Scientific background supporting the stock scenarios proposed in SC/J02/NP7

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- The stock structure scenarios proposed by Pastene, Goto and Kanda (options i) and ii) in SC/J02/NP7) are based on the results of extensive and intensive genetic analyses based on hypothesis testing (see Appendix 1 of the Report of the Small Genetic Meeting), complemented with the results of the analysis of other non-genetic data. The analyses have been based on the western North Pacific sub-areas, used under the RMP.

- Although the results suggested a temporal mixing of J and O Stocks in sub-area 11 (e.g. Pastene *et al.*, 1998), no strong evidence supporting additional stock structure in sub-areas 7, 8 and 9 has been found. These results indicate no evidence of clear multi-stock structure in sub-areas 7, 8 and 9, supporting our scenario i) in SC/J02/NP7.

- Option ii) in SC/J02/NP7 is based on the following considerations: Some genetic analyses based on mtDNA found low P values (but not significant at the 5% significant level) in the comparisons involving sub-area 9 (Taylor, 2000 for chi-square analysis; Goto and Pastene, 2000 for Fst analysis). To investigate the source of these low P values, Goto *et al.* (2000) conducted additional mtDNA analysis based on a post-stratification of the samples. They concluded that a possible source of mtDNA heterogeneity was attributed to minke whales sampled in the western part of sub-area 9 in 1995. When the 1995 9W sample is excluded from the analysis, no significant heterogeneity is observed at all in sub-areas 7, 8 and 9 indicating that whales distributed in these sub-areas mostly consist of the members of a single stock, and that members of other stock occasionally appear in 9W.

- A similar situation occurred in the samples from sub-area 9W in the 2000 and 2001 JARPN II surveys. It should be noted that the sample sizes in these cases were low, 16 and 29 whales, respectively and no definitive conclusion can be derived from such samples. Goto *et al.* (2001) demonstrated that the source of heterogeneity in the 1995 sub-area 9W sample was attributed to a frequency of a particular haplotype ('9'), which was higher than that observed in sub-area 9E in 1995 and those observed in sub-areas 7 and 8.

- When the samples from the western part of sub-area 9 in 1995, 2000 and 2001 were excluded from the analysis, no mtDNA heterogeneity was observed in sub-areas 7, 8 and 9 (SC/J02/NP10).

- Analysis based on nuclear DNA markers (microsatellite) suggested only a single (and weak) source of genetic heterogeneity attributed to the samples of sub-area 9W in 2001 (SC/J02/NP11).

- Considering that a) mtDNA heterogeneity in 1995, 2000 and 2001 could be attributed to sampling bias (e.g. the covering of JARPN surveys in these years could have been restricted both geographically and temporally), b) sample sizes in 9W in 2000 and 2001 are small, c) no evidence of the occurrence of W stock has been found in sub-area 9E and d) the results of other non-genetic approaches (morphometry, pollutant, reproductive data) indicate no evidence for additional structure in sub-areas 7, 8 and 9, we give more weight to option i) of the proposal presented in SC/J02/NP7. However we do not discard the possibility that the mtDNA heterogeneity found in sub-area 9W is due to the sporadic occurrence of a different stock. Then we also propose option ii) but with a lower weight.

References:

Goto, M. and Pastene, L.A. 2000. Population structure in the western North Pacific minke whale based on RFLP and sequencing analyses of mtDNA control region, using data from the 1994-1999 JARPN surveys. Paper SC/F2K/J311 presented to the IWC Scientific Committee Workshop to Review the Japanese Whale Research Programme under Special Permit for North Pacific Minke Whales (JARPN), Tokyo, 7-10 February 2000 (unpublished). 15pp.

Goto, M., Abe, H. and Pastene, L.A. 2000. Additional analyses of mtDNA control region sequences in the western North Pacific minke whales using JARPN samples. Paper SC/F2K/J32 presented to the IWC Scientific Committee Workshop to Review the Japanese Whale Research Programme under Special Permit for North Pacific Minke Whales (JARPN), Tokyo, 7-10 February 2000 (unpublished). 5pp.

Goto, M., Kanda, N. and Pastene, L.A. 2001. Genetic examination of western North Pacific minke whales including samples from JARPNII. Paper SC/53/RMP11 presented to the IWC Scientific Committee, July 2001 (unpublished). 11pp.

Pastene, L.A., Goto, M. and Kishino, H. 1998. An estimate of mixing proportion of 'J' and 'O' stocks minke whale in sub-area 11 based on mitochondrial DNA haplotype data. *Rep. Int. Whal. Commn* 48: 471-474.

Taylor, B. 2000. Genetic population structure in the western North Pacific minke whale: an analysis of mtDNA data. Paper SC/F2K/J6 presented to the IWC Scientific Committee Workshop to Review the Japanese Whale Research Programme under Special Permit for North Pacific Minke Whales (JARPN), Tokyo, 7-10 February 2000 (unpublished). 4pp.