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ICR comments on the paper "Are Antarctic minke whales unusually abundant because of 20th century whaling? By Ruegg *et al*. Molecular Ecology.

This study by Ruegg *et al*. estimates the long-term population size of the Antarctic minke whales prior to whaling by sequencing 11 nuclear genetic markers from 52 samples of this species. They concluded that their estimate of 670,000 animals is similar to or greater than contemporary abundance estimates suggesting that managing Antarctic ecosystem under the assumption that Antarctic minke whales are unusually abundant is not warranted. A similar version of this paper was presented and discussed at the IWC SC meeting in 2009.
Read the relevant part of the IWC SC report. (page58 ; 13.4 Review of other papers)

A previous paper by Roman and Palumbi (2003) dealing with genetic analyses to estimate long term population sizes in North Atlantic large baleen whales was also presented and discussed at the IWC Scientific Committee (IWC SC). The IWC SC welcomed these novel analyses but at the same time agreed that initial pre-whaling population sizes have considerable more uncertainty than reported. In 2004 the IWC SC identified several works to address these uncertainties and such work is ongoing.

Calculation of the long term population size using genetic data depends on two important factors, first on the assumptions used to estimate genetic diversity (on which the effective population size is based) and second on the assumptions used to convert effective population size into census population size. The study by Ruegg *et al*. is valuable in the sense that the authors dealt with some of the uncertainties identified by the IWC SC some years ago to estimate genetic diversity. However the results were not convincing. For example results of their tests for nuclear markers were consistent with neutrality and equilibrium. Based on this, they estimated the genetic diversity keeping growth rate=0, i.e. forcing the estimation to assume that populations size has been constant, which is in clear conflict with previous mtDNA studies by Palumbi and other authors.

Regarding the second factor the IWC SC meeting last year noted that caution is needed in using genetic methods to make inferences on absolute numbers. The absolute estimates will also be sensitive to the ratio of effective to mature population size. The IWC SC also noted that comparison with survey abundance estimates is complicated due to whales in unsurveyed areas of sea ice habitat.
Read the relevant part of the IWC SC report. (page58 ; 13.4 Review of other papers)

Apart from the issue of uncertainties mentioned above the most relevant issue is whether or not evolutionary estimates are useful for management of whales. Ruegg *et al*. used an evolutionary estimate of the effective population size. Such estimates can not be assigned to a point in time narrow enough to assure that the estimates apply to the period just prior the start of the harvest of the Antarctic minke whales. Then evolutionary estimates are of no utility for management purposes.

In summary their results on long term population abundance can not be used for management purpose.

In part of this paper the authors suggest that “….some agencies advocate culling minke whales as a way to reduce competition with fisheries and to support the recovery of other over-harvested whales species’. This is just a misunderstanding of what the JARPA II (Japanese whale research program) is doing in the Antarctic. One of the objectives of the JARPA II is to “Modeling competition among whale species and future management objectives”. In the context of this objective and in addition to the “Krill surplus hypothesis” mentioned in the Ruegg *et al*. paper, several other hypotheses are being tested through the development of ecosystem modeling. JARPA II contributes with important input data for the development of these ecosystem models such as abundance and stomach contents of whales.
Read the JARPAII research plan.