

DETERMINATION OF NATAL ORIGINS OF GREEN (*Chelonia mydas*) AND HAWKSBILL
(*Eretmochelys imbricata*) TURTLES AT FEEDING GROUNDS IN MALAYSIAN WATERS

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Abstract of thesis presented to the Senate of Universiti Malaysia Terengganu in fulfillment of the requirement for the degree of Master of Science

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Genetic, flipper tagging and telemetry studies have demonstrated that sea turtle migrate extensively between nesting and feeding grounds. However, in Malaysia, sea turtle conservation efforts concentrated mainly on nesting populations, hence little is known about the turtles at feeding grounds. In recent years, harvesting of sea turtles at feeding grounds in Malaysia has become more serious. Therefore, this research aimed to identify the feeding grounds and to determine the natal origins of sea turtle occupying each feeding habitat using mitochondrial DNA control region sequences.

A total of ten sampling locations were identified (Redang Island, Perhentian Island, Talang-Satang National Parks, Pulau Tiga, Layang-Layang Island, Mantanani Island, Tanjung Tuan, Sungai Pulai, Tun Sakaran Marine Parks and Sipadan Island), and about 103 green and 25 hawksbill turtles were caught for this study. Besides, this study also analyzed 30 tissue samples from sea turtle carcasses seized in the 2007 Hainan poaching incident.

Fourteen haplotypes were detected from the green turtle samples, of which five were new haplotypes and nine were previously reported by Dethmers *et al.* (2010). As for the hawksbill turtle, 11 haplotypes were detected, of which four were new haplotypes and the remaining seven haplotypes were previously identified by previous study. The genetic results suggested that the feeding grounds in Malaysia consist of sea turtles from multiple nesting populations around Southeast Asia and the Western Pacific.

The Mixed Stock Analysis suggested that most of the green turtle feeding populations were originated from the Sulu Sea and South-Eastern Sabah (63.16%) and Long Island, Papua New Guinea (16.42%). As for the hawksbill turtle, most feeding populations were originated from Bataan, Philippines (32.13%), Coco Island, Myanmar (21.10%) and Davao Gulf, Philippines (19.42%).

This research is important for the understanding sea turtles migration patterns, identifying the inhabited feeding grounds and identifying which nesting populations contributed to the feeding populations in Malaysia. Undoubtedly, better management is needed to conserve both nesting and feeding populations as well as their habitats. Effective protection of sea turtle feeding populations in Malaysia may enhance the nesting populations of sea turtles located thousands of kilometers away.

Abstrak tesis yang dikemukakan kepada Senat Universiti Malaysia Terengganu sebagai memenuhi keperluan untuk ijazah Master Sains

MENENTUKAN ASAL USUL PENYU AGAR (*Chelonia mydas*) DAN PENYU SISIK (*Eretmochelys imbricata*) DI KAWASAN PERMAKINAN DI SEKITAR PERAIRAN MALAYSIA

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Kajian genetik, penandaan dan telemetri telah menunjukkan bahawa penyu berhijrah secara meluas di antara kawasan persarangan dan kawasan pemakanan. Namun, di Malaysia, usaha pemuliharaan penyu hanya bertumpu kepada populasi persarangan, jadi kurang maklumat diketahui mengenai penyu di kawasan pemakanan. Kebelakangan ini, pemburuan penyu secara haram di kawasan pemakanan di Malaysia telah menjadi semakin serius. Oleh kerana itu, tujuan utama kajian ini adalah untuk mengenalpasti kawasan pemakanan penyu dan juga untuk menentukan asal usul penyu yang mendiami di setiap kawasan pemakanan dengan menggunakan “mitochondrial DNA control region sequences”.

Sejumlah 10 lokasi persampelan telah dikenalpasti (Redang Island, Perhentian Island, Talang-Satang National Parks, Pulau Tiga, Layang-Layang Island, Mantanani Island, Tanjung Tuan, Sungai Pulai, Tun Sakaran Marine Parks and Sipadan Island), dan sebanyak 103 ekor penyu agar dan 25 ekor penyu karah telah ditangkap untuk kajian ini. Selain itu, kajian ini juga menganalisis 30 sampel tisu daripada bangkai penyu yang disita dari Pemburuan Haram Hainan pada tahun 2007.

Empat belas haplotipe telah dikesan daripada sampel penyu agar, di mana lima sampel adalah haplotipe baru dan sembilan sampel merupakan sampel yang dilaporkan sebelum ini oleh Dethmers *et al.* (2010). Bagi penyu karah, 11 haplotipe telah dikesan, di mana empat adalah haplotipe baru dan tujuh haplotipe merupakan sampel yang sebelum ini dikenal pasti oleh kajian lama. Hasil kajian genetik mencadangkan bahawa kawasan pemakanan penyu di Malaysia adalah terdiri daripada populasi penyu yang bertelur di sekitar kawasan Asia Tenggara dan Pasifik Barat.

“Mixed Stock Analysis” menunjukkan bahawa kebanyakan populasi penyu agar di kawasan pemakanan berasal dari Laut Sulu dan Selatan-Timur Sabah (63.16%) dan Long Island, Papua New Guinea (16.42%). Bagi penyu karah, kebanyakan populasi di kawasan pemakanan adalah berasal dari Bataan, Philippines (32.13%), Coco Island, Myanmar (21.10%) dan Teluk Davao, Philippines (19.42%).

Kajian ini adalah penting untuk memahami penghijrahan penyu dan mengenalpasti populasi persarangan yang menyumbang kepada populasi di kawasan pemakanan di Malaysia. Oleh itu, pengurusan yang lebih baik diperlukan untuk memelihara populasi penyu di kedua-dua kawasan persarangan dan kawasan pemakanan dan juga habitat mereka. Perlindungan penyu di kawasan pemakanan secara berkesan di Malaysia akan dapat meningkatkan populasi persarangan penyu berlokasi beribu-ribu kilometer jauhnya.