



Population genetic structure of harbour porpoise *Phocoena phocoena* across Europe: implications for management.

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The harbour porpoise (*Phocoena phocoena*) is a species of conservation concern and there is a need to define Special Areas for Conservation (under the EU Habitats Directive). Population genetic structure can provide an understanding of relationships between populations and so inform management. Relationships between porpoises from Iberia (n=189), northern Europe (n=113), and Turkey (n=16) were established by genotyping 10 microsatellite DNA loci. Structure-based analysis for the best supported number of a posteriori genetic populations identified three groups: Iberian Peninsula, Turkey and North Europe. As porpoises from Turkey are a different subspecies (*P. p. relicta*) the differentiation of this population was expected. Principal coordinate analysis confirmed a level of population structure among samples dividing Iberia, North Europe, and Turkey. FST differences between the three groups were significant. DNA sequence variation across 334 base pairs of the mitochondrial control region was also used to determine population structure. In total 167 samples from areas across Europe were obtained and combined with 1352 previously published sequences from Europe, West Africa, Aegean, Marmara and Black Sea. 111 different haplotypes were found; 3 were newly discovered and found only in Iberia. A median-joining network shows no clear population clustering based on sampling origin but haplotypes present in the Aegean, Marmara and Black Seas appear to form a distinct group. However, FST values were significant between all the populations except for Spain versus Portugal and West Greenland versus Iceland. Combined this information identifies Iberian porpoises as a single genetic population that could be defined as a different subspecies and this should be considered in the future designation of SACs and management plans in the study area.