



# mtDNA variation of the critically endangered hawksbill turtle (*Eretmochelys imbricata*) nesting on Iranian islands of the Persian Gulf

M. Tabib, H. Zolgharnein, M. Mohammadi, M.A. Salari-Aliabadi, A. Qasemi, S. Roshani, H. Rajabi-Maham and F. Frootan

Department of Marine Biology, Faculty of Marine and Oceanic Science, Khorramshahr Marine Science and Technology University, Khorramshahr, Iran

Corresponding author: H. Zolgharnein  
E-mail: zolgharnein@kmsu.ac.ir

Genet. Mol. Res. 10 (3): 1499-1503 (2011)  
Received November 10, 2010  
Accepted January 3, 2011  
Published July 25, 2011  
DOI 10.4238/vol10-3gmr1148

**ABSTRACT.** Genetic diversity of sea turtles (hawksbill turtle) was studied using sequencing of mitochondrial DNA (mtDNA, D-loop region). Thirty dead embryos were collected from the Kish and Qeshm Islands in the Persian Gulf. Analysis of sequence variation over 890 bp of the mtDNA control region revealed five haplotypes among 30 individuals. This is the first time that Iranian haplotypes have been recorded. Nucleotide and haplotype diversity was 0.77 and 0.001 for Qeshm Island and 0.64 and 0.002 for Kish Island, respectively. Total haplotype diversity was calculated as 0.69, which demonstrates low genetic diversity in this area. The data also indicated very high rates of migration between the populations of these two islands. A comparison of our data with data from previous studies downloaded from a gene bank showed that turtles of the Persian Gulf migrated from the Pacific and the Sea of Oman into this area. On the other hand, evidence of migration from populations to the West was not found.

**Key words:** Genetic diversity; Sea turtles; Persian Gulf; D-loop; Mitochondrial gene; Phylogenetic analysis