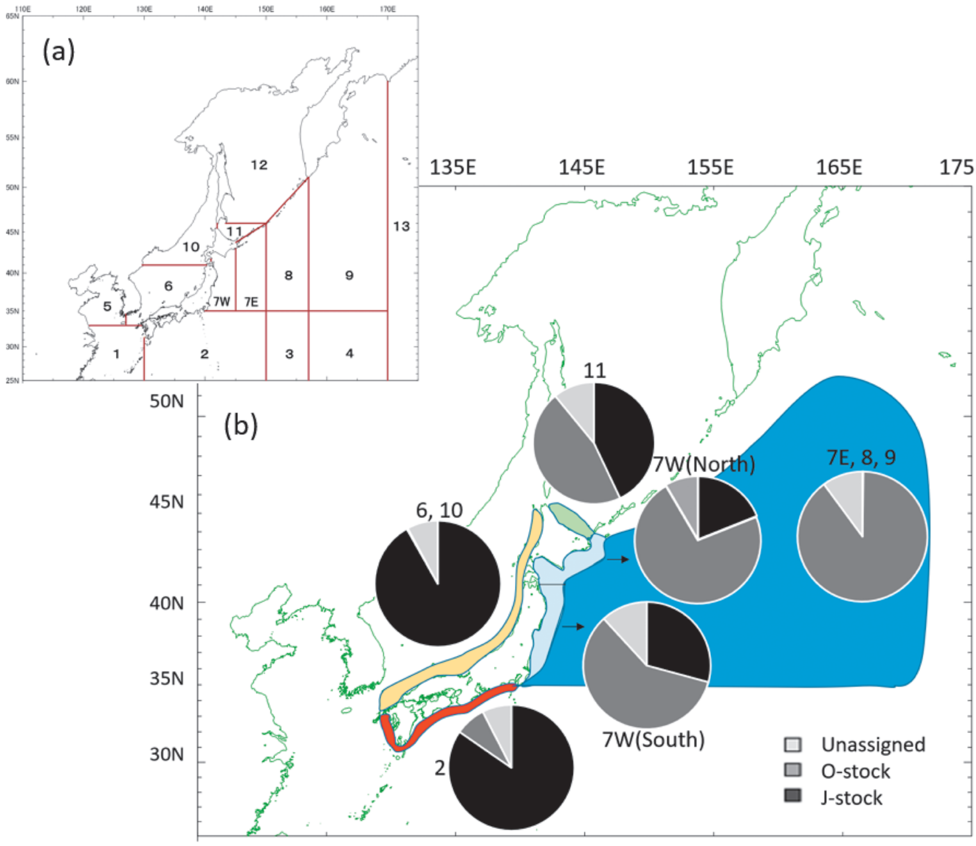


Fig. 2. (a) The 13 sub-areas defined for North Pacific common minke whale management trials (modified after IWC, 1994) and (b) spatial occurrence of O- and J-stock common minke whales in each sub-area around Japan based on genetic individual identification (modified after Goto *et al.*, 2017).

Distribution and movement

Spatial distribution of the J-stock along the coast of Japan

As shown in Fig. 2(b), almost all the individuals collected from the Sea of Japan side belong to the J-stock, whereas almost all of the individuals from the offshore North Pacific belong to the O-stock (Goto *et al.*, 2017). The southern part of the Pacific side of Japan was mainly occupied by the J-stock, while Northern Hokkaido and the northern part of the Pacific side of Japan are areas where both stocks overlap geographically (Goto *et al.*, 2017). Areas relevant for the J-stock are sub-areas 2, 6, 7W and 11.

Temporal distribution along the Pacific coast of Japan

Goto *et al.* (2017) showed the monthly occurrence of O- and J-stocks in sub-areas 2 and 7W (South) on the Pacific side of Japan (Fig. 3). In the southern part of the Pacific side of Japan (sub-area 2), J-stock was predominant throughout the year (around 80% in proportion). In the southern part of the Pacific side of Japan (sub-area 7W (South)), the proportion of the J-stock increased in autumn/winter and decreased in spring/summer. Conversely, the proportion of O-stock decreased in autumn/winter and increased in spring/summer. Goto *et al.* (2017) postulated that the fact that the J-stock is distributed in the southern part of the Pacific side of Japan throughout the year suggests that the Kuroshio Current—one of the strongest west boundary currents of the subtropical gyre—is serving as a dynamic stock boundary between O- and J-stocks.

