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# A note on mismatch distributions of mtDNA control region sequences in baleen whales from the western North Pacific

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## ABSTRACT

This study examined the distribution of the number of nucleotide substitutions between all pairs of individuals within western North Pacific O and J stock common minke, Bryde's, sei and right whales, to investigate whether the pattern of distribution is indicative of exponential population growth (in evolutionary terms), and thus of non-equilibrium. According to Slatkin and Hudson (1991), unimodality of the frequency distribution is indicative of exponential population growth, and this pattern was found in the O stock common minke and sei whales. In contrast multimode pattern in the frequency distribution was found in the J stock common, Bryde's and right whales, which is inconsistent with exponential population expansion.

## INTRODUCTION

The 2009 JARPNII review workshop noted that the genetic analyses conducted under JARPNII assumed mutation-drift-migration equilibrium but that some evidences suggested exponentially expanding population, and thus non-equilibrium (IWC, 2010). Consequently the workshop recommended that tests for population genetic equilibrium should be undertaken. Furthermore it recommended that estimation of divergence between sample partitions should be undertaken using non-equilibrium approaches, and suggested the IM approach by Hey and Nielsen (2004).

As a starting point to respond the workshop recommendation above, the distribution of pairwise differences among mtDNA control region sequences were estimated (Slatkin and Hudson, 1991) for several western North Pacific baleen whale species. Previous analyses suggested that the mismatch distributions in population samples from North Pacific O stock common minke whales were consistent with exponential population expansion (and thus non-equilibrium) however the sample of J stock common minke whale had multiple mismatch distributions, which was inconsistent with exponential population expansion (Pastene *et al*., 2007).

In this study we used all the available sequences till 2014 to estimate the mismatch distributions in samples of western North Pacific O and J stocks common minke, sei, Bryde's and right whales, to investigate whether the pattern of distribution is indicative of exponential population growth, and thus of non-equilibrium.

## MATERIALS AND METHODS

### Samples and DNA extraction

Samples and DNA extraction procedures used in this study for J and O stocks common minke, Bryde's, sei and North Pacific right whales were the same as in the studies in Pastene *et al*. (2016a: SC/F16/JR38, 2016b: SC/F16/JR40; 2016c: SC/F16/JR44, 2016d: SC/F16/JR46, 2016e: SC/F16/JR50).

### mtDNA control region sequencing analysis

Sequencing procedures for J and O stocks common minke, Bryde's, sei and North Pacific right whales were the same as in the studies in Pastene *et al*. (2016a: SC/F16/JR38, 2016b: SC/F16/JR40; 2016c:

SC/F16/JR44, 2016d: SC/F16/JR46, 2016e: SC/F16/JR50). The lengths of the mtDNA control region segments used in those species were 487bp, 487bp, 299bp, 487bp and 275bp, respectively.

### Mismatch distribution analysis

The distribution of the number of nucleotide substitutions between all pairs of individuals of common minke (J and O stocks), Bryde's, sei and right whales within the western North Pacific, was computed and compared to the Poisson distribution (Slatkin and Hudson, 1991) expected if the population had undergone exponential growth. We used the computer program Arlequin ver. 3.01. A total of 10,000 simulations were made. The agreement of the observed distribution with the expected distribution was evaluated using the chi-square test.

## RESULTS AND DISCUSSION

Figure 1 shows the observed distribution of pairwise differences compared with the number of expected distributions assuming a Poisson distribution for O stock common minke (A), J stock common minke (B), Bryde's (C), sei (D) and right (E) whales. All observed distributions were significantly different than the expected Poisson distribution. However, unimodality (as opposed to more than two modes) of the frequency distribution is indicative of exponential population growth (Slatkin and Hudson, 1991). This was the case of the O stock common minke and sei whales (Figures 1 A and D, respectively). It was not the case of the J stock common minke, Bryde's, and North Pacific right whales (Figures 1B, C and E).

In the case of the Bryde's whale when total samples were used, there is a mode at zero and then a steady decline, which is similar to what Excoffier (2004) shows for scenarios where there is a range expansion, but more recent.

