STUDIES ON THE POPULATION GENETICS OF GREEN TURTLE (*CHELONIA MYDAS*) AND HAWKSBILL TURTLE (*ERETMOCHELYS IMBRICATA*) IN MALAYSIA USING MICROSATELLITE

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Introduction

This study applies modern molecular genetic techniques to address aspects of Malaysian Sea turtle biology that have remained unresolved using conventional methods. The endangered or threatened status of sea turtles in Malaysia dictates aggressive and comprehensive management plans to expedite population recoveries. In light of that, specific studies were undertaken to determine the genetic variability within and among the various nesting populations, assessing the extent of differentiation among these populations and to determine their conservation status. Our ultimate aim is to provide the first complete genetic appraisal of diversity and stock structure for Malaysian green and hawksbill turtles in response to the need to identify conservation priorities. We hoped to establish conditions that permit nesting populations to increase in numbers to some level at which a species is no longer at appreciable risk of extinction.

Materials and Methods

Blood samples from hatchlings will be collected from various nesting populations in Malaysia. A standard bleeding technique will be used as described by Owens and Ruiz (1980), where blood is drawn from the dorsal cervical sinus using ½ CC insulin syringe. Samples are preserved in a lysis buffer (Dutton, 1996) and stored at –20°C. Genomic DNA from blood samples are then extracted using the Qiagen tissue kit protocols. All microsatellite amplifications will be performed in a 20 µl mixtures containing template DNA, PCR buffer, $MgCl_2$, dNTP's, taq polymerase and microsatellite primers. 17 microsatellite primers (Dutton, 1995; FitzSimmons et al. 1995; Kichler, *internet pers. comm.*) were used and amplifications were performed using the Perkin-Elmer 2400 PCR system. Aliquots of PCR products will be run on 4% Nusieve agarose 3:1 gels, stained using ethidium bromide and visualized on the UV transiluminator. Non-radioactive confirmation tests for the heterozygots will also be done using 6% sequencing acrylamide gels.

Results and Discussion

Blood samples were collected from various nesting populations in Malaysia, *viz.*, Sabah (Sabah Turtle Islands Park and Pulau Sipadan), Melaka, Johor, Perak, Pahang and Terengganu (Pulau Redang and Setiu). Further sample collection was also done from Sarawak Turtle Islands and Terengganu (Pulau Perhentian and Setiu). So far, we managed to screen all the green and hawksbill turtle's blood samples from Sabah Turtle Islands. Anyhow, we haven't done any statistical analyses yet on the results obtained. Currently, we have standardised our molecular genetic techniques and expected to finish the lab analyses in May, 1999. We hope to finish this project by the end of the year 1999 and submit a complete genetic appraisal of diversity and stock structure of Malaysian sea turtles.

Conclusions

Our preliminary results demonstrate that microsatellite technique can be used as a rapid and sensitive genetic marker for the detection of polymorphism and to study the population genetics of sea turtles in Malaysia.

References

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