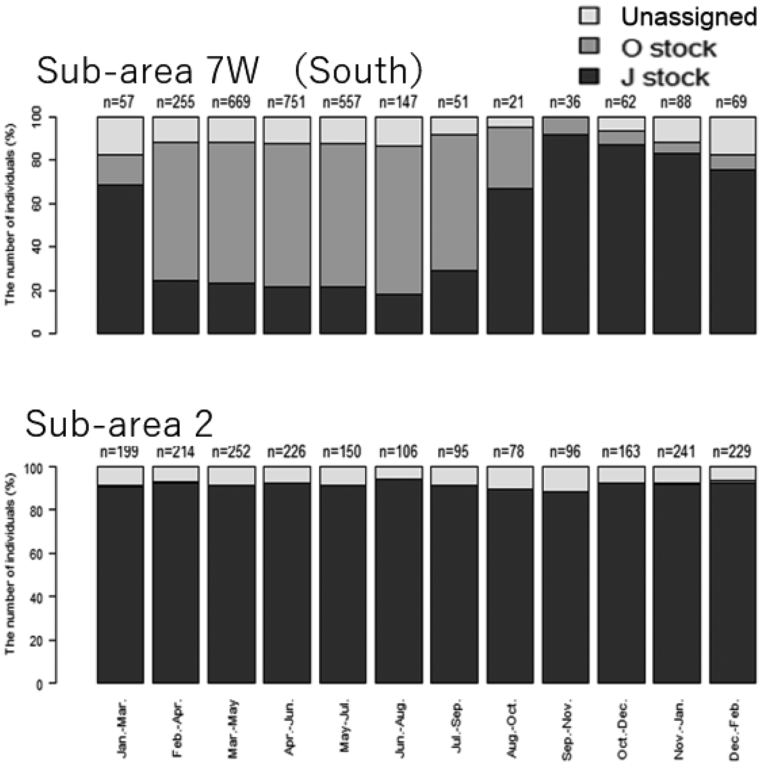


Fig. 3. Monthly occurrence of O- and J-stock common minke whales in sub-areas 7W (South) and 2 on the Pacific side of Japan. Each bar is expressed as a three-month moving average. Sample size (*n*) is shown on the top of each bar (modified after Goto *et al.*, 2017).

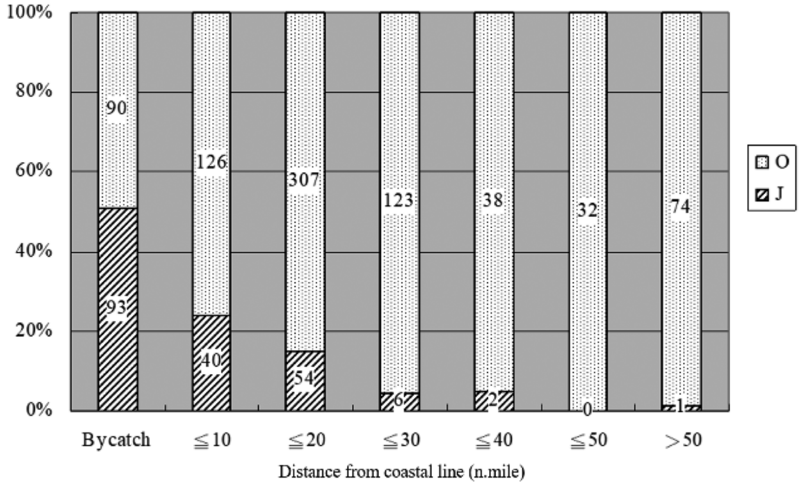


Fig. 4. Proportion of the common minke whales assigned to the J- and O-stocks collected from sub-area 7W by the distance from Japan's coastal line (after Kanda *et al.*, 2010). The numbers in the bars indicate sample size. Bycatches occur within 3 n.miles from the coastal line.

Distance from the coastal line

Kanda *et al.* (2010) estimated the proportion of the minke whales assigned to the J- and O-stocks collected from sub-area 7W by the distance from the Japanese coastal line (Fig. 4). J-stock whales have a more coastal distribution in comparison with the O-stock. The proportion of the J-stock whales decreased from coastal areas towards offshore areas. Such a clinal distribution supports the mixing of the two stocks in sub-area 7W. This means that the main migration routes of J-stock animals, especially juveniles which are predominant in the bycatch samples (Pastene *et al.*, 2016a), might be along the nearshore areas that follow the coastal line of Japan on the Pacific and Sea of Japan sides. The distribution of J-stock animals on the Pacific side of Japan decreased from coastal areas towards offshore areas (Fig. 4).

Migratory routes

Based on the studies by Hatanaka and Miyashita (1997) and Goto *et al.* (2010), it was assumed that the migratory routes of adult and juvenile J-stock animals to feeding areas were as shown in Fig. 5. Although the breeding area(s) of these animals had not been identified at this stage, migratory routes to breeding area(s) were assumed to be the reverse in the case of adults. Adult animals were assumed to migrate northward and southward for feeding and breeding, respectively, through the central corridor of the Sea of Japan. The northward migration limit was not clear at this stage because there were no genetic samples available from the central and northern parts of the Okhotsk Sea. In the case of juveniles, it was assumed that they were making short northward and southward migrations along the coastal area for feeding because bycatch juvenile animals were reported throughout the year on the Japanese coast (Pastene *et al.*, 2016a; Goto *et al.*, 2017).

