

GE03 GENETIC DIVERSITY OF BOTTLENOSE DOLPHIN (TURSIOPS TRUNCATUS) FROM THE CROATIAN PART OF THE ADRIATIC SEA

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The bottlenose dolphin (*Tursiops truncatus*) is the only resident marine mammal species in the Croatian part of the Adriatic Sea with a total number of individuals estimated at around 250. This extremely low number and potential geographical isolation render this population prone to extinction. The bottlenose dolphin is considered an endangered species and is legally protected in Croatia. The maintenance of the genetic variation within populations is a general concern for the conservation of endangered species. Genetic variability is thought to be essential to the long-term persistence and adaptability of populations. We analysed microsatellite loci in 30 individuals found dead from 1994 until 2003 and a fragment of the mitochondrial DNA control region in 22 individuals. DNA was extracted from tissues of carcasses. Multiplex polymerase chain reactions were performed in which 12 polymorphic dinucleotide repeat cetacean microsatellite loci (EV1, EV14, EV37, EV94, TexVet3, TexVet5, TexVet7, D08, D14, D18, D22, D28) were amplified. PCR products were analysed on ABI PRISM 310 Genetic Analyzer. Genetic variation analysis was performed using the Genetix 4.05 program. Fragments of the mtDNA control region were sequenced using universal forward MTCRf primer and a newly-designed reverse primer named "DUPr". Sequence alignment was performed using ClustalW. MtDNA analysis was performed with the ARLEQUIN. The mean allelic diversity per microsatellite locus was 7.17, ranging from three to 15 alleles and the mean expected heterozygosity was 0.69, ranging from 0.34 to 0.89. The microsatellite results reveal relatively high genetic variability in the population of bottlenose dolphins in Croatia. Mt DNA sequence analysis identified only four unique haplotypes with 22 polymorphic sites in 22 individuals. Both haplotype diversity and nucleotide diversity of the Croatian bottlenose dolphin population were relatively low (0.403 and 0.008,

respectively). These genetic results should prove valuable for future molecular genetic investigations of the Adriatic bottlenose dolphins.

GE04 GENETIC ANALYSIS OF HARBOUR PORPOISE (*PHOCOENA PHOCOENA*) POPULATIONS LIVING ALONG BRITTANY COASTS

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Eight microsatellite loci previously cloned from the porpoise (*Phocoena phocoena*) genome have been analyzed on individuals stranded along brittany coasts of North-west France. Allelic variations are strong for the eight loci, and heterozigosity levels high. At the opposite, ISSR (Inter simple Sequence Repeats) analysis produced strongly homogeneous patterns, which are species specific. Investigation of ISSR on seven species, belonging to the Delphinidae and Phocoenidae families, allowed us to reconstruct a phylogenetic tree, strongly differentiating species and delphinidae-subfamilies. We are now comparing our results (ISSR analysis and single microsatellite length variations) with those of porpoises originating of north or celtic seas, and from south of France. This should allow us in near future to determine the geographical origin(s) of porpoises living along brittany french coasts, and to evaluate the genetic homogeneity of this population.

GE05 GENETIC STUDY OF COMMON DOLPHIN *DELPHINUS DELPHIS* IN THE CENTER/NORTH REGION OF PORTUGAL

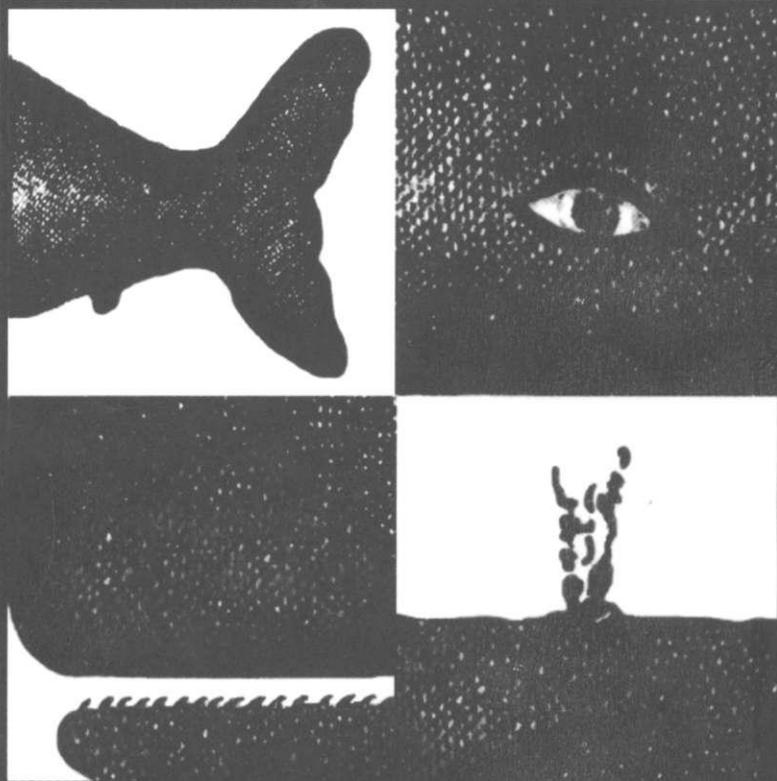
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