



Genetic variation among full-sib families and the effect of non-genetic factors on growth traits at harvest in *Clarias magur* (Hamilton, 1822)

Roshan Rameez^a, Shrinivas Jahageerdar^{a,*}, Thongam Ibemcha Chanu^b, Jayashankar Jayaraman^c, Rama Bangera^d

^a ICAR-CIFE, Mumbai, India

^b ICAR-CIFE, Kakinada, Andhra Pradesh, India

^c ICAR-CMFRI, Kochi, India

^d AKVAFORSK GENETICS, Sunndalsøra, Norway

ARTICLE INFO

Keywords:

Heritability
Genetic correlation
Non-genetic factors
Magur
Growth traits

ABSTRACT

Magur (*Clarias magur*) is an Indian catfish species with a good potential for aquaculture. The expansion of magur aquaculture is hindered because of low reproductive and survival rates. Furthermore, males need to be sacrificed to collect milt for artificial fertilization. At present, magur seed production mainly depends on the wild-caught juveniles and to a smaller extent, from broodfish whose genetic potential is unknown. The availability of high-quality seeds in a sustainable way can be ensured through the selective breeding program for magur. The knowledge of factors influencing growth traits and their genetic parameters is a pre-requisite for implementing a genetic selection program. The present study aimed to quantify the performance of *C. magur* reared in a two-year class and estimate their heritabilities at stocking and harvest and also to estimate the genetic and phenotypic correlations among them. The growth traits such as Body Weight (BW), Total Length (TL), Body Depth (BD), Head Width (HW), and Average Daily Gain (ADG) were recorded from 1413 animals belonging to 78 fullsib families produced by adopting single pair mating design, after one year of pond culture (traits at harvest). Genetic parameters were also estimated for body weight (BW₀) and total length (TL₀) measured from 2328 fish from 78 fullsib families at the time of stocking. Magur attained an average BW of 135 g and 24.5 cm TL after one year culture period. The heritabilities of BW, TL, and ADG were 0.44 ± 0.07 , 0.32 ± 0.06 , and 0.42 ± 0.07 , respectively and may be biased upwardly due to the single pair mating design. Genetic correlations between harvest traits were all positive and varied in magnitude between traits (0.74 to 0.99). The results obtained from the current study indicate the presence of genetic variation in magur population for growth traits and selection based on genetic merit can produce improvement in these traits.

1. Introduction

Clarias magur (Hamilton 1822) is an Indian catfish popularly known as magur and is distributed across India, Nepal, Bhutan, Bangladesh, and other countries (Ng and Kottelat, 2008). Magur has the potential to be a candidate species for freshwater aquaculture in India. Magur fetches a better market price due to its high consumer preference, good taste, and nutritional profile (Sinha et al., 2014). The lack of good quality seed in sufficient quantity is the primary constraint for the commercial aquaculture of magur. Presently, magur culture is based on the broodfish/seeds collected from natural breeding grounds, which eventually put pressure on natural stocks. The genetic improvement

program will help to supply the desired number of high-quality broodfish to establish commercial hatcheries, and is an important long-term and sustainable way to increase the magur aquaculture in India.

Selective breeding offers an opportunity for continuous genetic gain for traits under selection, which is permanent. The benefits of accumulated genetic gain across the generations in a nucleus can be multiplied and expressed in a large number of individuals in the production sector (Farias et al., 2017). The selective breeding programs in aquaculture species have been usually aimed at enhancing growth performance and reducing rearing cycle duration, which leads to more efficient production and higher benefits (Gjedrem and Baranski, 2009). Body size traits are usually synonym with growth traits and are

* Corresponding author.

E-mail addresses: rameez.fgbpa503@cife.edu.in (R. Rameez), jahageerdar@cife.edu.in (S. Jahageerdar), thongam@cife.edu.in (T.I. Chanu), jjssankar@gmail.com (J. Jayaraman), rmbangera@gmail.com (R. Bangera).

<https://doi.org/10.1016/j.aqrep.2020.100411>

Received 9 October 2019; Received in revised form 9 April 2020; Accepted 15 June 2020

Available online 17 July 2020

2352-5134/ © 2020 The Authors. Published by Elsevier B.V. This is an open access article under the CC BY license (<http://creativecommons.org/licenses/by/4.0/>).

important economic traits in aquaculture species. Since growth cannot be subjected to direct evaluation, body weight, and/or length at a fixed age is used as a criterion for evaluating the performance of a species used for aquaculture. Knowledge of non-genetic factors affecting the growth traits and their genetic parameters are prerequisites for starting any efficient selective breeding program (Gjedrem and Robinson, 2014). The information on non-genetic factors affecting the economically important traits helps to optimize the aquaculture practice for maximum growth. The extent of genetic improvement in successive generations is proportional to the existing genetic variation within the population. Heritability estimates for body weight at harvest and other economically important traits in several aquaculture species have been well documented (Gjedrem, 1983; Gjedrem and Robinson, 2014). In magur, limited information is available on non-genetic factors affecting growth traits and their genetic parameters. Jousy et al. (2018) reported 145.9 and 137.6 as average body weight at one-year pond age in magur under mono and polyculture systems respectively; they also reported a high heritability for body weight. In the present study, the effect of non-genetic factors on growth traits of magur produced across two batches at stocking and harvest were quantified, and the genetic parameters of these traits were estimated.

