STUDY ON GENETIC VARIABILITY OF OYSTER (*Crassostrea iredalei*, FAUSTINO) IN PENINSULAR MALAYSIA USING RAPD-PCR TECHNIQUE

WAN BAYANI BINTI WAN OMAR

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Chairperson : **Associate Professor Sayed Mohd Zain S. Hasan, Ph.D.**

Member : **Associate Professor Mariana Nor Shamsudin, Ph.D.**
: **Noraznawati Ismail**

Faculty : **Agrotechnology and Food Science**

The random amplified polymorphic DNA (RAPD) technique was used to examine the genetic variability and relationship among individuals within and between populations of oysters (*Crassostrea iredalei)* from Terengganu, Kelantan, Perak and Kedah. The result of optimization of polymerase chain reaction (PCR) machine (Hybaid PCR Express, UK) showed that the best concentration of genomic DNA, magnesium chloride, dNTP-mixture, Fermentas Taq DNA Polymerase and primer for *C. iredalei* RAPD study were 50 ng, 3.0 mM, 0.4 mM, 2 U/µl and 0.4 µM (10 picomoles) respectively. The machine produced clear RAPD banding patterns with an optimal annealing temperature of 36°C for 45 cycles. The genomic DNA was extracted from the oysters tissues by using phenol chloroform method. Twenty oligonucleotide primers (Kit A, Operon Technologies, Inc. Alameda, California) were screened and four primers were selected to amplify DNA from 80 samples of *C. iredalei* from the four populations. A total of 159 RAPD fragments (RAPDs) with 122 polymorphic fragments (76.73%) with the size ranging from 250 to 2000 base pairs (bp) were scored from the population. The highest level of

polymorphisms were detected in samples from Terengganu (84.10%) followed by Kelantan (78.13%), Perak (73.17%) and Kedah (71.43%). Genetic distance level between populations varied from 0.56 to 0.65. The dendrogram constructed from the data of RAPD banding patterns revealed two main clusters of *C. iredalei* population in Peninsular Malaysia. The first cluster consists of Terengganu and Kelantan populations and the second cluster consists of Perak and Kedah populations.