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G02

AMBIGUOUS EVIDENCE OF A RECENT BOTTLENECK IN THE ADRIATIC BOTTLENOSE DOLPHINS (*TURSIOPS TRUNCATUS*)

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The bottlenose dolphin (*Tursiops truncatus*) is an endangered and legally protected species in Croatia, whose demographic history is poorly known. It is the only resident marine mammal species in Croatian part of the Adriatic Sea, with number estimated at around 250 individuals. There are indications that there has been intensive eradication operations in the mid 20th century that might have caused reductions in the effective population size and might have resulted in a loss of genetic variation. Therefore, we aimed to investigate a possibility of recent population size contraction and to compare the level of genetic diversity in the bottlenose dolphin population from the Croatian part of the Adriatic Sea with other bottlenose dolphin populations. Thirty samples were genotyped at 12 dinucleotide microsatellite loci. Bottleneck analysis gave ambiguous evidence for a recent population decline in the investigated bottlenose dolphin population. M ratio test, with two sets of parameter values, suggested a recent bottleneck; whereas analysis by Bottleneck program under two mutation models (TPM and SMM) showed no evidence for a genetic bottleneck. In addition, there was no evidence for a significant deviation from the normal L-shaped distribution of allele frequencies as expected for a stable population under mutation-drift equilibrium. Furthermore, both allelic richness (6.956) and expected heterozygosity (0.676) of the Adriatic population are above mean of all compared populations (5.993 and

0.658, respectively), confirming relatively high level of genetic diversity in the investigated Adriatic population. Due to ambiguous results, further research is needed to elucidate demographic history of this bottlenecked dolphin population.



G03

GENETIC DIVERSITY AND POPULATION STRUCTURE OF THE EUROPEAN HARBOUR SEAL (*PHOCA VITULINA VITULINA*) IN WESTERN EUROPE

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The European harbour seal, (*Phoca vitulina vitulina*), has been subjected to a number of demographic perturbations, both natural and anthropogenic. Two epizootics of phocine distemper virus affected up to 50% of the population in some areas. Some of these areas are showing signs of recovery, such as in the Netherlands, whereas other regions show signs of further decline, such as in Scotland. Contaminants, hunting pressure and habitat loss have also contributed to population declines in parts of their range. Such contractions and expansions in population size can have an effect on the overall population structure. Eight regions in Western Europe (Western Scotland (n=15), Orkney, Scotland (n=15), Eastern Scotland (n=15), the Wash, Eastern England (n=8), the Thames, Eastern England (n=8), Chichester, Southern England (n=6), Baie du Mont Saint Michel, France (n=5), Dutch Wadden Sea, the Netherlands (n=8)) were sampled. Samples were analyzed for genetic differences based on variation at 6 microsatellite loci to investigate population structure over Western Europe. There was a significant correlation ($p < 0.05$) between geographic distance and genetic distance and a significant F_{ST} value of 0.25 between Scotland and southeast England-western Europe. This suggests two distinct subpopulations. These results are consistent with the findings of previous studies where regional philopatry was observed on the range of 300-500 km.





ABSTRACT BOOK

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