

CONSERVATION GENETICS OF NORTH ATLANTIC LOGGERHEAD SEA TURTLES: ANALYSIS OF NUCLEAR AND MITOCHONDRIAL DNA

C. Monzón-Argüello¹, C. Rico², E. Naro-Maciel³, A. Marco², and L.F. López-Jurado⁴

1 Instituto Canario de Ciencias Marinas, Telde, Gran Canaria, España

2 Estación Biológica de Doñana, CSIC, Sevilla, España

3 Center for Biodiversity and Conservation and Sackler Institute for Comparative Genomics American Museum of Natural History, New York, USA

4 Universidad de Las Palmas de G.C. Campus de Tafira, Gran Canaria, España

Abstract

Complex population structure has been described for the loggerhead sea turtle (*Caretta caretta*), revealing lower levels of population genetic structure in nuclear compared to mitochondrial DNA assays. This may result from mating during spatially overlapping breeding migrations, or male-biased dispersal as previously found for the green turtle (*Chelonia mydas*). To further investigate these multiple possibilities, we carried out a comparative analysis from twelve newly developed microsatellite loci and the mitochondrial DNA control region (~804 bp) in adult females of the Cape Verde Islands (n=158), and Georgia, USA (n=17). The Cape Verde archipelago harbours the third largest loggerhead sea turtle nesting aggregation in the world, after the populations of south Florida, USA and Masirah, Oman. Cape Verde is also the sole major confirmed nesting area for this species in the eastern Atlantic. Our results reveal levels of gene flow across different genetic markers between North Atlantic loggerhead sea turtle rookeries, providing insight into the mechanisms leading to complex population genetic structure that would provide immediate conservation applications.