A short note on suggestions for future analyses to elucidate the population structure of North Pacific minke whales.

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CURRENT DATA ANALYSES

The genetic data collected by the Institute of Cetacean Research from North Pacific minke whales is extensive compared to most genetic assessments under the IWC SC. However, the level of spatial genetic heterogeneity among North Pacific minke whales to the east of Japan is generally low, which creates challenges with respect to the application of current "standard" population genetic inference methods. In other words, it is very difficult to obtain reasonably precise estimates of migration rates, which in turn makes it difficult to provide solid advice to the IWC SC. For most population genetic inference methods it is also unclear whether the low spatial genetic heterogeneity is caused by "high" historic and zero current migration rates, or high current migration rates.

Matters are further complicated by the fact that the samples are collected in a migratory corridor when the minke whales are *en route* to feeding grounds. Most analyses, including the recent re-analysis by Gagiotti and Durand (2010), assume that the spatial distribution of genetic variation is temporally stable. In other words, individuals from each population are expected to follow the same migratory route every year. In addition, methods employing successive clustering, such as Boundary Rank by Martien and Taylor, are usually spatially constrained, such that only samples from adjacent area can be clustered. If migration routes change across years then such spatial constraints make little sense. Indeed, the analysis conducted by Gaggiotti and Durand (2010) demonstrated that the inferred population structuring changes radically when such spatial constraints are lifted. In other words, a clustering approach is highly sensitive to such *a priori* assumption about which we actually have poor knowledge.

The last and final issue, which Gaggiotti and Durand (2010)(and the email group) have considered to great length, is the removal of minke whales from the genetically distinct Sea of Japan (J) "population". Leaving unrecognized J individuals in the analysis may introduce a false signal of population genetic structure. In contrast removing all individual with an "odd" genetic profile may result in the removal of non J-stock individuals which in turn reduces the likelihood of detecting any additional population genetic structure. It is tempting to employ the genetic data in assignment methods, such as STRUCTURE, to assess putative J-stock individuals and remove those based upon their admixture probabilities. I think that using the same data to select individuals and later conduct the assessment of population structure is less than optimal. Since population assignment to J-stock is not 100% (i.e., diagnostic) then there is no way of knowing if any subsequent heterogeneity in later analyses stems from J-stock individuals. Even using mtDNA may yield incorrect assignments as we do

not know for sure what in fact are J-stock individuals. Under any circumstances, any removal of J-stock individuals should be conducted with data that are independent from the subsequent identification of population structure, and ideally with data that are diagnostic for J-stock.

SUGGESTION TO APPLY KINSHIP-BASED ANALYSES

The main concern from a management perspective is overexploitation, in this case from small North Pacific minke whale populations. This could be either (i) a too large catch of J-stock individuals not recognized as such, (ii) and/or catches from a small undetected costal population inhabiting the areas with the largest catches. I think that kinship-based analyses might be a better alternative to elucidating possible substructure, and it is conceivable that the current data is sufficient (in terms of markers) to get at least a preliminary impression (Palsbøll *et al.* in press). Briefly, assuming equal samples sizes, the number of pairs of closely related individuals (kin) is inversely related to population size (Palsbøll 1999; Peery *et al.* 2008). Hence, if a substantial number of catches is taken from a small unrecognized coastal population this should emerge as an elevated number of pairs of samples of close kin in the costal samples (Peery *et al.* 2008). Similarly the spatial distribution of pairs of close kin on a larger scale will also inform about population structure and migration routes (Økland *et al.* 2010; Peery *et al.* 2008).

It is probably worthwhile to conduct individual-based simulations in parallel to assess the expected power and precision, which to a large extent will depend upon the proportion sampled of each population (Peery *et al.* 2008).

CITED LITTERATURE

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