STUDIES ON THE POPULATION STRUCTURE OF HAWKSBILL TUTLE (*Eretmochelys imbricata*) FROM INDONESIA USING MITOCHONDRIAL DNA (mtDNA) CONTROL REGION SEQUENCES

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2008

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By

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PENGAKUAN DAN PENGESAHAN LAPORAN
PROJEK PENYELIDIKAN I DAN II

Adalah ini diakui dan disahkan bahawa laporan penyelidikan bertajuk:

Studies on the Population Structure of Hawksbill Turtle (*Eretmochelys imbricata*) From Indonesia using Mitochondrial DNA (mtDNA) Control Region Sequences

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Suffian Bin Muzahar

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LIST OF ABBREVIATIONS

bp	Base pair
DNA	Deoxyribonucleic Acid
$MgCl_2$	Magnesium Chloride
ml	Milliliter
mm	Millimiter
mM	Millimolar
mtDNA	Mitochondrial DNA
nm	Nanometer
°C	Degree celcius
PCR	Polymerase Chain Reaction
STIP	Sabah Turtle Island Park
µl	Microliter
V	Volt

ABSTRACT

This is a collaboration of University Malaysia Terengganu (UMT) with South East Asian Fisheries Development Center (SEAFDEC). Genetic diversity of hawksbill turtle (*Eretmochelys imbricata,* Linnaeus, 1970) population from Kimar, Belitung, Indonesia was analyzed using mitochondrial DNA (mtDNA) control region sequences. All samples were amplified using Polymerase Chain Reaction (PCR) method and were electrophoresed using agarose gel. The banding patterns of the amplified products were then visualized using UV light and purified using PCR purification kit before sending all the samples for sequencing. The sequenced data were analyzed using CHROMAS 2.33, ESEE3, Arlequin 3.11 and MEGA 3.0. Other samples from previous study done (Joseph, 2006) were also analyzed along with this study. Pairwise F_{ST} tests were conducted to obtain the population structure. Besides that, neighbour-joining tree of Kimura 2-parameter was also constructed to express the phylogenetic relationship between population. Extra haplotypes from the Caribbean based on the study by Bass *et al.* (1996) were obtained from Genbank to be rooted to the tree for comparison. Haplotype diversity (h) of the Kimar population was 0.60 and nucleotide diversity of 0.0096. This suggests that there is still hope to conserve the hawksbill turtles in Kimar despite of reported 88% population decline. Pairwise tests showed that nesting population from Kimar, Indonesia was genetically distinct compare to other nesting populations from Malaysia. This result was also supported by Neighbour-joining tree of Kimura 2-parameter.

KAJIAN STRUKTUR POPULASI PENYU KARAH (*Eretmochelys imbricata*) DARI KIMAR, INDONESIA MENGGUNAKAN KAEDAH KAWASAN KAWALAN URUTAN DNA MITOKONDRIA (MTDNA)

ABSTRAK

Kajian ini merupakan hasil kerjasama bersama Pusat Perkembangan Perikanan Asia Tenggara (SEAFDEC). Kepelbagaian genetik populasi penyu karah (*Eretmochelys imbricata,* Linnaeus, 1970) dari Kimar, Belitung, Indonesia telah dikaji menggunakan kawasan kawalan urutan DNA mitokondria (mtDNA). Sampel – sampel DNA diamplifikasi menggunakan teknik "Polymerase Chain Reaction" (PCR) dan seterusnya dielektroforesiskan menggunakan gel Agarose. Corak jalur yang terhasil dari produk amplifikasi kemudiannya dilihat menggunakan cahaya sinar UV dan dicuci dengan kit cucian PCR sebelum dihantar untuk disusun. Data yang telah disusun seterusnya dianalisis menggunakan pelbagai jenis aplikasi. Sampel – sampel dari kajian terdahulu (Joseph, 2006) juga digunakan sebagai perbandingan. Ujian "Pairwise F_{ST}" dijalankan untuk melihat struktur populasi penyu karah. Selain itu "neighbour-joining tree" juga dibina berdasarkan parameter Kimura-2 untuk menunjukkan hubungan philogeni di antara populasi. Haplotip tambahan dari Caribbean berdasarkan kajian oleh Bass *et al.* (1996) juga diambil dari Genbank untuk digunakan sebagai asas kepada perbandingan populasi tersebut. Kepelbagaian haplotip (h) untuk populasi dari Kimar adalah 0.06 dan kepelbagaian nukleotid adalah 0.0096. Ini menunjukkan bahawa masih terdapat harapan untuk menyelamatkan populasi tersebut biarpun terdapat penurunan populasi sebanyak 88% dilaporkan. Ujian "Pairwise F_{ST}" menunjukkan populasi dari Kimar, Indonesia adalah berbeza dari segi genetik berbanding populasi dari Malaysia.