GENOTYPE BY ENVIRONMENTAL INTERACTION FOR LIVE WEIGHT BETWEEN TWO PRODUCTION ENVIRONMENTS IN THE GIFT STRAIN (NILE TILAPIA, *OREOCHROMIS NILOTICUS*)

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SUMMARY

A genotype by environmental interaction study was conducted using the live weight data collected from three discrete spawning seasons of Genetically Improved Farmed Tilapia selective breeding program in Malaysia. Two production environments were used to grow-out the progeny, namely, cages and ponds. The analysis was carried by using animal mixed model and treating live weight in cages and in ponds as two different traits to determine the genetic correlation, which was used to quantify the genotype by environmental interaction for these two environments. The heritabilities estimated from the animal variance component were 0.34±0.061 and 0.40±0.067, for cages and ponds, respectively. The genetic correlation between live weight in cages and ponds was 0.75±0.091. Responses to selection were separately estimated for live weight in these two environments, and were 18.6% in cages and 15.3% in ponds after two generations of selection. Based on these results, we conclude that selection response was being achieved in both environments and that, despite the presence of a non-unity genetic correlation between live weight in cages and ponds, there was no significant evidence for genotype by environmental interaction for these two main aquaculture systems in Malaysia.

INTRODUCTION

The two main culture systems in Malaysia for tilapia farming are cage and pond (Hanafi and Chua 2008). Due to the rich natural resources in Malaysia, cage culture system is considered more economic in terms of land used and management compared to the pond system (Hanafi and Chua 2008). In Asia most of the selective breeding programs for Nile tilapia were conducted under intensive pond culture system, including the GIFT (Genetically Improved Farmed Tilapia) breeding program by the WorldFish Center in Malaysia (Eknath *et al.* 1993; Bolivar 1998; Eknath and Acosta 1998; Tayamen 2004; Ponzoni *et al.* 2005). This situation raises the issue of genotype by environment interaction (GxE) between pond and cage culture systems. It is important to know if genetic gain is being realised even if fish are grown in an environment that is different from that in which selection is taking place.

In the context of animal breeding, GxE describes the situation where different genotypes do not respond in the same way to different environments, so that the genetic and environmental effects are not additive. In order to examine the issue of genotype by environment interaction, we treated live weight at harvest in each culture environment as two different traits (Falconer 1952). The objectives of this study were to estimate the genetic parameters for live weight expressed in cage and pond environments, to evaluate the response to selection in both environments, and to determine the genotype by environment interaction between cage and pond culture systems.

MATERIALS AND METHODS

The data used in this study consisted of 10,065 fish with phenotype from three discrete generations (spawning season 2002 to 2004) of the GIFT selective breeding program in Malaysia. The breeding program had two lines: a selection line (selected for high breeding value for live weight) and a control line (selected on average breeding values for live weight). There were a

total of 177 sires and 244 dams involved in both lines. The details of base population, mating scheme and selection method are described in Ponzoni *et al.* (2005).

For the GxE study, the individually tagged fingerlings from each full-sib family were separated into two groups of equal size and grown out either in cages or earthen ponds. For the cage environment, the fingerlings were reared at cages of size 3m x 3m, with initial stocking density of 55 fish per square meter of water surface. For the pond environment, earthen ponds of 0.1 hectare were used and the initial stocking density was three to four fish per meter square. At both environments, the fish were fed twice a day with commercial dry pellet feed that contained 32 percent of protein.

The fish in both environments were harvested after approximately 120 days of grow-out. At harvest, the fish were recorded for live weight (grams), standard length (cm), width (cm), depth (cm) and sex. Based on the spawning date and harvesting date, the age (in days) of each fish was computed. Only the results corresponding to the GxE for live weight are presented in this paper.

The phenotypic and genetic parameters for live weight (square root transformed) were estimated using ASReml (Gilmour *et al.* 2002). In order to quantify the GxE between cage and pond environments, the genetic correlation was estimated by treating live weight in cage and pond as two different traits in a bivariate analysis. A mixed model was fitted to the data, with spawning season, line and sex as fixed effects, and animal and dam (solely accounting for the maternal and common environmental effect on the progeny, without a genetic structure) were fitted as random effects. Age was fitted as a covariate with the spline function available in ASReml.

The selection responses for both environments were calculated based on the average estimated breeding values by line and by generation, and it was expressed as a percentage of the least square mean on control line.

RESULTS AND DISCUSSION

The number of observations, simple means, minimum and maximum, standard deviation and coefficient of variation values for body weight and age at harvest in the cage and pond environments are presented in Table 1. The mean weight for the fish grown in ponds was greater than that for fish grown in cages.

Table 1. Descriptive statistics for live weight (g) and age (days) at harvest in cage and pond

Variable	Environment	N	Mean	Minimum	Maximum	Standard deviation	Coefficient of variation (%)
Live weight	Cage	5086	146.5	13	591	77.8	53
	Pond	4979	223.0	7	682	104.4	47
Age at harvest	Cage	5086	240	151	289	27.5	11
	Pond	4979	230	125	302	32.7	14

Table 2. Analysis of variance of live weight ($g^{0.5}$) **in cage and pond: Tests of fixed effects using PROC MIXED (SAS Institute Inc. 1997)**

Effect	Cage		Pond	
	F value	Prob. > F	F value	Prob. > F
Spawning season (SS)	65.22	< 0.0001	56.21	< 0.0001
Line (L)	13.93	0.0002	24.52	< 0.0001
Sex (S)	498.16	< 0.0001	440.65	< 0.0001
SS x S x L	3.91	0.0015	20.84	< 0.0001
Age at harvest	72.41	< 0.0001	409.67	< 0.0001
Residual variance	4.0277		3.4832	

Table 2 shows the statistical significance for the fixed effects and the linear covariate (age at harvest) for cage and pond, respectively. All main effects and the covariate were statistically significant ($P<0.05$).

