

Corrections to Gray Whale Analysis: Document SC/62/AWMP1

In order to get a document to the IWC in time for consideration at this meeting, we had to conduct some of this work rather hastily. After submission, we have gone through all aspects of the analysis at our desired pace, and have found a few errors and/or corrections that need to be made. These are presented below, with a revised interpretation at the end of this document.

1. Reduction in Sample Size

The topic that we have received the most comments on regarding this paper is that we did not mention whether or not we accounted for the potential for some of the samples to have originated from the same individual. All samples were collected in association with photo-identification data as part of an ongoing study, and we presumed this was understood. However, since submission of the manuscript we have reviewed all collection and photo-identification data, and this led to the sample size being reduced in two ways. First, we did find some duplicates that had been overlooked and second we narrowed our definition of 'summer resident' using only samples from whales either identified in multiple summers or present between July and Nov 15 to ensure that the samples did not represent migrants temporarily passing through the area. The revised sample set contains data from 40 individuals, with the haplotypes indicated below.

	1 1 1 1 1 1 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2																										N	S			
Hap	2 6 6 8 8 8 9 9 9 9 0 0 0 0 2 2 7 2 2 4 6 6 6 6 7 8 8 8 9 9 9	6 7 8 0 8 9 0 1 3 8 2 4 5 6 4 9 1 0 8 4 5 6 6 7 1 4 8 9 0 9	F	F	Total																										
1	A	T	C	T	T	T	C	G	G	T	T	T	T	A	A	T	A	C	G	C	G	T	C	G	T	C	C	6	4	10	
3	G	2	0	2
4	.	.	.	G	2	0	2
5	.	C	T	.	C	.	T	C	C	.	G	G	C	.	T	.	T	.	C	.	.	.	T	.	1	0	1
6	.	.	T	.	C	C	T	C	C	.	G	.	.	T	.	T	A	.	T	.	.	T	.	2	3	5	
7	.	.	T	.	C	C	T	.	.	.	C	C	.	.	G	.	.	T	A	T	A	.	T	.	C	.	.	3	3	6	
8	.	.	T	.	C	.	A	C	.	.	G	.	C	.	T	.	T	.	C	.	.	T	T	1	0	1	
9	.	.	T	.	C	.	T	.	A	.	.	C	.	.	G	.	.	T	.	T	T	.	T	.	1	0	1
10	.	.	T	.	C	.	T	.	.	C	.	C	.	.	G	.	.	G	T	.	T	.	C	.	.	T	.	1	0	1	
11	.	.	T	.	C	.	T	.	.	C	.	C	.	.	G	.	.	T	.	T	.	C	.	.	.	T	.	1	0	1	
12	.	.	T	.	C	.	T	.	.	C	.	C	.	C	G	.	.	T	.	T	.	C	4	1	5	
13	.	.	T	.	C	.	T	.	.	.	C	C	.	C	G	.	.	T	A	T	A	.	T	3	4	7	
14	.	.	T	.	C	.	T	.	.	.	C	C	.	C	G	.	.	T	A	T	A	C	T	2	0	2	
15	.	.	T	.	C	.	T	.	.	.	C	C	.	C	G	.	.	T	.	T	A	C	T	A	.	.	.	1	7	8	
16	.	.	T	.	C	.	T	.	.	.	C	C	C	C	G	.	.	T	.	T	A	C	T	2	1	3	
17	.	.	T	.	C	.	T	C	C	.	G	.	C	.	T	.	T	.	C	.	.	.	T	.	1	1	2
18	.	.	T	.	C	.	T	C	.	C	G	.	.	T	.	T	A	.	T	7	1	8	
19	.	.	T	.	C	.	T	C	.	C	G	.	.	T	.	T	A	C	T	6	0	6	
20	.	.	T	.	C	.	T	C	.	C	G	.	.	T	.	T	A	C	T	A	.	.	.	10	2	12	
21	.	.	T	.	C	.	T	C	.	.	G	.	C	.	T	.	T	.	C	.	.	.	T	.	4	1	5
22	.	.	T	.	C	.	T	C	.	.	G	.	C	.	T	.	T	T	.	2	1	3
23	.	.	T	.	C	.	T	C	.	.	G	.	.	T	T	.	10	1	11
24	.	.	T	.	C	.	T	C	.	.	G	.	.	T	.	T	.	C	T	.	3	1	4
25	.	.	T	.	C	.	T	C	.	.	G	.	.	T	.	T	A	C	T	A	.	.	.	5	6	11	
26	.	.	T	.	C	.	T	C	.	.	G	.	.	T	.	T	A	C	T	.	C	.	.	2	0	2	
27	G	.	T	.	C	.	T	C	.	.	G	.	.	T	T	.	1	0	1
29	.	.	T	.	C	.	T	C	.	.	G	.	.	T	0	1	1
30	.	.	T	.	C	.	T	.	.	C	.	C	.	C	G	.	.	T	.	T	.	C	.	.	.	T	.	.	0	1	1
31	.	.	T	.	C	.	T	.	.	.	C	C	.	C	G	.	.	T	.	T	A	C	T	0	1	1
Total																												83	40	123	

