STUDIES ON THE POPULATION GENETICS OF GREEN (Chelonia mydas) AND HAWKSBILL (Eretmochelys imbricata) TURTLES IN MALAYSIA USING DNA MICROSATELLITES

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By

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Thesis Submitted in Fulfilment of the Requirements for the Degree of Master of Science in the Faculty of Science and Technology Kolej Universiti Terengganu Universiti Putra Malaysia

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December 2000

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Faculty: Science and Technology

Genetic diversity of six populations of green turtle (*Chelonia mydas* Linnaeus, 1958) from Terengganu, Pahang, Perak, Sarawak, Sabah Turtle Islands Park and Pulau Sipadan and four populations of hawksbill turtle (*Eretmochelys imbricata* Linnaeus, 1766) from Melaka, Johor, Terengganu and Sabah were analysed using 14 microsatellite markers. The amplified DNA product was electrophoresed using Nusieve Agarose gel 3:1 and the banding patterns were visualized by using UV light. High levels of polymorphism were observed over all populations of green turtle, with up to 12 alleles per locus and expected heterozygosities ranging from 0.5 to 0.7. In hawksbill turtle populations, these loci were also polymorphic, with up to 8 alleles per locus and expected heterozygosities from 0.2 to 0.6. The difference in the level of genetic variability in the two species of marine turtles needs explanation and may have profound implications for the management of these endangered species. Low genetic differentiation and intra-specific gene flow was observed among the nesting populations assayed in this study. Genetic distance between populations of green and hawksbill turtle ranged from 0.0352 to 0.1101 and 0.0626 to 0.0989, respectively. Cluster analysis using populations as node show a clustering of populations according to geographical localities. This indicates that the genetic relationships are associated with geographical distances, whereby populations are subdivided through space and thus these local populations should be recognised and monitored as separate management units.

This study has identified the first microsatellite DNA in green and hawksbill turtles from Malaysia and allowed the estimation of the previously incomplete genetic information of these species. It uncovered that some of the nesting populations of green and hawksbill turtles in Malaysia are rapidly approaching extinction, especially the Perak green turtle population and the Terengganu and Johor populations of hawksbill turtle. Hence, strict conservation measures and management practices should be enforced to prevent these populations from becoming extinct. The most significant result from the microsatellite analyses is the evidence for the presence of four genetically differentiated stocks in Malaysian waters; the eastern part of Peninsular Malaysia represented by the East coast and Johor populations, the western part of Peninsular Malaysia represented by the Perak and Melaka populations, the Sarawak population and the Sabah population. In addition, this study also showed the potential usefulness of microsatellite DNAs in addressing evolutionary and conservation issues regarding endangered populations of marine turtles.

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