Genetic parameters for early growth traits in *Lates calcarifer* (Bloch)

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Abstract

Genetic parameters for early growth traits such as body length at 21st, 50th and 80th day and body weight at 50th and 80th day were estimated using the data from a sample of 497 progeny of 4 sets or pair matings in *Lates calcarifer*. The progeny were produced by the induction of natural spawning using reproductive hormone LHRH-a. The heritability (h^2), genetic and phenotypic correlations were estimated using single pair matings model of analysis of variance and covariance. The coefficient of variation ranged from 21.57 to 37.95 for body length and 64.98 to 89.41 for body weight. The h^2 estimates ranged from 0.15 to 0.96 and 0.50 to 0.77 for body length and body weight respectively. The pooled data estimates of h^2 are higher than the single environment data estimates and the h^2 increased along with the age. The genetic and phenotypic correlations between body length and weight were found to be high, positive and significant in 50 day and 80 day old fingerlings of *L. calcarifer*.

Growth rate of fish is very crucial for achieving better production in a culture system. Growth as such is influenced by a large number of genes and environmental factors to which the animal is exposed (Dickerson, 1954). So to analyse the growth of an animal it is important to partition the phenotypic expression of growth into genetic, environmental and other interaction components by understanding the sources of variation and covariation for the growth traits. Heritability (h^2) and genetic correlation (r_G) are the two important genetic parameters which are essential in designing breeding programmes. Early growth is also of great importance because of the maternal and common environmental effects affecting the size groups during the fry stage.

The Asian seabass, *Lates calcarifer*, is a commercially important brackishwater fish and a priority species for diversification in farming. There is a growing demand for seabass seed because of its great prospects in culture. As growth rate is of economic importance in aquatic species and the body weight shows a very high phenotypic variation in all species of fish and shell fish (Gjedrem, 1983); this study was undertaken to estimate genetic parameters of the early growth traits. There are no reports available with regard to seabass genetic parameters. Application of quantitative genetics in aquaculture as such is in a dormant stage in India. The h^2 estimates of 0.25-0.77 for 60 day body weight (Busack and Gall, 1983), 0.16-0.86 for 56 day body weight (Busack, 1983) in mosquito fish (*Gambusia affinis*) and 0.10-0.38 for 1 year weight in rainbow trout (Linder *et al*, 1983) have been reported. The genetic correlations between body

length and body weight were reported to be close to unity in salmonids (Refstie, 1980) and in Rohu (Gjerde and Reddy, 1996). This study was taken up to fill up the gap in the knowledge of the genetic parameters for early growth traits in *L. calcarifer*.

Material and methods

The captive broodstock of *Lates calcarifer* developed at the CIBA field experimental station, Muttukadu, was used as the source of the breeders in the present study. The stock consisted of a heterogenous group of randomly collected wild specimens from nearby coastal areas during the period 1995-96. They are being maintained in the 100 ton net water capacity RCC tanks with 80% water exchange daily and are fed with frozen trash fish @ 5% of the body weight.

Female fishes with ova diameter of above 450μ and oozing males were selected for induced breeding experiments. The induction of spawning was done by LHRH-a hormone treatment @ 60-70 μg/kg body weight for females and @ 30-35 μg/kg body weight for males. Spawning occured naturally after 32-36 hrs of hormonal treatment and the fertilised eggs were transfered to 500 l incubation tanks for hatching (Kailasam *et al.*, 1998). After hatching, the larvae were maintained initially on rotifers for the first 10 days and *Artemia* nauplii and rotifers upto 15 days. From 15th day onwards minced meat was given along with *Artemia* nauplii and slowly *Artemia* feeding was discontinued within one month. Thereafter the fry were fed exclusively on boiled/minced trash fish meat.

The data for genetic analysis in the present study was generated by measuring the early growth traits *i.e.* body length and body weights of 497 progeny sampled from 4 sets/pair matings namely LC1, LC2, LC3 and LC4. The progeny of all these four matings were reared in the hatchery (environment 1) and the measurements on growth traits were taken at 21st day, 50th day and 80th day intervals. Measurements on growth traits at 50th day and 80th day were also obtained from a sample of progeny of LC1 and LC3 sets, which were reared in farmers hatcheries/ponds (environment 2).

