Mitochondrial sequence variation in the Bering/Chukchi/Beaufort Seas bowhead whales

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Abstract

Sequences of the mitochondrial control region were used to test for spatial, temporal and cohort structure in bowhead whales from the North Pacific. χ^2 and F_{st} tests were used to test spatial comparisons (North Slope vs. S. Lawrence Island (SLI), North Slope vs. Savoonga and North Slope vs. Gambell), temporal comparisons (fall vs. spring migrations for the North Slope and for Barrow only), and age groups (old vs. young). All tests yielded non-significant results.

Introduction

In SC/56/BRG13 and SC/56/BRG15, LeDuc and Taylor tested for spatial and temporal differences within bowhead whales from the Bering/Chukchi/Beaufort Seas stock using mtDNA sequence data. Although no significant differences were found, the spatial tests suffered from small sample sizes from one of the strata (SLI), and the temporal comparison of fall vs. spring yielded a non-significant but low p-value of 0.102 (see also analyses in Pastene et al. 2004). For all of these comparisons, additional analyses were called for with greater sample sizes and hence increased power. Since then, many more samples have been collected for most strata, including sequences from bone (n = 27) and baleen (n = 12) samples from SLI. Furthermore, additional information about ages and age classes of many samples has enabled the comparison of different age groups. Comparisons with bowhead samples from the Chukotka region of Russia will appear in a separate document.

Materials and Methods

A sequence from a 397 base pair region of the mitochondrial control region was generated from each sample. Laboratory methods for harvest samples are as described in the previous bowhead papers; laboratory methods specific to bone and baleen samples are as described in Morin et al. (in press). It is possible that some of the bone and baleen samples used in the present analyses are from whales previously represented in the set of skin samples taken from the harvested animals. The association of skulls to harvested animals was determined using comparisons of the catch records of different whaling captains with the estimated body length of the whales as determined by regression analysis with skull dimensions (George et al. 2005). In most cases the skulls were associated with whales not represented in the skin sample set. However, because some skull samples (and most baleen samples) could not be associated with particular harvested whales with any certainty, duplicate sampling cannot be completely ruled out. There were 27 bone and 12 baleen samples added to the sample set. Table 1 presents the sample sizes for each comparison, both in the present study and in the previous papers. To compare age groups, the old whale strata included animals rated as "geezer" 2 or 3 (for rating methods, see file "geezer index.readme.doc" submitted to IWC Secretariat), or any animal estimated at over 50 years old. The young whale strata included any animal under 25 years old or less than 13m in length. For age estimation methods and ages, see George et al. (2004), Lubetkin et al. (2004), Rosa et al. (2004) and Lubetkin et al. (2006). All

comparisons were made using a permutation χ^2 test (as in the previous studies) and F_{st} . P-values were determined using 10,000 permutations.

Results and Discussion

Table 2 presents the results for all the temporal and spatial comparisons, as well as the p-values from the earlier studies. None of the comparisons yielded significant results, even with the greater sample sizes.

Stratum	Previous sample size	New sample size
North Slope	205	286
St. Lawrence Is.	11	62
Savoonga	7	20
Gambell	4	42
Fall (North Slope)	99	151
Spring (North Slope)	104	135
Old	N/A	50
Young	N/A	217

Table 1. Sample sizes for strata used in the new analyses and in previous analyses.

Comparison	χ^2 2006 p-value (2004 p-value)	F _{st}	p-value
N Slope vs. St. Lawrence Is.	0.4191 (0.538)	0.00135	0.256
N Slope vs. Savoonga	0.7473 (0.678)	0.000016	0.3893
N Slope vs. Gambell	0.1770 (0.310)	0.004267	0.1380
North Slope Fall vs. Spring	0.5609 (0.102)	-0.001532	0.7302
Barrow Fall vs. Spring	0.6317 (N/A)	0.000336	0.3574
Old vs. young	0.2428 (N/A)	-0.001031	0.5139

Table 2. Results of chi-square and F_{st} tests using mtDNA control region sequences. P-values from earlier papers are given in parentheses.

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