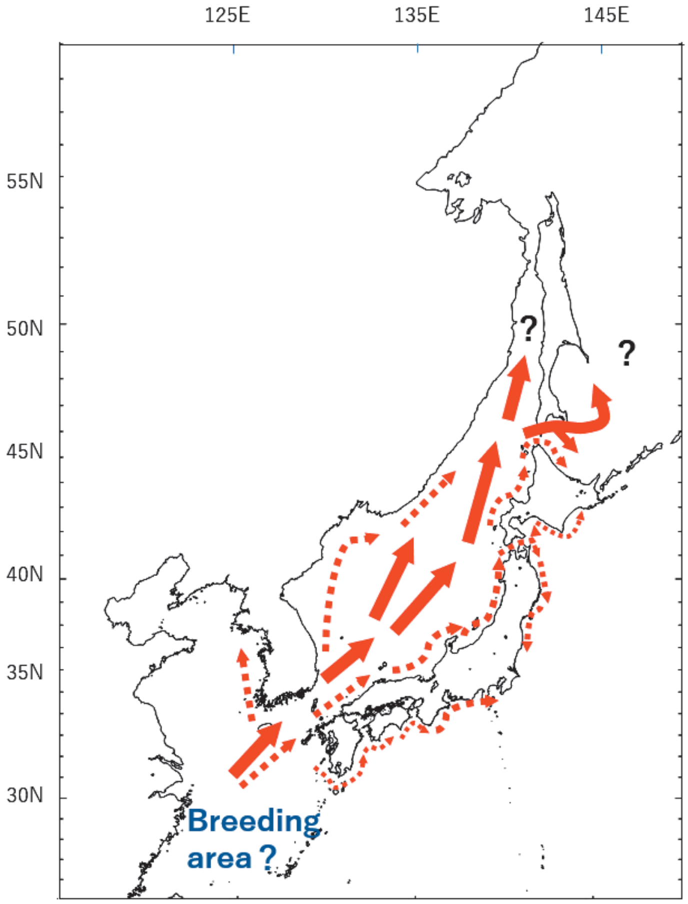


Fig. 5. Assumed feeding migration route of J-stock common minke whales (modified after Hatanaka and Miyashita, 1997 and Goto *et al.*, 2010). Solid red arrows: mature animals, dotted arrows: immature animals. The northward migration limit and the breeding areas of these animals has not been identified at this stage. Adult animals were assumed to migrate northward through the central corridor of the Sea of Japan, while juveniles were assumed to make short northward and southward migrations along the coastal area.

Morphology and morphometry

Morphology

Nakamura *et al.* (2016) studied the white patch on the flipper, which is characteristic of common

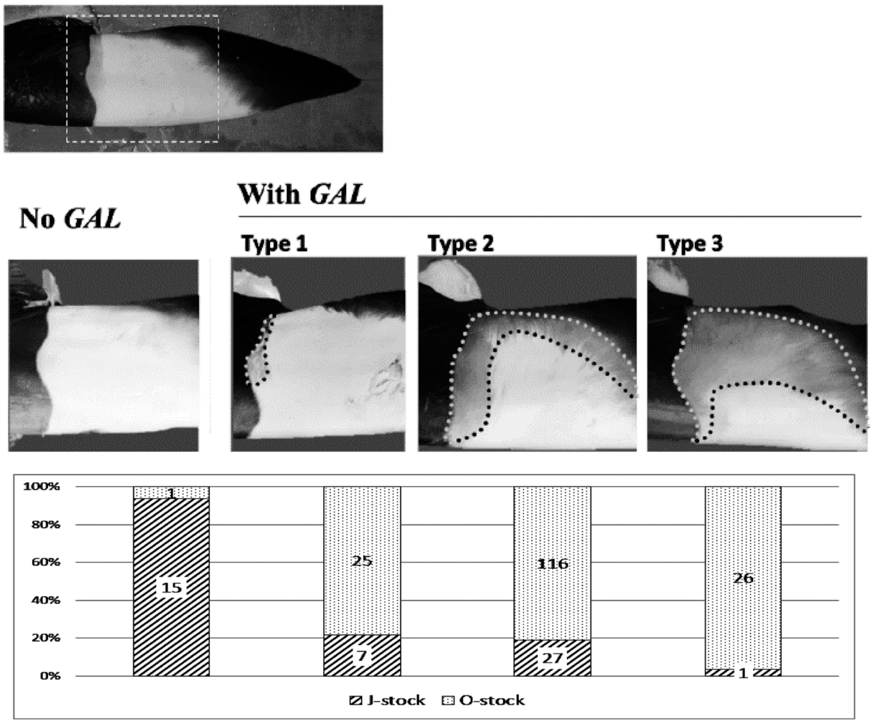


Fig. 6. Characteristics of the white patch along the ventral part of the flipper in common minke whales from the western North Pacific. The pictures show the basis for the classification based on the *GAL* types (*GAL*: surrounded by dotted line), and the bar plots show the proportion of each GAL types between J- and O-stocks (modified after Nakamura *et al.*, 2016). Bar figures indicate number of individuals.

