BASE POPULATION STRUCTURE STUDIES FOR *MACROBRACHIUM ROSENBERGII* USING MICROSATELLITE MARKERS.

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ABSTRACT

Giant freshwater prawn farming is startlingly increasing in Malaysia, yet little is known about the patterns of genetic diversity of its domesticated and wild stocks. Making use of populations with different gene resources is a way to increase genetic diversity of *Macrobrachium rosenbergii* in Malaysia.

Availability of microsatellite markers (‘western’ form) which are highly polymorphic enables the divergence study of this species to be conducted for genetic improvement. This project successfully identified potential base populations for a genetic improvement program. Mean observed heterozygosity across four populations was in the range of 0.55 to 0.62 while the mean expected heterozygosity ranged from 0.85 to 0.87. Mean number of alleles was found to be the highest in the Kg Acheh population at 15.40. The highest genetic distance was found between Kampung Acheh and Sg Perak populations with a value of 1.29 with an Pairwise F_{ST} value of 0.15. Population Teluk Kumbar and Sg Perak showed a high genetic identity with a value of 0.57 and a low Pairwise F_{ST} value of 0.09. The Kg Acheh and Sg Perak populations were the most divergent among the other populations and are the best pair to be crossed.

For a successful genetic improvement program, genetic relatedness between parents from different locations is crucial. Many farm operators are mixing different populations for the sake of genetic diversity without having a proper genetics data. The number of different populations does not confirm the accumulation of variant alleles where genetic bottleneck could happen without proper relatedness data.

ABSTRAK

Penternakan udang galah secara komersial telah meningkat secara mendadak di Malaysia, namun corak kepelbagaian genetik spesies ternakan dan liar tidak banyak diketahui dengan sepenuhnya. Pengaplikasian populasi dengan pelbagai sumber bahan baka merupakan salah satu cara untuk meningkatkan kepelbagaian genetik *Macrobrachium rosenbergii* di Malaysia.

Mikrosatelit tersedia yang diekstrak daripada struktur *M. rosenbergii* ‘western’ and ‘eastern’ dengan kadar polimorfik yang tinggi memungkinkan kajian kepelbagain spesis ini untuk penambahbaikkan genetik. Projek ini telah mengenalpasti populasi yang digunakan sebagai populasi asas untuk program penambahbaikkan genetik. Purata heterozigositi yang diperhatikan sekitar 10 lokus terletak dalam linkungan 0.41563 kepada 0.56250, manakala, purata heterozigositi yang dijangkakan adalah diantara 0.76166 to 0.85149. Populasi Kampung Acheh memberikan purata bilangan alel yang tertinggi iaitu 15.40. Perbezaan genetik yang tertinggi dijumpai di kalangan individu-individu dalam populasi Kampung Acheh dan Sg Perak dengan nilai 1.2944 serta nilai tertinggi ‘Pairwise F_{ST}’ adalah 0.14635. Selain daripada itu, populasi Teluk Kumbar dan Sg Perak menunjukkan nilai persamaan genetik yang tertinggi, 0.5727 dan nilai ‘Pairwise F_{ST}’ yang rendah pada 0.09217. Populasi Kg Acheh dan Sg Perak merupakan pasangan yang paling berbeza dari segi genetik dan boleh digunakan dalam pembiakan silang.

Perhubungan genetik di antara pasangan udang galah yang terlibat dalam pengeraman telur untuk membentuk kepelbagaian genetik merupakan perkara mustahak yang perlu diberi keutamaan. Ramai pihak mencampur-adukkan udang galah demi membentuk kepelbagaian genetik.

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µg	microgram
µl	microlitre
1X	one times
bp	basepair
dATP	deoxyadenosine triphosphate
dTTP	deoxythymidine trop[hosphate
dGTP	deoxyguanosine triphosphate
dCTP	deoxycytidine triphosphate
ddH_2O	double distilled water
DNA	deoxyribonucleic acid
EDTA	ethylenediamine tetraacetic acid
M	molar
Mg/ml	milligram per milliliter
$MgCl_2$	Magnesium Chloride
mM	millimolar
OD	optimal density
PCR	polymerase chain reaction
TBE	tris-borate-EDTA buffer
UV	ultraviolet
mya	million years ago
rRNA	ribosomal ribonucleic acid
mtDNA	mitochondrial DNA
H_o	observed heterozygosity
H_e	expected heterozygosity
n_a	observed number of alleles
n_e	effective number of alleles
Fis	Inbreeding coefficient
A_n	mean number of alleles
St. Dev	standard deviation
HWE	Hardy-Weinberg Equilibrium
IHHNV	Infectious Hypodermal and Hematopoeitic Necrosis Virus
PL	post larvae