
Targeted studies to decipher humpback whale genetic diversity

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Abstract

Humpback whales are a typical example of a highly mobile marine mammal species, and yet show strong intra-specific genetic structure. Fidelity to feeding and breeding grounds may strongly influence the population structure. In particular, regional differences in mitochondrial DNA (mtDNA) could mirror cultural transmission of the migration route, thus leading, over generations, to fidelity to specific feeding and breeding grounds. We attempted to decipher the complex structure of humpback whale genetic groups in the Madagascar breeding ground (in collaboration with the NGO Cetamada, CNRS and University of Paris XI), and in two feeding grounds: in the Bering Sea (with the University of Moscow, the Pacific Geographical Institute and FEROP project) and around Saint-Pierre-et-Miquelon Island (in collaboration with the NGO FNE SPM, DTAM, CNRS and University of Paris XI). Our results support those of other studies and shed light on the actual levels of genetic diversity in humpback whales and their local variations. Comparative analysis of nuclear and mitochondrial DNA polymorphisms is highly informative, and can lead to contrasting results. For instance, we showed that two groups of humpback whales from Russian Pacific waters, separated by approximately 500 km within what has been considered the same feeding ground, are unexpectedly genetically different. In contrast to nuclear DNA polymorphisms, which show no differences between humpback whales sampled in the two groups, a significant difference in mtDNA was observed between the two areas. Fidelity to specific feeding sites, maternally learned and corresponding to a cultural transmission between generations, could therefore occur at smaller geographic scales than generally thought, and reflect some heterogeneity in feeding grounds. Such diversity should be taken into account with regard to conservation since the loss of a specific site used by humpback whales, even at a small geographical scale, could well correspond to the loss of genetic heritage.

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