minke whales, based on individuals assigned genetically to the J- and O-stocks. For the analyses on morphological differences the authors used whales sampled by the Japanese Whale Research Program under Special Permit in the western North Pacific Phase II (JARPNII) during 2012 and 2013. They focused on the morphological differences in the size and pattern of the white patch on the flipper of each whale. The length of the white patch along the anterior (ventral) margin of the flipper tended to be proportionally smaller in the J-stock. The pattern of the boundary area of the white patch named as the ‘Grayish Accessary Layer (GAL)’ was remarkably different between the two stocks (Fig. 6). Among animals with ‘no GAL’ type, 94% were J-stock. Conversely, 96% of the animals with GAL expanding over half of the flipper width were O-stock.

Fluke color pattern

Nagatsuka (2008) found that common minke whales had different black and white color patterns in the ventral fluke pigmentation and characterized their color patterns into three types, according to the proportion of white and black colors: white fluke, intermediate fluke and black fluke (Fig. 7). Statistically significant differences in the frequencies of these three types were observed between the individuals assigned genetically as J- and O-stocks sampled during the 2007 JARPNII survey in sub-area 7W. The white type was predominant in the J-stock whales while the intermediate and black types were predominant in the O-stock.

Morphometry

Hakamada and Fujise (2000) examined external measurement data of whales obtained during the 1994–1999 JARPN surveys (external measurements for V1–V9 in Fig. 8 and additional data for length of tip to posterior insertion and maximal width of flipper, and for width of fluke tip). They found statistically significant differences between the individuals identified genetically as J- and O-stocks. The

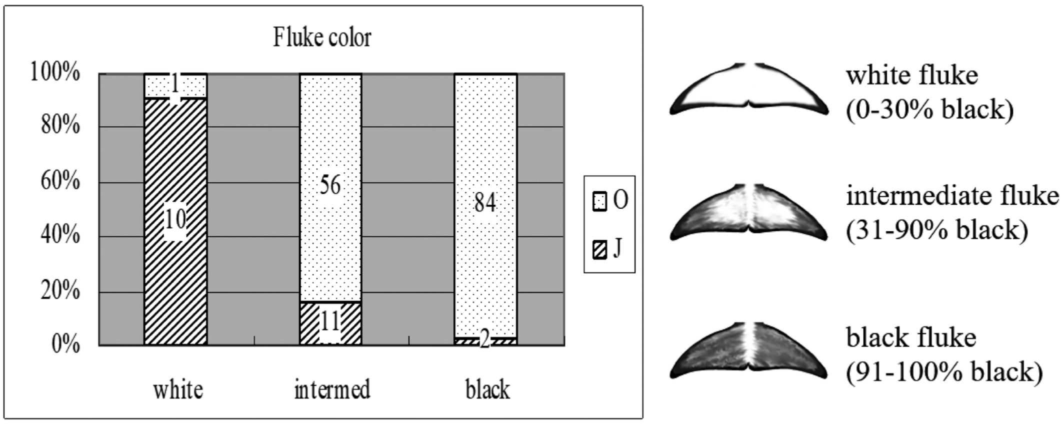


Fig. 7. Proportion of J- and O-stock-assigned common minke whales collected from sub-area 7W by the fluke ventral color pattern, and diagram of the three patterns (after Kanda *et al.*, 2010). The numbers in the bars indicate the sample size.

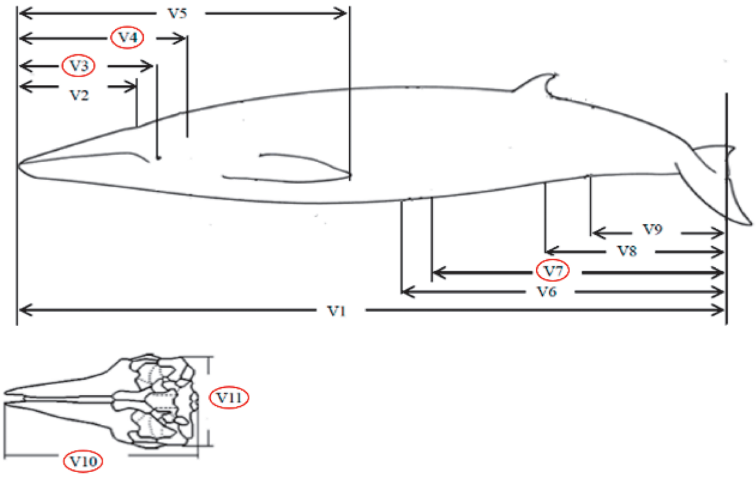


Fig. 8. External measurements of western North Pacific common minke whales examined for comparative stock analyses (after Hakamada and Bando, 2009). Measurements V3, V4, V7, V10 and V11, indicated with red ellipses, showed significant differences in morphometrics between J- and O-stocks.

average marginal mean of the length of the measurements V2–V4, width of flipper and width of fluke tip were longer for J-stock animals than for O-stock animals.

