

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

Mediador: Fabrício Rodrigues dos Santos, UFMG, Belo Horizonte, MG, Brasil

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

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

Naro-Maciel, E¹; Bondioli, ACV²; Martin, M³; Baptistotte, C⁴; Bellini, C⁵; Almeida, AP⁶; Marcovaldi, MA⁶; Santos, AJB⁷; Torezani, E⁸; Amato, G⁹

¹Biology Department, College of Staten Island, City University of New York, Staten Island, NY, 10314, USA. ²Projeto Tartarugas, Instituto de Pesquisas Cananéia – IPeC, Rua Tristão Lobo 199, 11990-000 Cananéia, SP, Brasil.

³Yale School of Forestry and Environmental Studies, New Haven, CT, 06511, USA. ⁴Projeto TAMAR-ICMBio, Vitória, Espírito Santo, 29900, Brasil. ⁵Projeto TAMAR-ICMBio, Av. Alexandrino de Alencar 1399, Tirol Natal RN, Brasil.

⁶Projeto TAMAR-ICMBio, Praia do Forte, Bahia, 40210, Brasil. ⁷Fundação Pró-TAMAR, Alameda do Boldró s/ número, Fernando de Noronha PE, Brazil.

⁸Sackler Institute for Comparative Genomics, American Museum of Natural History, New York, New York, 10024, USA

Eugenia.NaroMaciel@csi.cuny.edu

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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

Fabrício Rodrigues dos Santos^{*1}, Sibelle Torres Vilaça^{*1}, Sarah Maria Vargas^{*1}, Paula Lara-Ruiz², Érica Molfretti³, Estéfane Cardinot Reis⁴, Gisele Lôbo-Hajdu⁵, Luciano Soares⁶

^{*}Laboratório de Biodiversidade e Evolução Molecular (LBEM), Instituto de Ciências Biológicas, Universidade Federal de Minas Gerais (UFMG), Av. Antônio Carlos, 6627, 31.270-010 Belo Horizonte, MG, Brazil. ¹Department of Biology and Evolution, University of Ferrara, Via L. Borsari 46, 44100 Ferrara, Italy. ²Universidade Federal do Espírito Santo, Av. Fernando Ferrari, 514, 29075-910 Vitória, ES, Brazil. ³Laboratório de Genética Marinha (LGMAR), Departamento de Genética, Universidade do Estado do Rio de Janeiro (UERJ), Rua São Francisco Xavier, 524, 20.550-013 Rio de Janeiro, RJ, Brazil. ⁴Projeto TAMAR-ICMBio, C.P. 2219, 41950-970, Salvador, BA, Brazil.

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*)*

Sandro Luis Bonatto, PUC/RS, Porto Alegre, RS, Brasil

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.

Genetic diversity of loggerhead sea turtles (*Caretta caretta*) along the Brazilian coast: phylogeographic aspects and cases of hybridization

Gisele Lobo-Hadju, UERJ, Rio de Janeiro, RJ, Brasil

The loggerhead sea turtle, *Caretta caretta*, is the most common species of sea turtle nesting in Brazil and is listed as endangered by the IUCN. Our study characterizes the genetic structure of loggerheads in Brazil based on the variability of the mitochondrial DNA control region and presents a hypothesis for the colonization of Brazilian rookeries. We analyzed 329 samples from Brazilian rookeries and an oceanic foraging ground from South Brazil, and compared our results with previously published data for other loggerhead populations. Brazilian rookeries had four haplotypes, none of which has been reported for rookeries outside Brazil. Six haplotypes were found in the foraging aggregation. We also found specimens considered hybrids because they present olive ridley's (*Lepidochelys olivacea*) mtDNA, but had the external morphology of *C. caretta*, or of a mixture of both species. Based on the two types of hybrids, it was hypothesized that at least two hybridization events had occurred: a more ancient one,

accompanied by introgression (F2 or later backcrosses), and a recent one (F1), both of which involving the same *L. olivacea* haplotype. The incidence of *L. olivacea* mitochondrial genome introgression into the *C. caretta* rookeries was only observed in Sergipe, which could be related to the large numbers of *L. olivacea* in this region and an overlap of reproduction periods of both species. The presence of the CC-A4 haplotype at all sampled sites and the low nucleotide diversity suggest a common origin for all rookeries, with CC-A4 being the ancestral haplotype of the Brazilian populations. The occurrence of haplotypes in the foraging aggregation that are known only from rookeries outside of Brazil is consistent with the transoceanic migratory behavior of loggerheads. Our results indicated that the colonization of Brazilian rookeries probably occurred from the southern USA stock. This recent colonization most likely followed a north to south route along the Brazilian coastline, influenced by, beside others, the Brazilian warm current. The occurrence of gene flow between different species of the Family Cheloniidae will significantly influence the development and implementation of management strategies in Brazil. Our results further suggest the existence of two genetic population units or evolutionary significant units (ESUs) of loggerheads in Brazil and corroborate natal homing behavior in loggerheads.

Key-words: conservation genetics, sea turtles, phylogeography, hybridization.
