

The genetic structure of harbour porpoises in the Baltic Sea relative to adjacent waters remains to be clarified: a reply to Berggren & Wang

A strong conservation focus on harbour porpoises *Phocoena phocoena* in the Baltic Sea is based on the presumption of a Baltic group genetically isolated from populations further west in the Belt-Kattegat area. This contention stems primarily from the results of a study (Wang & Berggren, 1997) claiming a statistically significant mtDNA haplotype frequency difference ($P < 0.05$) between the two regions. The result has been widely accepted as a scientific fact. We pointed out a flaw in Wang & Berggren's (1997) statistical analysis, noting that the difference is not significant using generally accepted criteria (Palmé et al., 2008). We argue that the genetic structure of the harbour porpoise in this region is unresolved, and stress the urgency of addressing this issue. The response by Berggren & Wang (2008) fails to clarify whether or not their mtDNA data support the existence of a genetically separate Baltic population.

In standard statistical hypothesis testing the probability of interest is obtaining (under the null hypothesis) an outcome as bad as or worse than the one observed. Wang & Berggren (1997) reported the probability of a worse outcome, not including the probability of the observation they actually made (or possible ties), thereby making it easier to obtain significance. Most basic statistics textbooks (e.g. Sokal & Rohlf, 1995) recommend such inclusion, which is reflected in the P-values we obtained using other software (Table 2; Palmé et al., 2008). Regardless of the P-value interpretation and the α -level, however, the observed F_{ST} based on Wang & Berggren's (1997) data is very low (0.007) and we show that for their data it is impossible to separate a case of complete panmixia from a discrete (10% migration) Baltic population. This analysis, based on Wang & Berggren's (1997) mtDNA data, reflects the female segment of the population, accounting for the stronger female philopatry claimed by Berggren & Wang.

Given the weakness of Wang & Berggren's (1997) data, the strong conservation focus on a genetically separate Baltic porpoise population currently lacks scientific support. This is so even if small sample sizes result in poor statistical power. The precautionary principle should, as always in conservation, be applied in the absence of adequate data but it should not be used to create sub-structuring that may not exist.

At present, we cannot separate the following basic scenarios (cf. Laikre et al., 2005) of possible Baltic harbour porpoise genetic structure in the Baltic-Belt-Kattegat Seas: (1) complete panmixia, (2) the Baltic representing a genetically distinct and separate population, (3) continuous genetic exchange over

this region. Effective conservation management is strongly dependent on which of these alternatives (or combination of them) is true. Palmé et al. (2004) suggested that the cumulative genetic data available for porpoises in this region should be analysed jointly using appropriate statistical techniques. To our knowledge this analysis has still not been carried out.

Cost effective species conservation requires scientifically valid information on population genetic structure over a species' distribution range. Such information provides the basis for focusing conservation management on relevant genetic units to minimize loss of intraspecific diversity, thus maximizing evolutionary potential. Given that the population genetic structure of harbour porpoise in the Baltic Sea and adjacent waters is unresolved, there is no scientifically valid genetic support for current costly conservation efforts. We thank Berggren & Wang for their attention to this problem, and hope that the present exchange, along with Palmé et al. (2008), will serve to stimulate investigations to clarify whether or not there exists a genetically and demographically separate Baltic harbour population.

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