STUDY ON GENETIC VARIABILITY OF LOKAN (*Polymesoda expansa*) BY USING RAPD-PCR TECHNIQUE

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Lihat sebelah

STUDY ON GENETIC VARIABILITY OF LOKAN (*Polymesoda expansa*) BY USING RAPD-PCR TECHNIQUE

By

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PROJEK PENYELIDIKAN I DAN II

Adalah ini diakui dan disahkan bahawa laporan penyelidikan bertajuk: Study on genetic variability of Lokan (*Polymesoda expansa*) by using RAPD-PCR technique oleh Anitha Sivanathan, no. matrik: UK 6734 telah diperiksa dan semua pembetulan yang disarankan telah dilakukan. Laporan ini dikemukakan kepada Jabatan Sains Biologi sebagai memenuhi sebahagian daripada keperluan memperolehi Ijazah Sarjana Muda Sains (Sains Biologi), Fakulti Sains dan Teknologi, Kolej Universiti Sains dan Teknologi Malaysia.

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bp	base pair
C	Cytosine
DNA	Deoxyribonucleic Acid
dNTP	2'-deoxynucleoside-5'-triphosphate(s)
G	Guanine
NTSYS-pc	Numerical Taxonomy and Multivariate Analysis System-personal computer
OD	Optical Density
PCR	Polymerase Chain Reaction
RAPD	Random Amplified Polymorphic DNA
RFLP	Restriction Fragment Length Polymorphism
SAHN	Sequential, Agglomerative, Hierarchical and Nested Clustering
TBE	Tris-Borate-EDTA buffer
TE	10 mM Tris-Cl, 1 mM EDTA
UPGMA	Unweighted Paired-Group Method of Arithmetic
VDS	Video Documentation System
w/v	weight/volume

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ABSTRACT

Genetic variability of the mangrove clam's *Polymesoda expansa* was detected using Random Amplified Polymorphic DNA-Polymerase Chain Reaction (RAPD-PCR) technique. The clams were collected from Pulau Semut and Pulau Dua populations of Setiu Wetland, Terengganu. The aims of this study were to assess the degree of polymorphism and establish the genetic database on the genetic variability of *P. expansa.* The genomic DNA was successfully extracted using the Promega Wizard™ Genomic DNA Purification Kit. Three primers were chosen from 1st BASE (OPA-01 to OPA-10); OPA-03, OPA-04 and OPA-09 based on the number and intensity of the fragments produced and used for amplification and yielded a total of 79 RAPD fragments with 63 polymorphic fragments (79.75%) with the size ranging from 200 to 2000 bp from combination of both populations. The highest level of polymorphisms were detected in samples from Pulau Dua population (81.40%) and followed by Pulau Semut population (77.78%). The dendrogram constructed from combination of both populations revealed two main clusters of *P. expansa* population. The effectiveness of RAPD analysis for the study of genetic variability in clam's *P. expansa* was demonstrated and this approach very useful for identification and phylogenetic study.

KAJIAN KEPELBAGAIAN GENETIK LOKAN (*Polymesoda expansa*) DENGAN MENGGUNAKAN TEKNIK RAPD-PCR

ABSTRAK

Kepelbagaian genetik Lokan bakau, *Polymesoda expansa* dikesan dengan menggunakan teknik polimorfisme DNA rawak teramplifikasi-tindakbalas berantai polimerase (RAPD-PCR). Lokan dikumpul dari populasi-populasi Pulau Semut dan Pulau Dua di Setiu Wetland, Terengganu. Tujuan kajian ini dijalankan adalah untuk menentukan darjah polimorfik dan menubuhkan pangkalan data kepelbagaian genetik bagi *P. expansa*. Genomik DNA dieksrak dengan Promega Wizard™ Genomic DNA Purification Kit. Tiga pencetus telah dipilih dari 1st BASE (OPA-01 hingga OPA-10); OPA-03, OPA-04 dan OPA-09 berdasarkan nombor dan intensiti fragmen yang terbentuk dan digunakan untuk amplifikasi dan menghasilkan sejumlah 79 jalur segmen RAPD dengan 63 jalur polimorfik (79.75%) yang berjulat antara 200 hingga 2000 bp daripada gabungan kedua-dua populasi. Paras polimorfik yang tinggi dikesan daripada sampel dari Pulau Dua populasi (81.40%) dan diikuti oleh Pulau Semut populasi (77.78%). Dendrogram daripada gabungan kedua-dua populasi menghasilkan dua kluster utama populasi *P. expansa*. Keberkesanan RAPD analisis untuk kajian kepelbagaian genetik bagi lokan *P. expans*a telah tercapai dan ini sangat berguna untuk kajian indentiti dan filogenetik.