Stock structure scenario of common minke whales from the Japanese waters as revealed by genetic data

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ABSTRACT
The Working Group on the in-depth assessment of western North Pacific common minke whales, with a focus on J stock, agreed to have four stock structure hypotheses for the J stock common minke whales in the sub-areas (SA) 5 and 6.   Although not listed as standing hypotheses, some members of the group also raised two additional stock structure hypotheses that extended covering geographic area to the Pacific east of Japan.   In this paper, although it is restricted to the Japanese waters, we evaluated how consistent the results from our recent genetic studies of common minke whales from the area (Goto *et al*., 2009; Kanda *et al*., 2009a, 2009b) to these hypotheses.

KEYWORS: COMMON MINKE WHALES, J STOCK, STOCK STRUCTURE HYPOTHESES.

INTRODUCTION
In order to investigate stock structure of common minke whales in the Japanese and Korean waters, Japanese and Korean scientists have worked together intersessionally to analyze the samples from Japan and Korea using genetic data (mtDNA and microsatellites).   On the basis of the results from the these analyses, the Working Group on the in-depth assessment of western North Pacific common minke whales, with a focus on J stock, agreed the following four stock structure hypotheses (IWC, 2007).

(1) One stock in the SA5 and SA6.
(2) Two stocks in the SA5 and SA6.   The one stock migrates along the Japanese coast, and the other migrates along the Korean coast.
(3) Two stocks.   One migrates up to the SA5 and the other migrates further north in the SA6 along the both Japanese and Korean coast.
(4) Two stocks.   Both migrate through the SA6 in different time of the year.

Last year at the SC meeting, some members of the group raised two additional stock structure scenarios (named (5) and (6) for this paper) that extended covering geographic area to the Pacific east of Japan, i.e., SA2 and SA7 although the working group disagreed to list as standing hypotheses (IWC, 2009).

(5) Two stocks in the SA5 and SA6.   This one is same to the (3) except the stock in the SA6 extends its distribution to the SA2 and co-occupies the SA7 with the O stock
(6) Four stocks.   One in the SA5, one migrating along the Korean coast, one migrating along the Sea of Japan coast, and the other migrating along the Pacific coast.

Common feature for the (5) and (6) different from the first four is that the SA2 is not the area for the O stock.

Plans were made to conduct analyses by the Japanese and Korean scientists to describe the stock structure of common minke whales around the Japanese and Korean waters and then to evaluate these hypotheses. Unfortunately the Korean data set was incomplete for proceeding with the analyses, and was not finalized by the 61SC.   Therefore, the most recent genetic analysis we present to this SC meeting (Goto *et al*., 2009; Kanda *et al*., 2009a, 2009b) examined the stock structure of the common minke whales around the Japanese waters using only the Japanese samples.

Questions to be addressed under the above 6 hypotheses are (a) how many different stocks exists around the Japanese waters, (b) if there are different stocks migrating along the Sea of Japan coast, and (c) if

there are different stocks in the SA6 and SA2 in addition to the O stock.

RESULTS AND DISCUSSION

Kanda *et al*. (2009a, i.e., SC/61/JR5) attempted to distinguish sampled minke whales into genetically distinct stocks using a combination of microsatellite analysis and a Bayesian clustering approach implemented in the computer program STRUCTURE (Pritchard *et al*., 2000).   Samples of 2542 minke whales were collected during the offshore component of JARPN and JARPNII from 1994 to 2007, during the coastal component of JARPNII from 2002 to 2007, and from bycatches in the set net fishery along the Japanese coast from 2001 to 2007, and were analyzed using 16 microsatellite loci.   Result of the clustering analysis indicated that the samples came from two genetically different groups of minke whales. Assignment of the individuals in the samples was conducted based on the membership probabilities obtained from the program, and more than 90% of the individuals were assigned into the either stocks with high membership probabilities.   After the assignment, these individuals were then grouped based on their sampling origins.   Spatial distribution of these individuals clearly indicated that these two stocks were the J and O stocks because individuals from the Sea of Japan and offshore North Pacific tended to be assigned in the different group.   The results also showed that the SA2 was mainly occupied by the J stock with some O stock individuals entered, and that both the J stock and O stock co-occupy the area in the SA7 very close to the coastal line.   In addition, the number of the J and O stock individuals and that of the immature mature individuals differed in between the bycatch and JARPN/JARPNII samples in the SA7 as well as SA11.

