

STUDY ON SEMI-FABRICATION OF *Guccinina* sp.
USING RADD-ROD TECHNIQUE

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Study on genetic variability of saccostrea sp. using RAPD-PCR
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**STUDY ON GENETIC VARIABILITY OF *Saccostrea* sp. USING RAPD – PCR
TECHNIQUE**

By

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Research Report submitted in partial fulfillment of
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Adalah ini diakui dan disahkan bahawa laporan penyelidikan bertajuk: STUDY ON GENETIC VARIABILITY OF *Saccostrea* sp. USING RAPD – PCR TECHNIQUE oleh MOHD. SYAHRILHIZRIAN BIN ZAINAL No. Matrik UK 6534 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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LIST OF ABBREVIATIONS

%	Percentage
°C	Degree Celsius
1X	One Time
A	Adenosine
bp	Base pair
C	Cytosine
cm	Centimeter
dH ₂ O	Distilled water
DNA	Deoxyribonucleic acid
dNTP mix	Deoxyribonucleotides mixture
EDTA	Ethylenediaminetetraacetic acid
g	Gram
G	Guanocine
M	Molarity
μg	Microgram
μL	Microlitre
μM	Micromolar
mg	Miligram
mL	Mililitre

mM	Milimolar
min	Minutes
ng	Nanogram
OD	Optical density
PCR	Polymerase Chain Reaction
Pmole	Picomole
Ppt	Part per trillion
RAPD	Random Amplified Polymorphic DNA
rpm	Rotation per minute
sec	Seconds
T	Thymine
TBE	Tris-borate-EDTA buffer
TE	10mM Tris Cl, 1 mM EDTA
Tris-HCL	Tris [Hydroxymethyl] aminomethane hydrochloride
UV	Ultra violet
V	Volt
VDS	Video Documentation System
v/v	volume/volume
w/v	weight/volume

ABSTRACT

The genetic variability and relationship among individuals between populations of oysters (*Saccostrea* sp.) from Setiu Wetland, Terengganu Darul Iman were examined using the random amplified polymorphic DNA (RAPD) technique. The genomic DNA was extracted from the oysters tissues using Kit Wizard™ Genomic DNA Purification (Promega). The results produced by the machine produced clear RAPD banding pattern. Twenty oligonucleotide primers were screened and three primers (OPA 15, OPA 19 and OPA 20) were selected to amplify DNA from twelve samples of *Saccostrea* sp. from Pulau Che Him and Pulau Semut, Setiu Wetland, Terengganu Darul Iman. A total of 80 RAPD fragments (RAPDs) with 64 polymorphic fragments (80%) with size ranging from 350 – 3000 bp were scored from the population. The highest level of polymorphisms were detected from Pulau Che Him (82.1 %) followed by Pulau Semut (78.1 %). Genetic distance for both populations ranges from 0.222 to 0.504.

KAJIAN MENGENAI KEPELBAGAIAN GENETIK *Saccostrea* sp. DENGAN MENGGUNAKAN TEKNIK RAPD- PCR

ABSTRAK

Kepelbagaian dan perhubungan genetik individu – individu di antara populasi tiram (*Saccostrea* sp.) dari Setiu Wetland, Terengganu, telah dikaji dengan menggunakan kaedah , Amplifikasi Rawak DNA Polimorfik (RAPD). Genomik DNA telah diekstrak daripada tisu dengan menggunakan Kit Wizard™ Genomic DNA Purification (Promega). Hasil keputusan yang diperolehi daripada mesin menghasilkan jalur – jalur RAPD yang jelas. Dua puluh pencetus telah diuji dan tiga daripada pencetus tersebut (OPA 15, OPA 19 dan OPA 20) telah dipilih untuk mengamplifikasi DNA daripada dua belas sampel yang dipilih daripada Pulau Che Him dan Pulau Semut, Setiu Wetland, Terengganu Darul Iman. Sejumlah 80 jalur RAPD dan 64 jalur RAPD yang polimorfik (80%) yang bersaiz diantara 350 – 3000 bp telah dihasilkan dan dikenalpasti. Tahap polimorfik yang tertinggi dikenalpasti daripada Pulau Che Him (82.1 %) dan diikuti sampel daripada Pulau Semut (78.1 %). Paras jarak perbezaan genetik antara kedua – dua populasi adalah daripada 0.222 sehingga 0.504.