Hakamada and Bando (2009) examined morphometric data (Fig. 8) of common minke whales sampled by JARPNII and identified genetically as J- and O-stocks. Measurements V3, V4, V7, V10 and V11 showed statistically significant differences between J- and O-stocks. This result suggested that external measurements can be used as a non-genetic marker to differentiate J-stock from the O-stock. For example, the average marginal mean of the length of the measurements V2–V5 were longer for J-stock animals than for O-stock animals. Measurements of V6–V9 were shorter for J-stock animals than for O-stock animals, while measurements of V10–V11 were longer for J-stock animals than for O-stock animals. These results suggested that J-stock animals tend to have bigger heads and shorter tail bodies than O-stock animals.

Reproduction

Conception date

Kato (1992) estimated conception date from fetal body length. He found two peaks of conception in samples from southern Okhotsk Sea and the Sea of Japan, one in autumn and another in winter. This

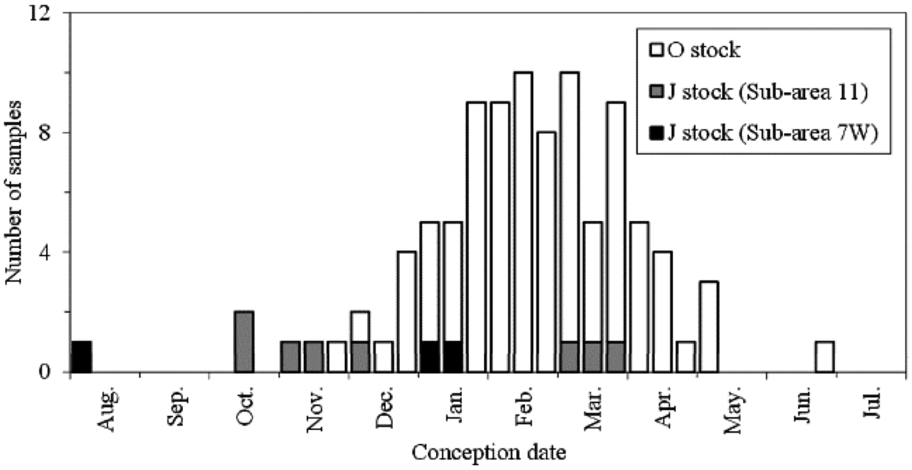


Fig. 9. Seasonal distribution of estimated conception dates of the J- and O-stock common minke whales in ten-day periods (after Bando *et al.*, 2010a).

was further endorsed by Best and Kato (1992). Subsequently, Bando *et al.* (2010a) examined conception dates of common minke whales sampled in sub-area 7W and sub-area 11 during the 1994–2007 JARPN/JARPN II surveys and identified genetically as either J- or O-stock individuals. Conception dates were estimated based on the formula of Kato and Miyashita (1991), which was developed for Antarctic minke whales and used for common minke whale in Kato (1992). In sub-area 7W the conception date of J-stock whales was in August ($n=1$) and January ($n=2$); in sub-area 11 it was between October and March ($n=8$) (Fig. 9). These results suggested that the conception period of the J-stock extends from autumn to winter, while the O-stock whales appear to have one peak in winter. However, the distributions of conception period for J- and O-stock overlapped with each other.

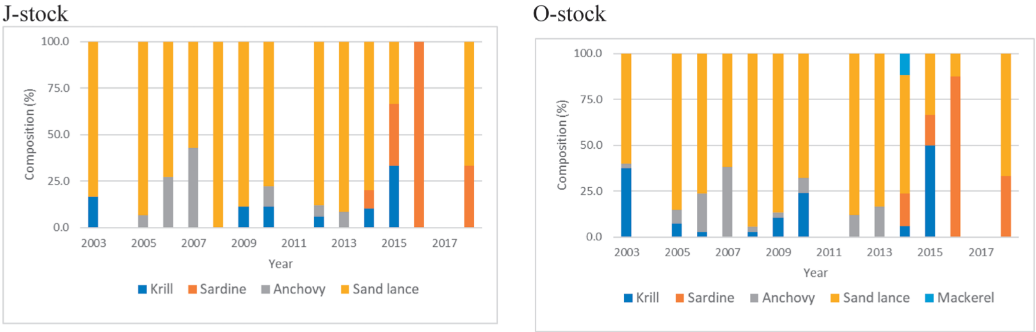
Feeding ecology

The feeding ecology of common minke whales around Japan has been examined by Kasamatsu and Tanaka (1992), Tamura and Fujise (2002) and Konishi *et al.* (2009). However, there have been few published papers specifically focused on the feeding habits of J-stock common minke whales. In order to simplify the comparison of feeding indices, Goto *et al.* (2021) divided prey species into the following based on the stomach contents of these whales: copepods, krill, Japanese sandlance *(Ammodytes personatus)*, Japanese anchovy *(Engraulis japonicus)*, Pacific saury *(Cololabis saira)*, walleye pollock *(Gadus chalcogrammus)*, Japanese common squid *(Todarodes pacificus)*, and others. The relative prey composition (%) in weight of each prey species in each month and sub-area was calculated. Results of the first analyses of genetically identified J-stock individuals showed that these whales fed on various prey species and that the main prey species changed both yearly and geographically (Fig. 10). These results suggested that the J-stock common minke whales are opportunistic feeders, changing their prey species in response to availability, having a feeding habit similar to the O-stock whales.

