Genetic Variation in Selected Thai *M. rosenbergii* Crossbreds Reared in Specific Environments[9]

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Introduction

AAGRDI has developed a domesticated and genetically improved stock of *Macrobrachium rosenbergii* for two generations. A wild stock has also been domesticated at the AAGRDI hatchery for one generation. Meanwhile, domesticated stocks from private hatcheries were also developed. Another improved stock from basically the two stocks of AAGRDI (genetically improved and the wild), together with the domesticated stock from a good private hatchery was used as base population for the selective breeding program. The improved stock therefore was developed to have a higher genetic diversity. This study is a continuation of Sodsuk *et al.* (2005)' s earlier work on the assessment of genetic diversity in crossbreds tested in different farm environments.

The objectives of this present study are: (1) to apply polymorphic allozyme markers in the evaluation of specific crossbreds identified earlier as ideal for rearing in specific environments (2) to assess/infer the genetic potential (based on genetic variability and performance trait data) and quality of the selected stocks chosen to be reared in the appropriate environment.

This study had hoped to cover a genetic assessment of selected parental stocks for each environment as listed below:

Environment	Male x Female
Uttaradit	FARM x AAGRDI
Buriram	AAGRDI x FARM
Chumphon	FARM x AAGRDI

However this report includes data mainly from the Buriram selective breeding trials.

Materials and Methods

Pleopods from about 40-60 individuals of parental and progeny stocks were sampled. Pleopods from each individual were cut and placed in separate microtubes. All pleopod samples in microtubes were preserved for further molecular analysis of allozyme markers. All preserved samples were electrophoretically analysed at 19-25 allozyme loci following a procedure already established by AAGRDI. All allozyme data from the laboratory analyses were collected and calculated as per locus averages of heterozygosities (H) and number of alleles (NoA) for genetic variation evaluation. The work was done using a software for population genetics studies (BIOSYS Release 1.7). Genetic variation, expressed as per locus averages of heterozygosities and number of alleles of the nine crosses were compared using the software SYSTAT (Wilkinson *et al.*, 1992).

Results and Discussion

The data for the Uttaradit and Chumphon have not yet been completely obtained due to unpredictable and uncontrollable effect of seasonal changes on the broodstock from these two sites. Thus far, only the data from the Buriram stocks have been completely analysed. These stocks include the AAGRDI and FARM parental stocks and their progeny (♀FARM x ♂AAGRDI) stock. Genetic variation data of the three Buriram stocks (AAGRDI, FARM and ♀FARM x ♂AAGRDI), analysed as observed heterozygosities (H) and number of alleles (A) at 21 allozyme loci are summarized in Table 1. The results from the present study show moderately higher observed heterozygosities and similar number of alleles compared to that obtained from an earlier

study by Sodsuk *et al.* (2005) also on three Buriram stocks (Table 2). The genetic variation data of the three Buriram stocks based on both studies confirm that the three stocks are not significantly different (p>0.05) from each other. Moreover, the present data also show genetic variability values close to those of natural stocks (Sodsuk and Sodsuk, 1998) (Table 3). This suggests that the ♀FARM x ♂AAGRDI progeny stock produced in Buriram is suitable and has the genetic potential for further use at the Buriram test site.

Table 1. **Observed heterozygosities (H) and number of alleles (A) of the three Buriram stocks (AAGRDI, FARM and ♀FARM x ♂AAGRDI) analysed at 21 allozyme loci (present study)**

Allozyme locus/ci	Heterozygosities (H)			Number of alleles (A)		
	AAGRDI	FARM	♀FARM x ♂AAGRDI	AAGRDI	FARM	♀FARM x ♂AAGRDI
1. AAT-1	0	0	0	1	1	1
2. AAT-2	0	0	0	1	1	1
3. ACP	0.333	0	0.083	2	1	2
4. AK	0.100	0.200	0	2	2	1
5. ALAT	0	0	0	1	1	1
6. EST	0.100	0.111	0	2	2	1
7. ESD-1	0	0	0	1	1	1
8. ESD-2	0	0	0	1	1	1
9. GPI	0	0	0	1	1	1
10. MPI	0.100	0	0.063	2	1	2
11. PGDH	0.100	0	0.125	2	1	3
12. XDH	0.100	0	0.063	2	1	2
13. IDHP	0.100	0.100	0.188	2	2	3
14. G3PDH-1	0.100	0.111	0.188	2	2	3
15. G3PDH-2	0	0.222	0.143	1	2	2
16. G6PDH	0.375	0.200	0.188	2	2	2
17. HK	0.100	0	0.125	2	1	2
18. MDH-1	0.100	0	0.150	2	1	2
19. MDH-2	0.100	0.100	0.375	2	2	2
20. LDH	0	0	0	1	1	1
21. PGM	0	0	0.125	1	1	2
Average (±SE)	**0.081 (±0.023)**	**0.050 (±0.017)**	**0.087 (±0.022)**	**1.57 (±0.11)**	**1.33 (±0.11)**	**1.71 (±0.16)**

