

Genética populacional e conservação das espécies de tartarugas-marinhas do Brasil

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Genética da conservação da tartaruga verde (*Chelonia mydas*) no Brasil

*Conservation genetics of the green sea turtle (*Chelonia mydas*) in Brazil*

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Protected areas successfully safeguard many organisms, and yet highly migratory species such as sea turtles may face serious threats when they leave the boundaries of these zones, underscoring the importance of understanding their population distribution. To investigate the population distribution of globally endangered green turtles in the Southwestern Atlantic Ocean, we sequenced a segment of the mitochondrial control region from turtles foraging at four sites in Brazilian waters, ranging from remote World Heritage Sites to highly urbanized areas (862 bp; n = 445), and analyzed them with respect to published data. At all sites the most common haplotypes were CMA-08 and CMA-05, and analysis uncovered several new sub-haplotypes. Results of “many-to-many” mixed stock analyses identified the primary natal sources of these feeding grounds, revealed the connectivity of the regionally important Trindade rookery, and highlighted the many threats outside of remote or protected areas. The study addressed calls for increased sampling in the Southwestern Atlantic, and provided data necessary for conservation and management of endangered green turtles within and outside of protected areas.

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Conservation genetics of Hawksbill Sea turtles from the Brazilian coast

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The Hawksbill (*Eretmochelys imbricata*) nests along the northeast coastline of Brazil, but over 90% of nests are registered in Bahia State where it is monitored by Projeto Tamar-IBAMA in Brazil. A preliminary

study detected a high occurrence of interspecific hybrids in Bahia, where 42% of morphologically characterized hawksbills displayed loggerhead mtDNA haplotypes. Although the relative importance of hybridization in conservation biology seems to be controversial among researchers, a detailed study of the process is needed to evaluate natural or anthropogenic causes of this regional phenomenon. We have analyzed a set of 12 nuclear markers together with mtDNA data to investigate in detail the hybridization events involving *Eretmochelys imbricata*, *Caretta caretta* and *Lepidochelys olivacea*. Our data indicates that mainly F1 hybrids were observed for the crossings *L. olivacea* x *E. imbricata*, and *L. olivacea* x *C. caretta*, whereas *C. caretta* x *E. imbricata* presents F1 and backcrosses with both parental species. In addition, the hybridization process observed between *C. caretta* x *E. imbricata* seems to be gender and species biased and we also found evidence of multispecies hybridization among *C. caretta* x *E. imbricata* x *C. mydas*. The results also indicate that hybridization is a very recent phenomenon that may be likely related to population decline due to anthropogenic causes, thus raising issues about the future conservation management of these populations.

Dinâmica populacional e filogeografia de tartaruga oliva (*Lepidochelys olivacea*)

*Global Genetic Structure and Phylogeography of Olive Ridley (*Lepidochelys Olivacea*)*

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The olive ridley turtle (*Lepidochelys olivacea*) has a global distribution across tropical and sub-tropical oceans, and is the most abundant marine turtles species. It is closely related to the Kemp's ridley (*L. kempii*) and the origin of both species is believed to be related to the closure of the Isthmus of Panama, about 3.5 to 5 million years ago. In this work we expand the previous study of Bowen et al. (1998) on the global phylogeography of olive ridley turtles using longer sequences of the mitochondrial DNA (mtDNA) control region and including fifteen nuclear DNA microsatellites (STRs) loci. A total of 324 olive ridleys, plus four Kemp's ridleys from all major nesting sites were sequenced and genotyped. The mtDNA revealed 29 olive ridley haplotypes, five haplotypes for the Atlantic Ocean (AT), nine for the Indo-Pacific (IP) region and 14 for the East Pacific (EP) and finally one haplotype for the Kemp's ridley. Phylogenetic and network analysis of the mtDNA found four distinct lineages within the olive ridley, two within the IP, one within AT, and one within the EP, and a closer relationship between a central haplotype found in Sri Lanka and Australia rookeries and haplotypes from Atlantic and East Pacific oceans. Olive ridleys show moderate to high genetic differentiation among regional rookeries separated by more than 500 km (pairwise F_{ST} was significant and varied from 0.1 to 0.88), but low genetic differentiation among closer rookeries (e.g. Surinam/French Guiana and Tiwi Island/McCluer Island (Australia) (pairwise F_{ST} from 0 to 0.04). However, Costa Rica/Mexico although separated by more than 500km, are not genetically distinct. The microsatellite analyses showed lower levels of genetic structure among regional nesting sites than did the mtDNA. Pairwise F_{ST} values varied from 0 to 0.04 between populations within the IP, from 0 to 0.08 between rookeries from AT, and from 0 to 0.02 between rookeries from EP. Between oceans, the pairwise F_{ST} vary from 0.03 to 0.18 between rookeries from IP and AT, from 0.04 to 0.24 between IP and EP, and 0.07 to 0.28 between AT and EP. Results from the software Structure indicated that our data support four genetic clusters that were also associated with Oceanic basins, and Kemp's ridley samples comprised a unique cluster.