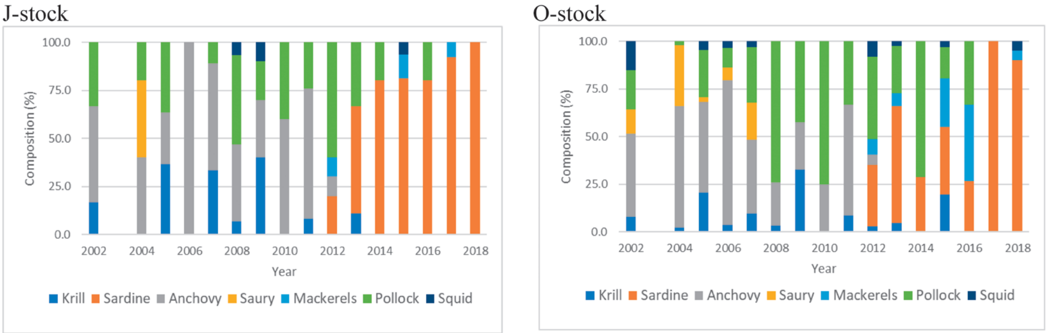
Environmental pollutant (total Hg) levels

Yasunaga and Fujise (2016) compared the accumulation patterns of total Hg concentrations in muscle and liver in genetically identified J- and O-stock common minke whales. Their analyses were based on J- and O-stock immature animals taken from sub-area 7W in the 2012 and 2013 JARPNII surveys (Fig. 11). Statistical analyses showed no significant differences in the level of pollutant concentration confounding factors such as age, sex, blubber thickness and year. This result suggests that there are few differences in trophic levels and food items between the J- and O-stocks of immature whales in sub-area 7W.

Sanriku (sub-area 7W, South)



Kushiro (sub-area 7W, North)



Abashiri (sub-area 11)

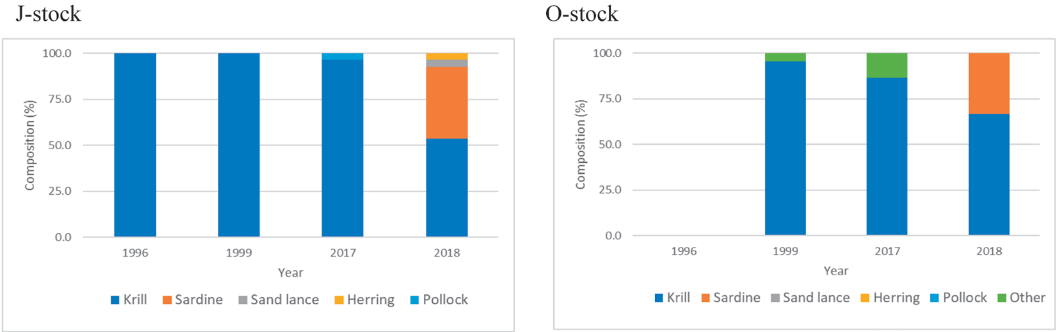


Fig. 10. Yearly and geographical change of main prey species of J- and O-stock common minke whales in Sanriku (southern part of sub-area 7W), Kushiro (northern part of sub-area 7W) and Abashiri (sub-area 11). (After Goto *et al.*, 2021; this study).

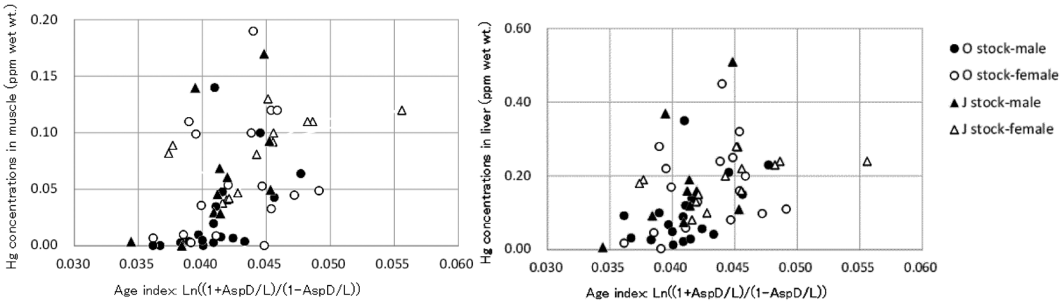


Fig. 11. Relationship between Hg concentrations (ppm wet wt.) and age in muscle (left) and in liver (right) in common minke whales from sub-area 7W (after Yasunaga and Fujise, 2016).

