POPULATION GENETIC ANALYSIS OF LOGGERHEAD TURTLES IN THE CAPE VERDE ISLANDS

Catalina Monzón-Argüello[1], Ciro Rico[2], Eugenia Naro-Maciel[3], Nuria Varo Cruz, Pedro López, Adolfo Marco [5], and Luis F. López-Jurado

[1] Instituto Canario de Ciencias Marinas, Las Palmas, Spain
[2] Estación Biológica de Doñana, CSIC, Sevilla, Spain
[3] Museo de Ciencias Naturales, New York, USA
[4] Cabo Verde Natura 2000, Boa Vista, Cabo Verde
[5] Estación Biológica de Doñana, CSIC, Sevilla, Spain
[6] Universidad de Las Palmas de Gran Canaria, Las Palmas, Canary Islands, Spain

Cape Verde harbors one of the world's largest nesting aggregations of loggerhead sea turtles *(Caretta caretta),with* thousands of females laying eggs on its beaches every nesting season. Cape Verde is an archipelago in Macaronesia, situated 600 km west of Senegal and comprised of 10 volcanic islands and five islets. The vast majority of nesting activity in Cape Verde occurs on the Boavista, Sal, Santa Luzia and Maio islands. Sequences of 391 b.p. of the mitochondrial DNA control region were analyzed in 158 adult females to elucidate population genetic structure and phylogeography. Samples were collected at four nesting sites; Boavista (n=62), Sal (n=49), Sta. Luzia (n=35) and Maio (n=12) between 2004-2005. The number of haplotypes, haplotype diversity (h), nucleotide diversity (Pi), haplotype frequencies and fixation indices (Fst) were obtained. We examined if latitudinal variation in genetic composition occurs throughout Cape Verde, since the most distant islands are more than 200 km aparto These results will indicate us if rookeries from different islands may be considered as one or different management unit.