

POPULATION GENETICS OF SEA TURTLES ALONG THE BRAZILIAN COAST

Proietti, M.C.¹; Secchi, E.R.¹; Monteiro, D.^{1,2}; Marins, L.F.³; da Silva, C.P.B¹; Reisser, J.⁴

¹Instituto de Oceanografia/FURG; ²Núcleo de Educação e Monitoramento Ambiental; ³Instituto de Ciências Biológicas/FURG; ⁴The Ocean Cleanup/Holanda

Sea turtles are long-lived, highly migratory marine animals that occupy several habitats and ecological niches throughout their lives. The complexity of their life cycle and the large geographical/temporal scales involved require indirect research of their ecology and biology, for example through molecular analyses. These techniques can help elucidate aspects such as population structure, natal origins of animals at foraging grounds, migrations, and interspecific hybridization. In this work we studied the mitochondrial DNA of immature green (*Chelonia mydas*) and hawksbill (*Eretmochelys imbricata*) turtle aggregations along the coast of Brazil, in order to determine diversity, structure, and natal origins, and investigate hybridization between species. For juvenile green turtles in South Brazil, we found overall low genetic diversity, and lack of genetic structure relative to all other Brazilian feeding grounds except Almofala, in the northeast; however, they were genetically different from all aggregations in the Caribbean and North America. Green turtles feeding at the southern region originated mainly from international rookeries (Ascension and Aves Islands; ~70% contribution), but the Brazilian nesting ground at Trindade Island also contributes to the feeding aggregation in ~17%. We found that these contributions were generally correlated with surface ocean currents. Juvenile hawksbill turtle aggregations at seven sites from northeast to south Brazil presented medium genetic diversity. Genetic profiles of these feeding areas were significantly different from other regions in the Caribbean and Africa, and a significant structure was observed between Brazilian feeding grounds grouped into areas influenced by the South Equatorial/North Brazil Current and those influenced by the Brazil Current. Our genetic analysis estimates that the studied hawksbill feeding aggregations originate mostly from the domestic rookeries Bahia and Pipa, but some contributions from African and Caribbean rookeries were also observed. Origins were also generally correlated with ocean currents, reinforcing the influence of this oceanographic feature on turtle dispersal. Finally, we report immature hawksbill x loggerhead (*Caretta caretta*) hybrids at three areas: Ceará (n = 1), Bahia (n = 1) and Rio Grande do Sul (n = 6) states. Despite the unusually high frequency of hybridization events between hawksbill and loggerhead breeding groups is at the Bahia rookery, ours was the first record of immature hybrids at the coast, and contributes to a more thorough understanding of the fate of to these animals after being born at Bahia. These hybrids were not present in important hawksbill feeding grounds of Brazil, being detected only at areas more common for loggerheads. This could indicate that these immature hybrids, which are morphologically similar to hawksbills, could be adopting behavioral traits more similar to loggerheads. The information presented here highlights the importance of national conservation strategies and international cooperation for the recovery of endangered green and hawksbill turtle populations. We also highlight the significance of better understanding the distribution and ecology of sea turtle hybrids in order to develop adequate management plans for these animals.

Keywords: SEA TURTLES; CONSERVATION GENETICS; HYBRIDIZATION