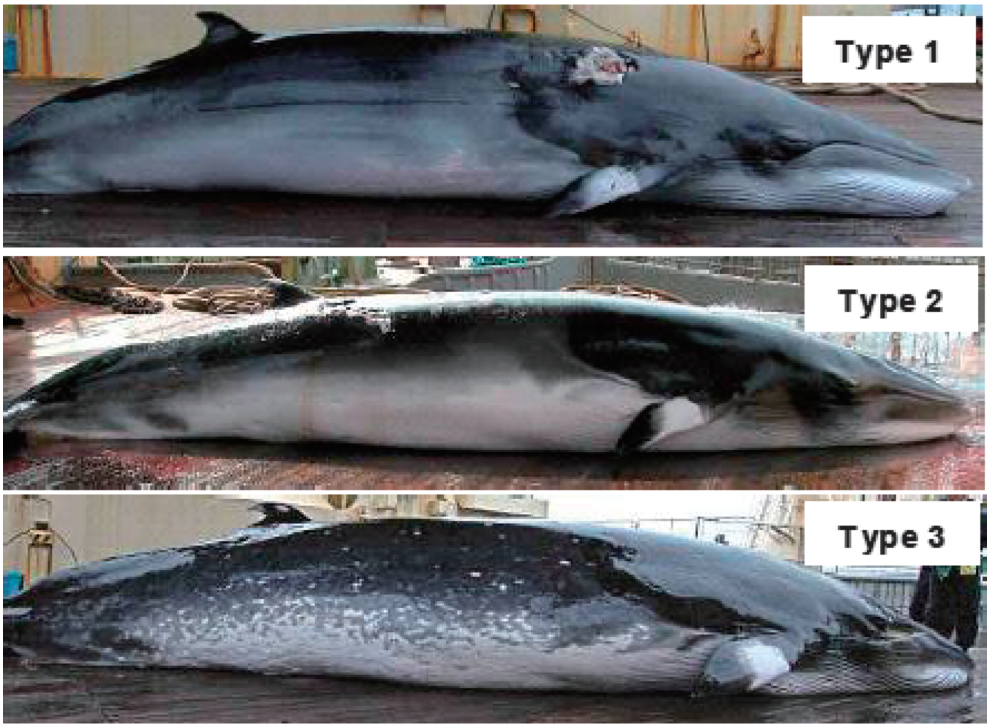


Fig. 12. Three types of cookie cutter shark-induced scar presence patterns in common minke whales. Type 1: no scars on the body (Sample No. 2006NP-M080: J-stock), Type 2: 1–20 scars on a single body side (2002NP-M061: J-stock), and Type 3: more than 20 scars on a single body side (2006NP-M067: O-stock) (after Bando *et al.*, 2010b).

Table 2. Types of cookie cutter shark-induced scars in common minke whales in the coastal areas of western North Pacific off sub-area 7W (North and South) and Pacific offshore area (sub-areas 8 and 9) (modified from Bando *et al.*, 2010b).

Sub-area	Type of scar		Microsatellite DNA		
			O	?	J
7W North	*Type 1*	None	0	2	17
	Type 2	1–20 scars	14	5	31
	Type 3	more than 20 scars	291	31	5
		Total	305	38	53
7W South	*Type 1*	None	0	3	19
	Type 2	1–20 scars	10	5	22
	Type 3	more than 20 scars	213	25	2
		Total	223	33	43
8	*Type 1*	None	0	0	0
	Type 2	1–20 scars	3	1	0
	Type 3	more than 20 scars	95	11	0
		Total	98	12	0
9	*Type 1*	None	0	0	0
	Type 2	1–20 scars	4	1	0
	Type 3	more than 20 scars	203	23	1
		Total	207	24	1

?: Unassigned.