Statilstical analysis was carried out to estimate h^2 of early growth traits, genetic and phenotypic correlations between growth traits by using single pair matings model of analysis of variance and covariance (Becker, 1984) and their significance was tested (Snedecor and Cochran, 1967). As the seabass induced breeding technique, in the present study, involved natural spawning by hormonal injection, the full sib and half sib families could not be produced to get the estimates of h^2 based on size and dam components seperately.

Results and discussion

The results of analysis of variance and the h^2 estimates along with phenotypic parameters for body length at 21st day, 50th day and 80th day (21 dL, 50 dL and 80dL) and body weight at 50th day and 80th day (50dW and 80dW) are presented in the tables 1 and 2. The analysis of variance and the h^2 estimates for 50d and 80d growth traits were estimated both from pooled data over two environments

Table 1. *Results of ANOVA, variance components and percent of variance in the analysis for different early growth parameters* of *L. calcarifer*

Source	D. F	Length				Weight			
		ms	F	var. co mp	% vari-ance	ms	F	var. comp	% vari-ance
21 day old									
Between matings	3	11.62	3.4*	0.28	7.59				
Between progeny	115	3.41		3.41	92.41				
50 day old									
Pooled									
Between matings	3	1596.25	39.76**	31.90	44.28	5.12	18.28**	0.10	26.31
Between progeny	201	40.14		40.14	55.72	0.28		0.28	73.69
ENV. 1									
Between matings	3	317.54	6.75**	8.61	15.48	4.47	11.46**	0.13	25.0
Between progeny	126	47.01		47.01	84.51	0.39		0.39	75.0
80 day old									
Pooled									
Between matings	3	13680.39	37.74**	334.20	47.97	1018.82	25.99**	24.58	38.54
Between progeny	169	362.50		362.50	52.03	39.19		39.19	61.46
ENV.2									
Between matings	3	4222.20	13.62**	141.49	31.33	119.50	14.84**	4.03	33.36
Between progeny	106	310.05		310.05	68.67	8.05		8.05	66.64

* significant at 5% level   ** significant at 1% level.

and also from environment 1 alone. The analysis of variance showed that the between matings component of variance is significant denoting highly significant differences in length and weight between the progeny of different matings (Table 1). High coefficient of variation (cv) for different traits, especially for body weights at different ages (Table 2), indicated the magnitude of phenotypic variation in these traits which could be exploited through selection for additive genetic effects. Gjedrem (1983) reported high coefficients of variation for juvenile body weight (26-78%) and juvenile body length (8-23%) for different species of fish such as rainbow trout, Atlantic salmon, common carp,

channel catfish and Tilapia. In the present study the cv for body weight ranged from 64.98 to 89.41% and for body length from 21.57 to 37.95%.

The h^2 estimates for body length and weight at different ages of early growth, in the present study, ranged from 0.15-0.96 and 0.50 - 0.77 respectively (Table 2). Gjedrem (1983) in his review reported h^2 estimates ranging from 0.06-0.24 for body length and 0.04 - 0.42 for body weight of juveniles in different fish species. In India, the h^2 estimates for body weight of Rohu were reported to be between 0.15 + 0.09 to 0.63 + 0.29 (Gjerde and Reddy, 1996). Gjerde (1986) concluded that the h^2 for body weight of juveniles is low (around

0.1) but for adult body weight it is in the medium range (0.2-0.4) in Atlantic salmon and Rainbow trout. The higher h^2 estimates obtained for body length and weight suggest a significant effect of additive genetic factors on growth traits, inspite of high environmental influence. The pooled data h^2 estimates are higher compared to single environemtal data estimates (T able 2), which can be explained by the fact that when the data is pooled from different environments, the genotype-environment interaction would inflate the h^2 estimate by entering the numerator component of the formula (Becker, 1984). This would have been the reason for the low h^2 estimates from single environment (env'1) data compared to pooled data estimates. The h^2 estimates showed an increase with the age in the present study. This observation was also made for growth traits in Atlantic salmon and Rainbow

trout (Gjerde, 1986; Su et al., 1996). However, in the present study only the early growth traits are taken and this observation need to be further checked with slaughter weights.