Note : Values in parentheses are standard errors (±SE)

Table 2. Observed heterozygosities (H) and number of alleles (A) of three Buriram stocks (AAGRDI, FARM and ♂AAGRDI x ♀FARM) analysed at 19-25 allozyme loci (Sodsuk *et al.*, 2005/2006)

Allozyme locus/ci	Heterozygosities (H)			Number of alleles (A)		
	AAGRDI	FARM	♀FARM x ♂AAGRDI	AAGRDI	FARM	♀FARM x ♂AAGRDI
1. *AAT-1*	0	0	0	1	1	1
2. *AAT-2*	0.333	0.034	0.100	2	2	2
3. *ACP*	0	0	0	1	1	1
4. *AK*	0	0	0	1	1	1
5. *ALAT*	0.037	0	-	2	1	-
6. *EST*	0	0	0	1	1	1
7. *ESD*	0.080	0	0	2	2	1
8. *FBALD-1*	0	0	-	1	1	-
9. *FBALD-2*	0	0	-	1	1	-
10. *G3PDH-1*	0	0	0.05	1	1	2
11. *G3PDH-2*	0	0	-	1	1	-
12. *G6PDH*	0	0.037	0	1	2	1
13. *GPI*	0.100	0.067	0	2	3	1
14. *HK-1*	0	0	0	1	1	1
15. *HK-2*	0	0	0	1	1	1
16. *IDHP*	0.250	0.069	0	3	2	1
17. *LDH*	0	0	0	1	1	1
18. *MDH-1*	0	0	0	1	1	1
19. *MDH-2*	0.367	0.233	0	2	2	1
20. *MEP*	0.100	0.333	-	2	3	-
21. *MPI*	0	0.033	0	1	2	1
22. *PGDH*	0	0	0	1	1	1
23. *PGM*	0.100	0.103	0.083	2	2	2
24. *XDH*	0	0	0	1	1	1
25. *ODH*	0	0	-	1	1	-
Average (±SE)	0.043 (±0.018)	0.036 (±0.016)	0.012 (±0.007)	1.36 (±0.11)	1.44 (±0.13)	1.16 (±0.09)

Note : Values in parentheses are standard errors (±SE)

Table 3. Genetic variation data, calculated for two parameters as per locus averages of heterozygosity (H) and number of alleles (A), in the three stocks from two studies (present and the Sodsuk *et al.* 2005/2006 study), in contrast with the data of natural stocks by Sodsuk and Sodsuk (1998)

Study	Parameter	Genetic variation			
		Per locus averages of various stocks			
		AAGRDI	FARM	♂AAGRDI x ♀FARM	Natural
Present study	H	0.081 (±0.023)[A]	0.050 (±0.017)[A]	0.087 (±0.022)[A]	-
	NoA	1.57 (±0.11)[B]	1.33 (±0.11)[B]	1.71 (±0.16)[B]	-
Sodsuk *et al.* (2005/2006)	H	0.043 (±0.018)[A]	0.036 (±0.016)[A]	0.012 (±0.007)[A]	-
	NoA	1.36 (±0.11)[B]	1.44 (±0.13)[B]	1.16 (±0.09)[B]	-
Sodsuk and Sodsuk (1998)	H	-	-	-	0.027-0.036
	NoA	-	-	-	1.29-1.33

Note : Values in parentheses are standard errors (±SE)

The same alphabetic superscription in the same line indicating non-significant differences (p>0.05)

Although the data of Uttaradit and Chumphon stocks have yet to be obtained, this study could attain the two objectives with the available data on the Buriram stocks.

The unaccomplished parts of the study are due mainly to the prevailing uncontrollable weather conditions. These, however, could be pursued and accomplished in 2007.

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