Additional analyses of mtDNA control region sequences in the western North Pacific minke whales using JARPN samples

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Goto and Pastene (1999) examined mtDNA control region sequence data of minke whales sampled during JARPN surveys in sub-areas 7, 8 and 9. They used the haplotype (Hst) and the sequence (Kst*) statistics to examine genetic differentiation among these three sub-areas. The comparison between sub-area 7 (n=89) and 8 (n=91) resulted in negative values (Hst=-0.0019 and Kst*=–0.0024) and their probabilities were high, 0.9109 and 0.9095, respectively. Comparison between sub-area 7 and 9 (n=188) and between 8 and 9 showed higher Hst and Kst* values, and although their probabilities were not significant, they were lower than those obtained in the comparison between sub-areas 7 and 8 (see Appendix).

Taylor (SC/F2K/J6) re-analyzed these data using the randomized chi-square test. Comparison between sub-area 7 and 8 showed a P=0.704, that between sub-area 7 and 9 showed a P=0.066 and that between sub-area 8 and 9 showed a P=0.068. Thus although these results showed no significant differences at the 5% significance level, the P values obtained for the comparison between sub-areas 7, 8 and 9 were even lower than those found by Goto and Pastene (1999).

In this Working Paper we examined further the mtDNA sequence data to understand the reasons for the low P values found in the comparisons involving sub-area 9.

First we compared sub-areas 7 and 8 pooled and sub-area 9. We found a significant Fst value (Table 1). Next we divided sub-area 9 in an eastern and western sectors at 162°E. Division at this longitude was made to optimize the differences between east and west in a post-stratification step.

We then compared sub-areas 9W, 9E and sub-areas 7 and 8. The results by Fst and PHIst are shown in Tables 2a) and 2b). All the comparison involving sub-area 9W showed a significant Fst and PHIst values.

Three JARPN surveys have been conducted in sub-area 9, in 1994, 1995 and 1997. We compared sub-areas 7 and 8 pooled and sub-area 9 in different years (Table 3). We found a significant difference in the Fst value for year 1995. Then we compared west and east sectors in sub-area 9 for that year. We found significant differences in both Fst and PHIst values (Table 4).

Next we compared sub-areas 7 and 8 pooled and sub-area 9 1995, excluding the eastern sector samples (Table 5). We found significant Fst and PHIst values.

Finally we compared sub-areas 7 and 8 pooled the total samples of sub-area 9, excluding the western sector samples of 1995. In this case we did not find significant differences in both statistics (Table 6).

Our results indicate that a possible source of mtDNA heterogeneity is attributed to minke whales sampled in the western sector of sub-area 9 in 1995, samples which were included in the analysis of Goto and Pastene (1999). Then the low P values obtained for the comparisons involving sub-area 9 in Goto and Pastene (1999) and Taylor (SC/F2K/J6) could be attributed to this group of samples.

It should be noted that a similar analysis using microsatellite, found no significant genetic heterogeneity (Table 7).

Table 1: Results of comparison by AMOVA between sub-areas 7+8 and 9.

	Sample size	Fst	P	PHIst	P
Sub-area 7+8	230	0.004	0.0175	0.003	0.1444
Sub-area 9	188				

Table 2:Pairwise comparison among sub-areas 7, 8, 9W (western samples by 162° E) and 9E (eastern samples by 162° E) by AMOVA analysis. Above diagonal: Probability, below diagonal Fst or PHIst value. Division at this longitude was made to optimize the differences between east and west in a post-stratification step.

a)Fst, Total Fst value = 0.003, P=0.0353

	Subarea 7	Subarea 8	Subarea 9w	Subarea 9e
	(139)	(91)	(103)	(85)
Subarea 7		0.7299	0.0120	0.3443
Subarea 8	-0.0018		0.0106	0.5210
Subarea 9w	0.0083	0.0091		0.0882
Subarea 9e	0.0006	-0.0006	0.0049	

b)PHIst, Total PHIst value =0.007, P=0.0397

	Subarea 7	Subarea 8	Subarea 9w	Subarea 9e
	(139)	(91)	(103)	(85)
Subarea 7		0.8029	0.0140	0.7873
Subarea 8	-0.0039		0.0325	0.5227
Subarea 9w	0.0156	0.0147		0.0090
Subarea 9e	-0.0040	-0.0021	0.0232	

Table 3: Results of comparisons by AMOVA between sub-areas 7+8 and 9 (in each year). Number in parenthesis show the sample size.

	Sub-area 7+8 (230)			
Sub-area 9	Fst	P	PHIst	P
1994 (21)	0.004	0.2341	-0.011	0.7722
1995 (100)	0.005	0.0286	0.001	0.2942
1997 (67)	0.000	0.3779	0.001	0.3564

Table 4: Results of comparison by AMOVA between western and eastern samples by 162° E in sub-area 9 in 1995. Division at this longitude was made to optimize the differences between east and west in a post-stratification step.

	Sample size	Fst	P	PHIst	P
West	78	0.029	0.0071	0.074	0.0041
East	22				

Table 5: Results of comparison by AMOVA between sub-area 7+8 and sub-area 9 in 1995 excluding eastern samples by 162° E. Division at this longitude was made to optimize the differences between east and west in a post-stratification step.

	Sample size	Fst	P	PHIst	P
Subarea 7+8	230	0.012	0.0004	0.013	0.0189
Subarea 9w(1995)	78				

Table 6: Results of comparison by AMOVA between sub-area 7+8 and sub-area 9 excluding western samples by 162° E from sub-area 9 in 1995. Division at this longitude was made to optimize the differences between east and west in a post-stratification step.

	Sample size	Fst	P	PHIst	P
Subarea 7+8	230	0.001	0.2967	-0.001	0.5415
Subarea 9	110				

Table 7: Probabilities of population differentiation test by microsatellite. Division at this longitude was made to optimize the differences between east and west in a post-stratification step.

Sub-areas	GT023	GATA028	GATA098	GT211	GATA417	GT509	EV37*Mn*	EV104*Mn*	Combined
7+8 & 9 (All)	0.3723	0.4737	0.4980	0.7768	0.7690	0.2079	0.7894	0.3859	0.7833
1995 (9E) & 1995 (9W)	0.8609	0.3888	0.3383	0.1231	0.8502	0.3701	0.7252	0.5778	0.7018
7+8 & 1995 (9W)	0.5313	0.3165	0.2252	0.5385	0.7904	0.2037	0.3231	0.3961	0.4848

Appendix

Results of the homogeneity test between Sub-areas
(from Goto and Pastene, 1999; SC/51/RMP8). Above diagonal:
Hst(a) and K-st*(b) values, below diagonal: probabilities.
In parenthesis is sample size.

(a) Hst

	Sub-area 6 (28)	Sub-area 7 (89)	Sub-area 8 (91)	Sub-area 9 (188)
Sub-area 6		0.0855	0.0902	0.0585
Sub-area 7	0.0000		-0.0019	0.0012
Sub-area 8	0.0000	0.9109		0.0015
Sub-area 9	0.0000	0.1383	0.0979	

(b) Kst*

	Sub-area 6 (28)	Sub-area 7 (89)	Sub-area 8 (91)	Sub-area 9 (188)
Sub-area 6		0.1667	0.1736	0.1207
Sub-area 7	0.0000		-0.0024	0.0010
Sub-area 8	0.0000	0.9095		0.0019
Sub-area 9	0.0000	0.2292	0.1186	