As the data is from single pair mating system and as the relationship among the breeders is not known because of their origin from wild; it is not possible to seperate additive genetic effects (V_A) from other common fullsib effects such as dominance effects (V_D), maternal effects (V_M), interation between additive and dominance effects. The between matings variance component (σ_S^2) in this estimation is equivalent to covariance of fullsibs (Becker, 1984) which estimates $1/2 \, V_A$, $1/4 \, V_D$, $1/4 \, V_{AA}$, $1/8 \, V_{AD}$, $1/16 \, V_{AAA}$ and V_M Hence the present estimates of h^2 set the upper limit of h^2 and more close to being genotypic heritability or heritability in a broad sense, which is given as V_G/V_P (Falconer,

Table 2. *Heritability (h^2) and Phenotypic parameters for different growth traits in L. calcarifer.*

Traits	Mean	C. V.	h^2	S. E	No. of matings or sets	Average No. of progeny sampled per set
Length (mm)						
1. 21 dL	6.82	30.43	0.15	0.16	4	28.99
2. 50 dL (pooled)	34.32	24.11	0.88	0.41	4	48.78
3. 50 dL (env. 1)	35.82	21.57	0.31	0.25	4	31.41
4. 80 dL (pooled)	66.73	37.95	0.96	0.42	4	39.85
5. 80 dL (env.1)	58.03	22.42	0.63	0.38	4	27.12
Weight (g)						
1. 50 dW (pooled)	0.77	81.80	0.53	0.33	4	48.78
2. 50 dW (env.1)	0.83	89.41	0.50	0.34	4	31.41
3. 80 dW (pooled)	6.11	89.05	0.77	0.40	4	39.85
4. 80 dW (env.1)	3.27	64.98	0.67	0.46	4	27.12

1989). The maternal effects entering the analysis should not be large as the off-springs are not nurtured and the most likely source of these variations could be egg size, juvenile size, clutch size etc., (Austin *et al.*, 1997). In seabass, another important environmental factor affecting the early growth traits is cannibalism (Parazo *et al.*, 1991) which determines the survival percentage and thereby effecting the stocking density and growth of the individuals. This constitutes the major environmentally induced differences in growth as also reported by Lutz and Wolters (1986) in cray fish. The standard errors of h^2 estimates are high (Table 2), probably because of less no. of sets/pair matings and less no. of progeny sampled per mating and hence the interpretation of the h^2 estimates should be done with caution.

The estimates of genetic and phenotypic correlation between length and weight are given in the Table 3. The correlations are high and significant. The high genetic correlations (r_G) between these two traits at 50d and 80d old indicate the existence of pleiotropy among additive genes *i. e.* the same set of genes determining both these traits (Falconer, 1989). The high and positive genetic correlations between body length and weight were also reported earlier in salmonids (Refstie, 1980), in Arctic char (Nilsson, 1992) and

in Rohu (Gjerde and Reddy, 1996). The estimation of genetic correlations is essential before planning a breeding programme; as this would give an indication about the possi-ble correlated responses in different traits when selection is done on a particular trait.

From the present study it can be concluded that the significant heritability estimates and high phenotypic variation for early growth traits in *L. calcarifer* indicate that it would be possible to improve growth rate by selection for body weight at an early age. In a selective breeding programme, by early selection it is possible to decrease the cost of maintaining broodstock over generations and reduces the generation interval component in estimating selection responses. However, the effectiveness of this approach depends on the relationship between growth rates at specific periods and their relationship to body weight at marketing age and also on the genetic variation and h^2 for body weight at the age of selection. Further, if selection for body weight at an early age is carried out as pre selection, it could reduce the accuracy of ranking of breeding candidates at target age and thereby reducing the expected response to the final selection.

Table 3. *Genetic and Phenotypic correlations between body length and body weight in L. calcarifer.*

	50 Day old	80 day old
1. Genetic correlation (r_G)	0.93**	0.89**
2. Phenotypic correlation (r_p)	0.88**	0.98**

** significant at 1% level.

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