As noted earlier the 2009 JARPNII review workshop recommended that estimation of divergence between sample partitions should be undertaken using non-equilibrium approaches, and suggested the IM approach by Hey and Nielsen (2004). This could be the case for O stock common minke, sei and possibly Bryde's whales. The IM approach estimates the divergence time and the migrations having occurred in the ancestry of two populations. It reports the posterior distributions of the ancestral population size, the divergence time, the relative initial population sizes, the growth rates and potentially asymmetrical migration rates between populations and the approach can use DNA sequence and microsatellite data. It should be noted, however, that this and other similar approaches face real difficulties when genetic differentiation among populations is low (*Fst*<0,01) (Gaggiotti, pers. communication).

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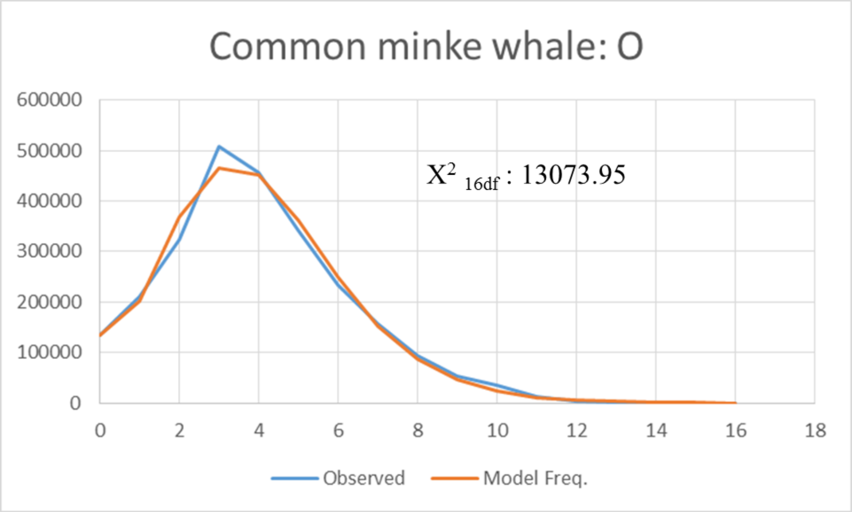
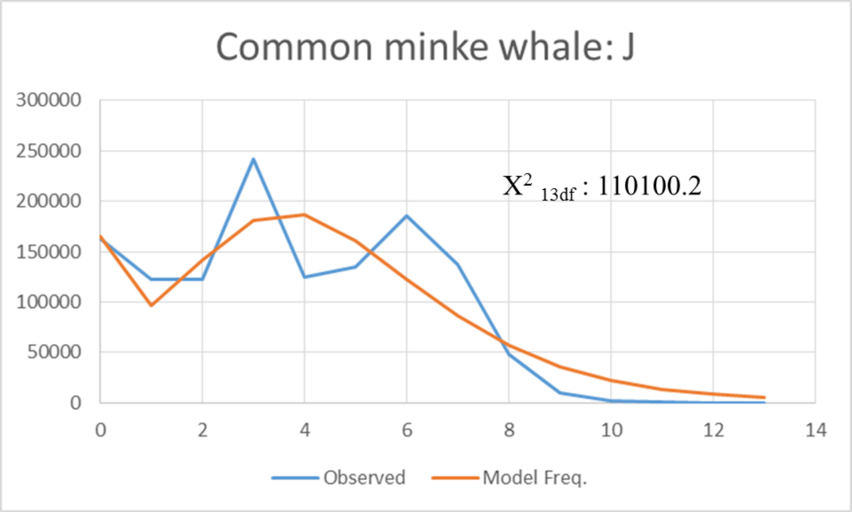
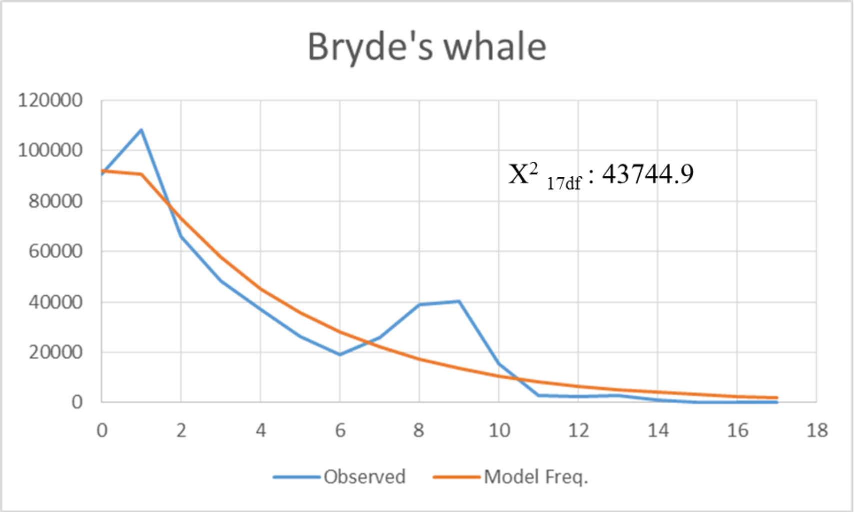
**A)**


