

GENETIC CHARACTERIZATION OF HAWKSBILL JUVENILES FORAGING AT CAPE VERDE ISLANDS INDICATES MAJOR UNDISCOVERED NESTING POPULATIONS IN THE REGION

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Abstract

The hawksbill sea turtle (*Eretmochelys imbricata*) is a circumglobal tropical species listed as Critically Endangered by the IUCN. While it is known that at least one stock occurs around the rookeries of São Tome and Príncipe and Bioko Islands, the eastern Atlantic remains genetically unexplored. We present the first analysis of mitochondrial DNA (mtDNA) sequences (n = 28) of hawksbill juveniles in a foraging aggregation at the Cape Verde Islands, an archipelago located in the eastern Atlantic. The mean size (minimum curve carapace length) of the studied individuals was 42.45 cm. The results showed three haplotypes non-reported in any nesting population to date: EATL (relative frequency 68%), Ei-A49 (14%) and Ei-A82 (4%). These three haplotypes were closely related to each other but highly divergent from all known Caribbean and Western Atlantic haplotypes. Furthermore, we detected three other haplotypes - Ei A (relative frequency 7%), Ei B (4%) and Ei F (4%) - that have been previously detected in rookeries from the western Atlantic. Cape Verde feeding ground showed a high degree of genetic differentiation with respect to known nesting populations and foraging areas. Furthermore, this juvenile aggregation presented the second lowest level of haplotype diversity and the highest value of nucleotide diversity from all the studied Atlantic foraging aggregations. We were not able to determine the population composition of this aggregation since more than 86% of the individuals carried orphan haplotypes whose origin has not been identified to date. These findings highlight the fact that the incomplete haplotype baseline of contributing nesting populations in the eastern Atlantic currently hampers progress of genetic studies and consequently, a priority for evaluation on the conservation and management issues related to foraging aggregations in this region. The results suggest that this aggregation appears to be composed primarily of turtles from regional nesting colonies (eastern Atlantic). Moreover, the finding of the haplotypes Ei A, Ei B and Ei F at low frequencies suggests the existence of occasional transatlantic movements. This study highlights the necessity of Cape Verde conservation and the need additional research, particularly expanding the genetic analysis throughout the westcoast of Africa to include unsampled areas.