

POPULATION GENETIC STRUCTURE OF THE HARBOUR PORPOISE (*PHOCOENA PHOCOENA*) IN ICELAND

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The harbour porpoise (*Phocoena phocoena*), one of the smallest cetaceans, has a circumpolar distribution, occurring in most temperate waters of the Northern Hemisphere. In general it is considered to be a coastal species and hence is subject to incidental take in commercial fisheries. It is therefore of utmost importance to identify which areas should be considered as different management units. Although Tolley et al (2001), using mtDNA, found Icelandic porpoises from the North and West of the country to be more similar to porpoises from the West Atlantic than to those from Norway, no other information has been published on the genetic population structure of the Icelandic harbour porpoise. In the present study, 169 animals from around the coast of Iceland (including animals from the Southeast never before genetically analysed), 77 Norwegian animals and an outgroup of 49 Irish individuals, were analysed using 10 microsatellite loci. Pairwise F_{ST} values, analysis of molecular variance (AMOVA) and assignment tests, all proved that these three areas were genetically distinct. More interestingly however, samples from the Southeast coast of Iceland were showing more genetic similarity to the Norwegian sample than to other Icelandic individuals (from the North and West). It is hypothesised that this could be the result of animals migrating to the Southeast coast of Iceland from other areas (possibly the Faroes) in pursuit of the capelin migration. A second hypothesis is that these Southeast Iceland samples could be the remnants of a Northward expansion after the last glaciation. This would have occurred in the East Atlantic along the European coastline to Norway, the Faroes and Southeast Iceland. Either way, these results will affect future management plans for the Icelandic harbour porpoise.

MITOCHONDRIAL DNA DIVERSITY OF THE COMMON DOLPHIN (*DELPHINUS DELPHIS*) IN THE CANARY ISLANDS

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The short-beaked common dolphin (*Delphinus delphis*) population of the Canary Islands is non-resident and can mainly be found in the archipelago between January and May. Nevertheless nothing is known about the geographic origin of this population. With this aim, 398 bp of the mitochondrial control region of 28 samples from stranded as well as free ranging animals, were sequenced and compared with those sequences described for populations from California, the Eastern Tropical Pacific, the Black Sea and the Mediterranean. For the 28 common dolphin samples, 21 haplotypes were described, being one of them identical to another one detected in the Black Sea. The nucleotide diversity values for the D-loop was 1.5% for the Canarian population. This population was found to be subdivided in two groups which were genetically closer respectively to the Mediterranean / Black Sea samples and to the California / Pacific samples than to one another suggesting different geographical origins of the animals found in the Canarian archipelago. However, the genetic distance value between those two groups is of the same order of magnitude as the one defined between the Californian sympatric morphotypes *D. delphis* and *D. capensis*, so that there is no support for the theory of them being different species.