Common minke whale: O
600000
500000
400000
300000
200000
100000
0
0
2
4
6
8
10
12
14
16
18
$X^2_{16df}$ : 13073.95
Observed
Model Freq.

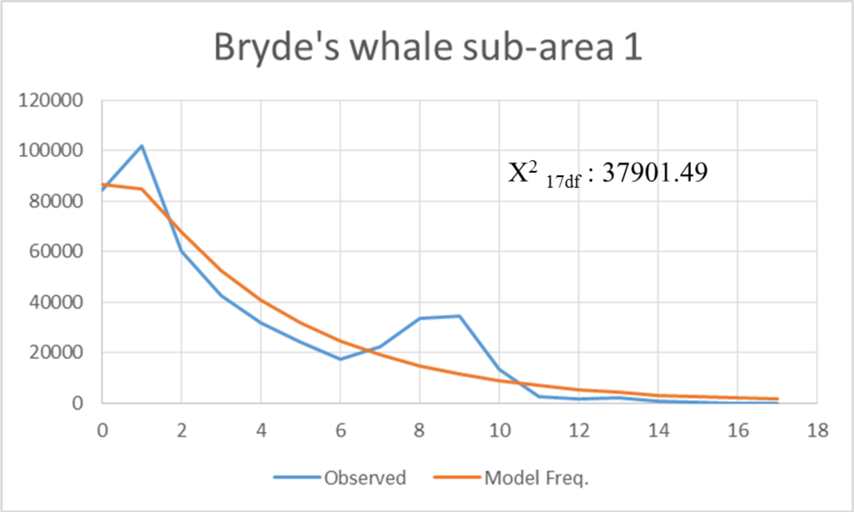
B)


Common minke whale: J
300000
250000
200000
150000
100000
50000
0
0
2
4
6
8
10
12
14
$X^2_{13df}$ : 110100.2
Observed
Model Freq.

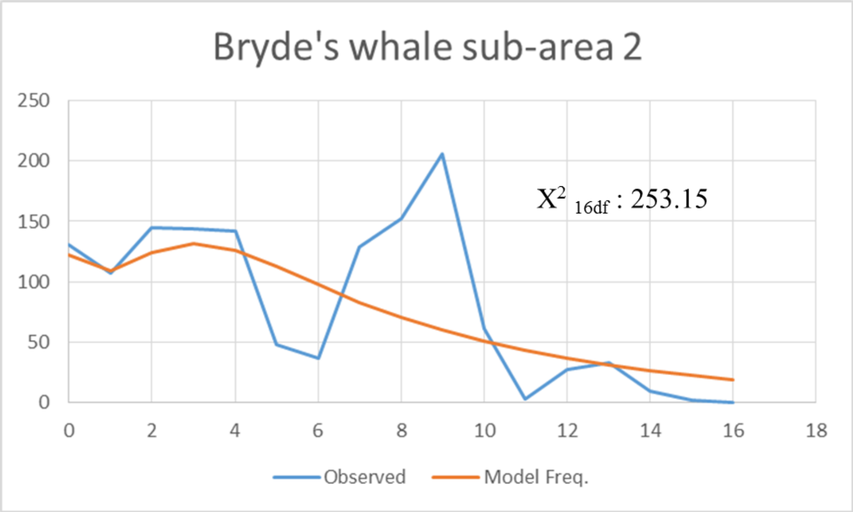
C)