The REML estimates of variance components, heritability, maternal common environmental effect and genetic correlation are shown in Table 3. The heritability estimates for cage and pond were slightly higher compared to other reported estimates in tilapia (0.24 by Gall and Bakar 1999; 0.20 by Gall and Bakar 2002; 0.34 by Ponzoni *et al.* 2005; 0.32 by Maluwa *et al.* 2006). The estimated maternal common environmental effects for cage and pond are in agreement with the estimates in literature (0.15 by Ponzoni *et al.* 2005; 0.21 by Rutten *et al.* 2005)

Table 3. Phenotypic and genetic parameters, and selection response for live weight (LW, $g^{0.5}$) in cage and pond

Parameter	REML estimate	
	LW in Cage	LW in Pond
Additive genetic variance (σ^2_A)	2.406	2.804
Maternal common environmental variance ($\sigma^2_D = \sigma_{M\_Ec}{}^2$)	1.282	1.666
Phenotypic variance (σ^2_P)	6.995	6.951
Heritability [h^2(s.e.)]	0.34 (0.06)	0.40 (0.07)
Maternal common environmental component [c^2(s.e.)]	0.18 (0.03)	0.24 (0.03)
Genetic correlation [r_g(s.e.)]	0.75 (0.09)	

The magnitude of the genetic correlation between cage and pond estimates the degree to which the same genes are involved in the expression of weight in these two environments. The genetic correlation estimated was 0.75±0.09 (Table 3). This result indicates that if selection were conducted in one environment (say, cages), but progeny were to perform in another environment (say, ponds), assuming equal heritability in both environments, selection in cages would capture 75 percent of the gain that could be achieved if it were carried out in ponds.

The estimates of genetic gain were encouraging, 18.6% gain in cages and 15.3% gain in ponds, after two rounds of selection. The response was large enough to indicate that genetic change was being achieved in both the cage and pond environments, and in the intended direction. Furthermore, the gains in cages and ponds, resulting from the bivariate analysis used in this study, were in good agreement with those resulting from a univariate analysis (treating the expression in both environments as a single trait) earlier reported by Ponzoni *et al.* (2005).

CONCLUSIONS

Falconer's (1952) approach of treating the expression of the trait in different environments as if they were different traits is useful in understanding and drawing practical conclusions from GxE studies. In the present case, the genetic correlation between live weigh in cages and in ponds indicates that if selection were conducted in one of the environments, 75 percent of the gain achieved in that environment would be captured in the other environment. The 95 percent confident interval for the estimated genetic correlation ranged from 0.66 to 0.84, which indicated moderate to low GxE. Coupled with the high heritability and selection responses obtained, we conclude that there was no evidence of GxE between cage and pond culture environments for tilapia farming in Malaysia that was large enough to warrant separate breeding programs. However, having or not a single breeding program should not be solely based on the genetic correlation, but also the economic importance of each culture environment and on the feasibility of implanting an additional program under the specific circumstances in question.

REFERENCES

Bolivar, R.B. (1998) PhD thesis, Dalhousie University, Canada.

Eknath, A.E. and Acosta, B.O. (1998) "Genetic improvement of farmed tilapias (GIFT) project: Final report, March 1988 to December 1997". International Center for Living Aquatic Resources Management, Makati City, Philippines.

Eknath, A.E., Tayamen, M.M., Palada-de Vera, M.S., Danting, J.C., Reyes, R.A., Dionisio, E.E., Capili, J.B., Bolivar, H.L., Abella, T.A., Circa, A.V., Bentsen, H.B., Gjerde, B., Gjedrem, T. and Pullin R.S.V. (1993) *Aquaculture* **111**:171

Falconer, D.S. (1952) *Amer. Nat.* **86**:293

Gall, G.A.E. and Bakar, Y. (1999) *Aquaculture* **173**:197

Gall, G.A.E. and Bakar, Y. (2002) *Aquaculture* **212**:93

Gilmour, A.R., Gogel, B.J., Cullis, B.R., Welham, S.J. and Thompson, R. (2002) ASReml User Guide Release 1.0, VSN International Ltd., Hemel Hempstead, HP1 1ES, UK.

Hanafi, H.H. and Chua, H.P. (2008) http://www.fri.gov.my/pppat/culture_protoc.htm [Consulted on December 4th, 2008].

Maluwa, A.O., Gjerde, B. and Ponzoni, R.W. (2006) *Aquaculture* **259**:47

Ponzoni, R.W., Hamzah, A., Tan, S. and Kamaruzzaman, N. (2005) *Aquaculture* **247**:203

Rutten, M.J.M., Komen, H. and Bovenhuis, H. (2005) *Aquaculture* **246**:101

SAS Institute Inc. (1997) "SAS/STAT® Software: Changes and Enhancements through Release 6.12", Cary, NC, USA.

Tayamen, M.M. (2004) *Proc. of 6th ISTA*, Manila, Philippines.