Kanda *et al*. (2009b) and Goto *et al*. (2009) then looked for any evidence of genetic differences in microsatellite allele and mitochondrial DNA (mtDNA) haplotype frequencies among these samples around Japan in order to look for evidence of sub-structuring of the J stock.   They used the JARPN and JARPNII samples from 1994 to 2007 at the SA7W (140-147°E) and SA11 and the bycatch samples from set net fishery along the Japanese coast from 2001 to 2007.   The individuals in the samples were labeled as either the J stock, O stock, or unknown origin based on the assignment in the Kanda *et al.* (2009a) for the heterogeneity tests.   The heterogeneity tests were conducted in the two ways: one used all the individuals in the samples and the other used only the J stock individuals in the samples.   The samples of all individuals contained not only the J stock individuals but also the O stock individuals and the individuals of unknown origins.   The proportions of the J and O stock individuals were quite different among the subareas while the proportion of the individuals of unknown origins was similar to each of the subareas.   Both analyses showed the same results.   Among all of the heterogeneity tests conducted, significant differences were detected only from the tests that included all individuals.   The genetic heterogeneity was found among the samples from the different sub-areas.   In addition, the genetic heterogeneity was observed in the SA7 between the samples collected from the different seasons of the year and between the samples from the JARPN/JARPNII and bycatch samples.   The authors of these papers then concluded that the genetic heterogeneities observed were most likely due to the spatial and temporal differences in the proportion of the J and O stocks, but not the existence of different stocks, indicating that only the single J stock with no sub-structuring existed around the Japanese waters.

With respect to the evaluation of how consistent the results of our genetic studies to the hypothesis, we believe useful new information has been obtained.   First of all, only two stocks distribute around the Japanese waters, the J and O stocks.   If the assignment of the whales to the J and O stocks conducted in Kanda *et al.* (2009a) had been unreliable, we could have detected statistically significant differences between some of the samples even in the only J stock individuals group.

Secondly, our results do not support the hypotheses proposing that minke whales from two different stocks migrate along the Japanese coast in the Sea of Japan at the different time of the year because we found no seasonal genetic difference in the SA6 samples.   We believe that the sample sizes for this test (Early = 188, Late = 223) was reasonably large to say that (Goto *et al*., 2009; Kanda *et al*., 2009b).

Thirdly, the SA2 is not the area for the O stock.   With respect to this, hypotheses (1) to (4) are equally unlikely.

Finally, no sub-structuring of the J stock was found around Japan, that is, the individuals from the same single J stock occupy the Japanese waters.   Simulation study we conducted indicated that from genetics standpoint the statistical power for testing the J sub-stocks with our data set was quite high (Kanda *et al*.,

2009b).   It might not be surprising that the microsatellite study (Kanda *et al*., 2009b) failed to find the genetic differences among the samples in the case of the only J stock individuals because the samples were grouped *a priori* based on the genetic variation at the microsatellite loci (i.e., Kanda *et al*., 2009a). However, that means one agrees our assignment analysis was reliable.   We also stress that the analysis using independent mtDNA marker showed the same results, increasing the confidence to our results (Goto *et al*., 2009).   Our results indicated the hypothesis (6) is unlikely.

Stock structure scenario we propose from our results is that only one J stock exists around Japan whose main distribution area is the Sea of Japan and SA2 of the North Pacific and share coastal zone of the SA7 with the O stock.   In the SA11, the J stock individuals appear to be dominant in the coastal area while both of the O and J stock ones exist in the offshore area.   In the SA12 of the Okhotsk Ocean, although small proportion of the J stock individuals appear to exist only south part and only the O stock ones enter the north part (e.g., Hakamada *et al*., 2009), no genetic data has been available so far.

It is important to note at this last moment is that sampling locations of the bycatches are restricted within 3 n.m. and most of them are immature whales (see Kanda et al., 2009a), suggesting that the number of the O stock individuals migrating into the offshore area of the SA2 may be higher than that expected from our studies as seen in the SA7 and SA11.

ACKNOWLEDGEMENTS

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