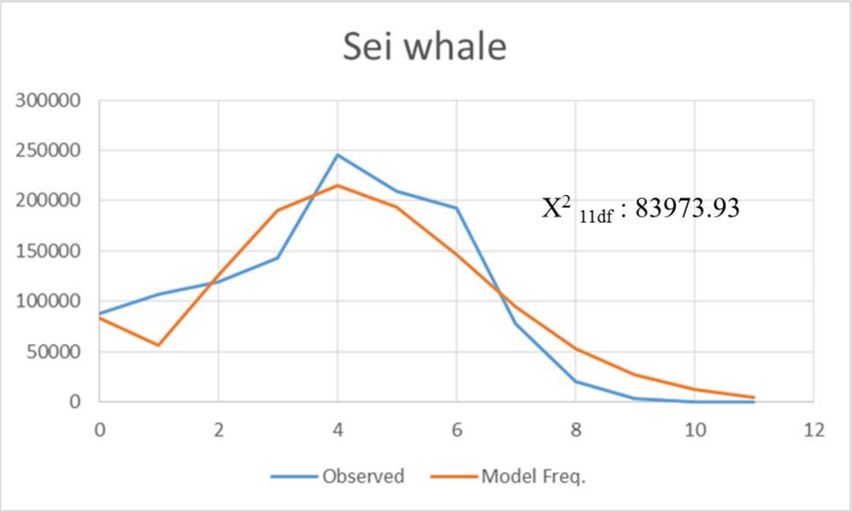
$X^2_{17df}$ : 43744.9



$X^2_{17df}$ : 37901.49


Bryde's whale sub-area 2
250
200
150
100
50
0
0
2
4
6
8
10
12
14
16
18
$X^2_{16df}$ : 253.15
Observed
Model Freq.

D)


Sei whale
300000
250000
200000
150000
100000
50000
0
0
2
4
6
8
10
12
$X^2_{11df}$ : 83973.93
Observed
Model Freq.

E)

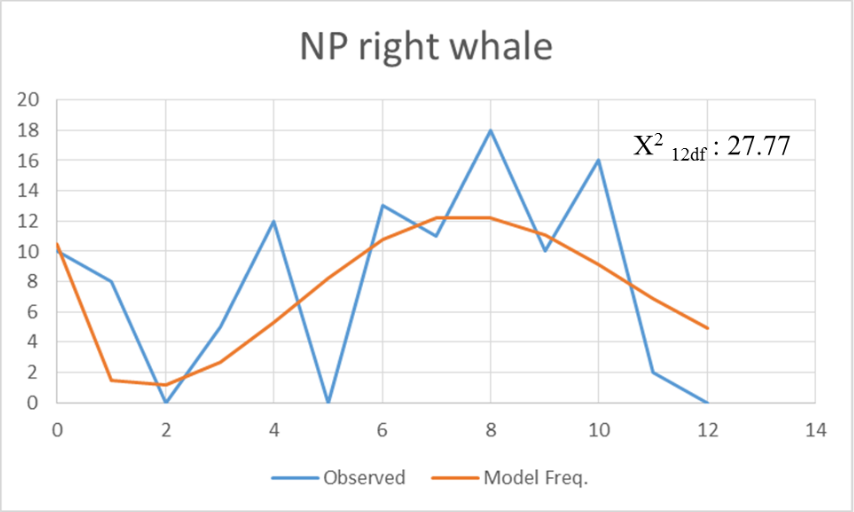


Figure1. Observed distributions of pairwise difference (blue line) compared with the number of expected distributions assuming a Poisson distribution (orange line) for each baleen whale species in the western North Pacific. The *x* axis is the number of substitutions, the *y* axis, the frequencies of the pairwise. A= O stock common minke whale; B= J stock common minke whale; C= Bryde’s whale; D= Sei whale; E= North Pacific right whale.