
MIXED STOCK ANALYSIS OF LEATHERBACK TURTLES FEEDING IN BRAZIL: RECORDS OVER FOUR YEARS

Sarah Vargas¹, Érica Molfetti², Sibelle Torres Vilaça³, Danielle Monteiro⁴, Sérgio C. Estima⁴, Luciano Soares e Soares⁵, Antônio P. Almeida⁵, Benoit de Thoisy⁶, Eugenia Naro-Maciel⁷, and Fabrício R. Santos²

¹ Laboratório de Biodiversidade e Evolução Molecular, ICB, UFMG, Belo Horizonte, MG, Brazil, Departamento de Ciências Biológicas, CCHN, UFES, Vitória, ES, Brazil

² Laboratório de Biodiversidade e Evolução Molecular, ICB, UFMG, Belo Horizonte, MG, Brazil

³ Department of Biology and Evolution, University of Ferrara, Ferrara, Italy

⁴ Núcleo de Educação e Monitoramento Ambiental, NEMA, Porto Alegre, RS, Brazil

⁵ Fundação TAMAR, Praia do Forte, BA, Brazil

⁶ Association Kwata, French Guiana

⁷ College of Staten Island, City University of New York, USA

The population of leatherback turtles (*Dermochelys coriacea*) nesting in Brazil is restricted to very few individuals, regularly nesting on the coast of the Espírito Santo State. However, a larger feeding aggregation occurs throughout Brazilian waters, with higher concentration off the south and southeast coasts. The objectives of this study are to estimate the contribution of source rookeries to a Brazilian feeding ground using population genetic measures and Mixed Stock Analysis (MSA), to describe the haplotypes found for two previously genetic undescribed rookeries: Gabon and Guadeloupe/Martinique, to increase the number of samples from Brazilian and French Guianan rookeries and to compare the data obtained with previous reports. To compare the sequences between leatherbacks from Brazil and elsewhere, we analyzed 496 bp of mitochondrial DNA (mtDNA) control region from leatherbacks stranded on beaches (n=90) and incidentally caught by fisheries in Brazilian waters (n=9) from January 2004 to December 2007. We also analyzed samples of nesting females from a rookery in Gabon (n=23) and from two rookeries in Guadeloupe and Martinica (n=29) and additional samples from rookeries in French Guiana (n=29) and Brazil (n=14). The MSA was run using haplotypes from the pelagic leatherbacks (n=99) and from 15 rookeries found worldwide from previously reports (overall n=386). Information from the literature regarding the number of females nesting per year in each population was used as a prior. An overall of 14 different haplotypes were described using the entire database. The most common haplotype, called A was found in 171 samples (44,30%). This haplotype was spread across all rookeries except for the Pacific coast of Mexico and Costa Rica. The haplotype A2, found for the first time only at the foraging area in Brazil, now was also found in samples in rookeries from Brazil and Gabon. Two new haplotypes (A5 e C3) were found in this study, both in samples from French Guiana. For the MSA, all chains consistently indicated a major contribution to the Brazilian pelagic aggregate from Gabon (77,7%), the largest populations of leatherback in the world. Efforts should be done in order to produce longer mtDNA and nuclear sequences in widespread worldwide samples to improve the confidence of data in phylogeography and MSA. Furthermore, MSA studies provide relevant data connecting nesting and feeding sites, and it is also important information for planning management strategies aiming to enhance conservation efforts worldwide. Acknowledgments: FAPES, Capes, CNPq, Fapemig and ISTS Program Committee