

this purpose we analyzed the genetic variation in the mitochondrial DNA control region from the Pulau Panjang aggregation (n=51) and compared with the genetic composition of the nesting aggregations of Sangalaki, Derawan and Blambangan (n=38) and previously assessed Australasian nesting grounds. After analysis of approximately 740bp of the mtDNA we identified 36 polymorphic sites (35 transitions and 1 transversion) that determined 11 different haplotypes that included three variants of haplotypes C3, two of C5, and two of haplotype D2. Molecular diversity estimates of all samples indicated a high haplotype and nucleotide diversity ( $h=0.853 \pm 0.014$ ;  $\pi=0.01098 \pm 0.01009$ ). High haplotype and nucleotide diversities were also found in nesting samples ( $h=7$ ;  $hd=0.778 \pm 0.045$ ;  $\pi=0.00381 \pm 0.01083$ ) as well as in feeding ground samples ( $h=10$ ;  $hd=0.845 \pm 0.028$ ;  $\pi=0.01535 \pm 0.01104$ ). The genetic composition of the nesting aggregations were dominated by haplotype C3 (39.47%) followed by haplotypes C14 (18.42%) and C5 (18.42%). Although haplotype C3 is common most of the nesting aggregations in Australasia, the genetic composition of the nesting aggregations from Derawan Islands is more similar to the rookeries of Malaysia, which are also composed by the combination of haplotypes C3, C5 and C14. The Pulau Panjang feeding ground was dominated by haplotype D2 (29.41%), D2A (19.61%), and A3 (13.73%) and results from mixed stock analysis suggest a genetic connectivity of the Derawan foraging aggregations with nesting grounds from Malaysia and Philippines. In addition, the Pulau Panjang feeding ground also seems to be home for Micronesian and Papua New Guinea nesting turtle populations, dominated by the presence of haplotype A3 and A4.

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## GENETIC DIVERSITY OF THE GREEN TURTLE (*CHELONIA MYDAS*) POPULATIONS IN SRI LANKA

**E.M.L. Ekanayake<sup>1</sup>, R.S. Rajakaruna<sup>2</sup>, P. Samaraweera<sup>3</sup>, K.B. Ranawana<sup>2</sup>, T. Kapurusinghe<sup>4</sup>, M.M. Saman<sup>4</sup>, and M.G.C. Premakumara<sup>4</sup>**

<sup>1</sup> Turtle Conservation Project, Duwemodara, Kosgoda, Post Graduate Institute of Science, University of Peradeniya, Sri Lanka

<sup>2</sup> Department of Zoology, University of Peradeniya, Sri Lanka

<sup>3</sup> Department of Molecular Biology & Biotechnology, University of Peradeniya, Sri Lanka

<sup>4</sup> Turtle Conservation Project, Duwemodara, Kosgoda, Sri Lanka

During the last few decades, marine turtle populations have been declining rapidly throughout the world, due to human interruption. They face many threats all around the world including slaughtering for meat and collecting eggs for human consumption. All seven species of marine turtles, including green turtles (*Chelonia mydas*), are listed as endangered or critically endangered by the IUCN. Although marine turtles are protected by government legislation, turtles are still being exploited in Sri Lanka. Population decline may cause the reduction in genetic variation of the turtle population. A relatively new thought based on evolutionary theory has argued that conservation efforts should focus on preservation of the genetic diversity that allows species to respond to changes and adapt for new conditions. The genetic diversity is widely believed as a base for the organismal diversity. Therefore, conservation projects are heading towards safeguarding genetic variation. The objective of this study is to determine the genetic diversity of the green turtle population that nest on southern coast of Sri Lanka. Small skin samples were collected from the nesting green turtles at Kosgoda turtle rookery, and preserved in 95% ethanol. Genomic DNA was extracted by chelex protocol. Microsatellites were amplified from genomic DNA by polymerase chain reaction (PCR). Six primers, Cm3, Cm58, Cm72, Cm84, Cc117 and Cc7 were used for the analysis. The PCR products were separated by polyacrylamide gel electrophoresis (PAGE) and the genetic diversity of the population was determined. Authors acknowledge the financial support from National Science Foundation, Sri Lanka (Grant Number: SIDA/2005/BT/01) and International Foundation for Science, Sweden (Grant number A/3863-1). Also we wish to acknowledge to symposium travel committee and to the Australian Government DEWHA, Queensland Environmental Protection Agency, Disney Animal Kingdom, Western Pacific Regional Fisheries Management Council, U.S. National Marine Fisheries Service, and the U.S. Fish and Wildlife Service (Marine Turtle Conservation Fund) for the travel grant.