2. Sampling Information

Thirty-nine biopsy samples were collected from gray whales present off the central west coast of Vancouver Island between June 15 and Nov 7, 1995 - 2006. In addition to the 39 living whales, one dead whale found off Campbell River on the east coast of the island in October 1997 was included in the analysis. Considering the date, this whale undoubtedly was a member of the southern population. This whale had a unique gender/haplotype combination, and therefore we can confirm that this individual is not accounted for in the biopsy sample set.

3. One Variable Site Missing

The original table reporting the variable sites for each haplotype (Table 2 in the paper) is missing one variable site at position number 299. That position is included in the revised table above.

4. Revision of Arlequin Analyses

All analyses had to be revised based on the new sample set described above. The results are below. Note that all analyses conducted with the program Arlequin were performed on the latest version (3.5) rather than version 3.1 as reported in the original paper.

A. F_{ST} :

$$F_{ST} = 0.01975, P = 0.00391$$

B. Φ_{ST} :

$$\Phi_{ST} = 0.01908, P = 0.06354$$

5. Revision of MIGRATE Analyses

Due to the lack of time for analyses in order to meet the IWC deadline, the MIGRATE runs reported in the paper are relatively short. We have now had time to run the program for more appropriate lengths with the revised data set. Specifically, it was run with a burn-in of 100,000 steps, and a run length of 10,000,000 steps with data recorded every 500 steps. The resulting data are below. The mode of the estimates is given above, with the 95% confidence interval in parentheses. Numbers represent the same values as reported in the original paper.

Iteration	$\Theta_{northern}$	$\Theta_{southern}$	$M_{southern-northern}$	$M_{northern-southern}$
1	0.0383 (0.0140-0.0780)	0.0213 (0.00750-0.0545)	383 (140-850)	423 (115-805)
2	0.0383 (0.0190-0.0770)	0.0183 (0.00700-0.0500)	378 (120-760)	433 (175-820)
3	0.0333 (0.0155-0.0800)	0.0198 (0.00650-0.0515)	383 (155-800)	473 (145-845)
4	0.0383 (0.0175-0.0745)	0.0198 (0.00850-0.0500)	378 (140-760)	393 (140-835)
5	0.0328 (0.0180-0.0775)	0.0183 (0.00700-0.0500)	383 (135-780)	483 (180-890)
Average	0.0352 (0.0168-0.0774)	0.0195 (0.00730-0.0512)	381 (138-790)	441 (152-839)

Moreover, the likelihood ratio test, testing the hypothesis of $\Theta_{northern} = \Theta_{southern}$ was rejected ($P = 0.000135$) with the new data set, as it was with the original.

6. Conclusions

The revised data set, and subsequent re-analysis of the data, does not change any of the original findings or conclusions. The significant F_{ST} value, and similar Φ_{ST} value (but with a slightly higher P-value), reject the hypothesis of panmixia between the two groups and are consistent with the hypothesis of a single breeding population with subdivision in feeding ground distribution based on maternally-directed site fidelity. Moreover, the significantly different θ estimates show that the maternal lineages of the southern feeding group are demographically independent of those of the northern feeding group. Combined, these data show that the southern feeding group qualifies as a separate management unit.