SC/F19/WNPM/05

Response to SC/F19/WNPM/01 'Preliminary analyses of population structure of North Pacific minke whales based on Japanese ‘bycatch’ and scientific whaling’ by Baker et al.

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INTERNATIONAL
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ABSTRACT

This paper responds some of the comments and conclusions made by Baker *et al*. in SC/F19/WNPM/01. Analyses conducted in SC/F19/WNPM/01 are very similar to those conducted by the same authors in the previous *Implementation Review* for western North Pacific common minke whale, and they do not refer to recent discussions and recommendations from the IWC Scientific Committee. It is very difficult the interpretation on stock structure of analyses conducted on strata containing O and J stock samples in different proportions. Furthermore, SC/F19/WNPM/01 did not consider results of recent clustering analyses and parent-offspring analyses which were difficult to reconcile with multiple O and J stocks proposed under the Hypothesis C.

RESPONSES AND COMMENTS

Texts from SC/F19/WNPM/01 are copied here in *italics*, and our comments and responses are given immediately below the text using plain letters.

Haplotype codes and quality control review

SC/F19/WNPM/01 noted that “*haplotype codes have been entirely revised in the current database, relative to the database made available for the previous Implementation Review (Baker et al., 2011). Although this may be internally consistent, the recoding complicated reference back to the previous analyses and will need to be considered in any effort to reconcile or integrate haplotype information from Korean samples*”.

Haplotype codes were revised as a result of additional check of the sequence data set. Specifically, at the 272th mtDNA control region site, a change was made from a polymorphic site (considered ambiguous) to ‘N’. The ambiguity could not be checked because of the loss of the original samples due to the 2011 tsunami.

SC/F19/WNPM/01 also noted that “*In total, the 4,707 samples represented 132 haplotypes, of which 41 were reported for only a single sample. Such a large number of ‘singletons’ is surprising given the very large sample size and could reflect minor sequencing error, similar to that found in quality control review for the previous IR (Steel et al., 2011)*”.

Following the comments in the previous *Implementation Review*, we have regularly re-checked all sequences considered ambiguous. For each individual sample, both forward and reverse sequences are typed for error check. After the first run, all of the ambiguous sequences, singletons, and sequences with the unusual number of transversions are re-sequenced for confirmation. Therefore, it is unlikely that the singletons in the data set represent sequencing error.

Genetic differentiation by strata

SC/F19/WNPM/01 calculated pairwise F_{ST} estimates and tested the difference in mitochondrial haplotype and microsatellite allele frequencies, and noted that ‘*the patterns of differentiation for both microsatellites and mtDNA were similar to that reported for the previous IR (Baker et al. 2011; Wade and Baker 2012)*’.

It is unfortunate that the authors did not take into consideration or refer to recent discussions and recommendations at the IWC SC on clustering methods (*e.g.*, IWC, 2018; 2019) to resolve stock structure questions. It is very difficult the interpretation on stock structure of analyses conducted on strata known to contain O and J stock whales in different proportions.

Preliminary conclusions
SC/F19/WNPM/01 concluded that "*results of the analyses presented here for the 1994 to 2016 dataset and previously for the subset of samples collected from 1994 to 2007 (Baker et al., 2011; Slikas and Baker, 2011; Wade and Baker, 2012) are consistent with the proposal to recognise 5 stocks, as described in Hypothesis C of the previous Implementation Review*".

As noted above, the statistical analyses were conducted for strata that contained J and O stock whales in different proportions therefore results from such analyses are difficult to interpret. Furthermore, the authors did not consider results of recent clustering analyses (*e.g.*, Pastene *et al*., 2016) and parent-offspring (P-O) analyses (Tiedemann *et al*., 2017). In particular several of the P-O pairs for the O stock were found between coastal and offshore areas in the Pacific side of Japan while that some of the J stock pairs were between the Sea of Japan and the Pacific side of Japan. These results are very difficult to reconcile with multiple O and J stocks as proposed by the Hypothesis C.

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