

## ORIGIN OF IMMATURE GREEN TURTLES (*CHELONIA MYDAS*) AT TWO FORAGING GROUNDS IN SABAH, MALAYSIA

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Understanding the population dynamics in both breeding and foraging habitats is a vital part of assessing the long-term viability of any species, particularly those that are highly migratory, such as green turtles, *Chelonia mydas*. Monitoring of the populations at the foraging grounds may help detect early signs of population trends that would otherwise take decades to be seen at the nesting beach. Mixed Stock Analysis (MSA) using molecular marker techniques provide an effective tool for estimating the origin of turtles sampled away from their nesting beach. Here we use sequence data from the mitochondrial DNA (mtDNA) of 96 immature green turtles at two foraging grounds at Mantanani Island and Layang Layang Island located northwest of Sabah, Malaysia. We used data from eight Australasian green turtle populations as the baseline data for tracing back the origin of turtles at the two foraging grounds. The origins of the turtles at the two foraging grounds were not different and the majority of these turtles originated from key rookeries at Sarawak in north western Borneo and from the Malaysia and Philippine Turtle Islands in SE Sabah. These same rookeries have a long tradition of using unshaded beach hatcheries that have resulted in mostly female hatchlings being produced. This may have contributed to the 1:4 female biases seen at the foraging grounds. We discuss the implications of hatchery practices at nesting beaches and recommend future research to improve the management of marine turtles in the region.

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## GREEN TURTLE (*CHELONIA MYDAS*) GENETIC COMPOSITION AT A FEEDING GROUND AND ROOKERIES IN THE WEST ATLANTIC: CONNECTIONS BETWEEN POPULATIONS

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Sea turtles are globally distributed reptiles that exhibit complex life traits, such as long generation time, oceanic habitat of juveniles, female homing and wide-ranging migrations. The migratory behavior outcomes in spatial segregation between breeding and nesting sites, resulting in successive stages of the mixing and isolation of genetic stocks, both spatially and temporally. The green turtle, *Chelonia mydas*, is threatened with extinction worldwide and understanding its history is important to assess population dynamics and make future projections on the population trends. The use of molecular techniques has enabled progresses in species conservation, such as characterization of population structure, genetic diversity and natal origins. Thus, the aim of this study is to characterize the genetic composition of *C. mydas* in a feeding ground (hereafter FG) (at north coast of Rio de Janeiro state, Brazil, n=175) and two rookeries (French Guiana, n=46, and Guadeloupe, n=24) in West Atlantic Ocean, as well as the genetic contribution of rookeries to the FG, based on mitochondrial DNA sequences. The FG is composed so far by 11 haplotypes: CM-A8 (72%), CM-A5 (17%) and the others with a frequency less than 5% (CM-A1, CM-A3, CM-A6, CM-A9, CM-A10, CM-A23, CM-A24, CM-A32 and CM-A42). Besides, two previously undescribed haplotypes were found, CM-A69 and CM-A70. The nesting rookeries are composed so far by CM-A5 (95%) and CM-A3 (5%) in Guadeloupe, and by CM-A5 (93%), CM-A8 (4%) and CM-A22 (3%)



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Baltimore, Maryland USA

5 to 8 February, 2013  
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Compiled by:

Tony Tucker, Lisa Belskis, Aliko Panagopoulou, Alan Rees, Mike Frick,  
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