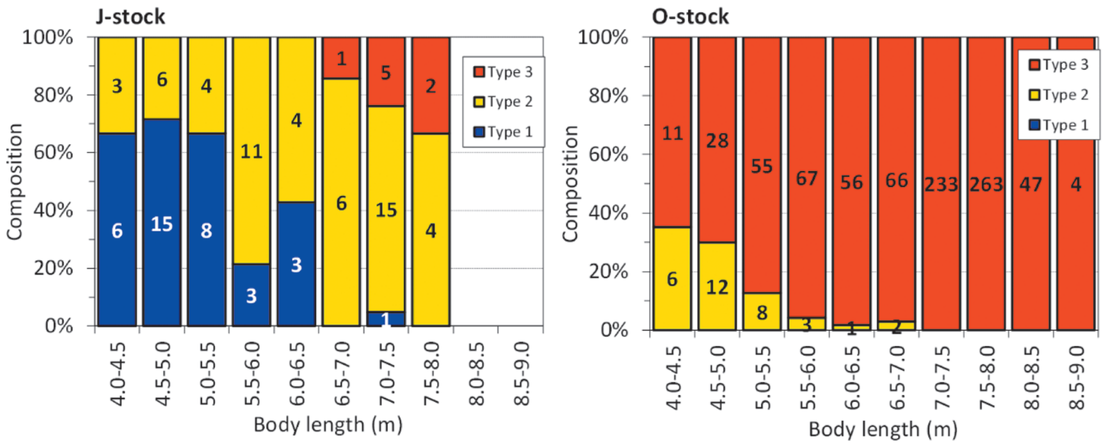


Fig. 13. Proportion of cookie cutter shark-induced scar types by body length class in J- and O-stock common minke whales. Bar numbers indicate sample size (after Bando *et al.*, 2010b).

Ecological markers

Cookie cutter shark scar

Bando *et al.* (2010b) investigated the presence of cookie cutter shark-induced scars in common minke whales identified genetically as J- and O-stock individuals. Whales examined were sampled in sub-areas 7W and 8 and 9 by JARPNII surveys during 2002–2007. Three types of common minke whales were identified from the density of scars found in the lateral side of the body: Type 1: no scars on the body, Type 2: 1–20 scars on a single side of the body, and Type 3: more than 20 scars on a single side of the body (Fig. 12). Prevalence of scars differed clearly between both stocks, and J-stock animals had fewer scars than the O-stock animals (Table 2 and Fig. 13). Although the scar prevalence increased with body length in both stocks, there are distinct differences consistent with their occurrence. J-stock whales with fewer scars were distributed in coastal areas while the O-stock whales with more scars were distributed in both coastal and offshore areas.

Conclusion

Table 3 shows a summary of the biological and ecological characteristics of genetically identified J-stock common minke whales. The individual identification from genetic marker analysis has been very useful in determining stock characterization and investigating differences in several features, such as distribution and movement, morphology and morphometry, reproduction, feeding ecology and environmental pollutants. Except for feeding ecology and environmental pollutant (total Hg) levels, these features indicate that J-stock individuals are biologically and ecologically differentiated from O-stock individuals. The existence of genetically, biologically and ecologically distinct and independent stocks mixing in a specific geographical area is unusual for baleen whales. The J-stock can be defined as a group of individuals sharing a common gene pool maintained by random mating and should therefore be managed independently. Some future works are being considered to improve the biological and ecological knowledge of the J-stock: i) investigation of the possibility whether some morphological and ecological features (e.g., white patch on the flippers and cookie cutter shark scars) can be used to identify J-stock individuals from the vessels in areas where biopsy samples for genetics cannot be collected (e.g. in the Russian territorial waters), ii) investigation of the northern limit of migration and distribution of J-stock animals by conducting sighting surveys and biopsy sampling in the relevant areas, iii) undertaking focused research to understand migratory corridors and breeding ground locations using the satellite tagging and to collect and analyze the genetic, biological and ecological information from these localities and iv) estimate other biological and ecological characteris-

Table 3. Summary of the biological and ecological features of the genetically identified individuals of J-stock common minke whales examined in this study.

Feature	Overview
Spatial distribution	Whales occupy the Sea of Japan side and the southern part of the Pacific side of Japan; they overlap geographically with O-stock in northern Hokkaido and the northern part of the Pacific side of Japan.
Temporal distribution	Whales are predominant throughout the year in the southern part of the Pacific side of Japan. Their proportion increases in autumn/winter and decreases in spring/summer in the northern part of the Pacific side of Japan.
Distance from the coastal line	Their proportion decreases from coastal towards offshore areas.
Flipper color pattern	Characterized for almost no GAL* in their flippers in comparison with the O-stock (Fig. 6).
Fluke color pattern	Characterized by a higher proportion of white color in the ventral side of flukes in comparison with the O-stock (Fig. 7).
Morphometry	Characterized by bigger heads and shorter tail bodies in comparison with the O-stock.
Conception date	Most likely extends from autumn to winter.
Feeding ecology	Feeding habits are similar to those of the O-stock.
Environmental pollutant (total Hg) levels	Levels are similar to those of the O-stock in the coastal waters of Japan. Levels suggest that the health risk is low.
Cookie cutter shark scar	Fewer scars in comparison with the O-stock (Fig. 13).

*: Grayish Accessory Layer.

tics such as abundance, growth and maturity. It is also important that efforts are made to investigate the occurrence, distribution and stock structure of common minke whales migrating around Chinese and Korean Peninsula waters, and the genetic, biological and ecological relationship with whales distributed in the sub-areas around Japan. Investigation of the stock structure in those waters is important as a number of annual bycatches have been reported from the Korean Peninsula through the collaboration with Korean scientists. All such projects would be aimed at further enhancing the assessment and the understanding and management of J-stock common minke whales.

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