2. Materials and methods

2.1. Ethics statement

The present experiment was part of a research project approved by the Institute Research Council (IRC) of ICAR- Central Institute of Fisheries Education (Deemed University), Mumbai, India (Project code: CIFE-2012/7). The experimental procedures followed were in compliance with the guidelines of IRC.

2.2. Broodfish selection and induced breeding

The stocks used in the present study were collected from the natural waters of Andhra Pradesh (AP), Assam, and the West Bengal states of India during May-June 2013. These fish were maintained at Fresh Water Fish Farm (FWFF), ICAR-Central Institute of Fisheries Education, Balabhadrapuram-Kakinada, AP, India, to form a base population to initiate a genetic improvement program of magur. The collected fish weighed approximately 50–100 g and were transported by air and road to the FWFF. After initial quarantine for two weeks and observing for disease and deformity, the fish were tagged with Passive Integrated Transponder (PIT) tag. The sex of the collected magur was identified, and males and females were segregated and reared separately in 200m² earthen ponds for a minimum period of one year before they were used for breeding. These fish were fed twice a day with commercially available high protein content feed (minimum 30 %) at the rate of 3% of the body weight twice a day. The matured broodfish were collected for induced breeding, after the complete draining of the pond and further selected based on morphological characteristics. The fish with about 150 g body weight were selected as broodfish, and besides, females were selected if they were oozing eggs upon applying gentle pressure on their abdomen. The breeding in magur coincides with the monsoon period, and in the present study, the breeding period spanned from July to September.

A single dose of commercially available hormone Ovatide®, a synthetic analog of Gonadotropin-Releasing Hormone (GnRH), was used as the inducing agent. An intramuscular injection of Ovatide® at the rate of 0.1 and 0.2 mL per 100 g body weight was administered to males and females to induce breeding. After the injection, male and female fish were kept in separate FRP tanks till harvesting the gametes. The eggs were collected in dry plastic trays by stripping the females after 17 h of Ovatide® injection. In males, the milt cannot be obtained through stripping. Therefore the milt was collected directly from the testis; to collect the testis, the males were anesthetized in a plastic tub containing

5 L water and clove oil @ 2 ppm and then the abdomen was incised and testis were removed, and after that the fish were sacrificed by immersing in the water containing clove oil in high concentration. The sperm suspension was prepared by macerating the testis in normal saline solution (0.9 % NaCl) in a mortar with pestle. The sperm remain under the dormant condition in normal saline solution. Fertilization was induced by mixing the eggs collected in the plastic tray with sperm suspension and mixed thoroughly along with water, which activates the sperm. The fertilized eggs were washed twice with water before being released into hatching units.

2.3. Production of families

2.3.1. Mating design

A single pair mating design, where one male is mated with one female, was used to produce full-sib families. A total of 162 full-sib families were bred in two batches, and a separate set of broodfish were used in each of the batches. In batch-1 (2014), 98 full-sib families were bred, and in batch-2 (2015), 64 full-sib families were bred. Out of 162 families, only 100 full-sibs families could successfully hatch, and 78 full-sib families survived till tagging (39 each from batch-1 and batch-2).

2.3.2. Larval rearing

The fertilized eggs from different full-sib families were incubated separately in an indoor hatching unit (1.25m × 0.45m × 0.2 m) facilitated with flow-through systems for water exchange. The fertilized eggs were transferred into the hatching tubs by attaching them on to the roots of water hyacinth (*Eichhornia*). Hatching of the fertilized eggs took place after 24–27 hours of fertilization, and the hatchlings got detached by themselves from the *Eichhornia* roots. The unfertilized eggs, which are opaque-white in color, were still attached to the roots of *Eichhornia*, which made it easy to clean the hatching tubs. Larvae after the complete yolk sac absorption (3 days post-hatch) were fed *ad libitum* with live feed (Zooplankton dominated with *Moina*). After ten days of hatching, early fry of 10–12 mm size were shifted to a rectangular outdoor rearing unit of dimensions 3m × 0.6m X 0.45 m. During outdoor rearing, the early fry were fed three times a day that is in the morning, noon, and evening with zooplankton, which was collected from the specially prepared earthen pond. Further, the zooplankton was supplemented with crumbled starter feed (< 250 microns) containing 35 % protein at the rate of 3% body weight, followed by artemia flakes at the rate of 5% body weight, preferably in evening hours. The juveniles (full-sib families) were reared in the outdoor rearing units for 30 days and after that were transferred to separate cement tanks of dimensions (4 m Lx 1.5 m W x 1 m H) at a stocking density of maximum of 200 no per tank for family-wise rearing until they attained a tagging size of average 10–15 g.

2.3.3. Tagging and communal rearing

From each full-sib family, 30 fish were randomly selected for tagging with PIT tags. A total of 2328 fish were PIT tagged from 78 full-sib families. Body weight and total length were recorded at the time of tagging. After tagging, the fish were kept under observation for 48 h to check for mortality due to tagging stress. No significant mortality was observed within this period, and if any mortality was observed, additional fish were tagged to maintain the family size. After two days of tagging, the fish were released into earthen ponds of size 200 m² for communal rearing under both monoculture and polyculture systems. The monoculture was practiced only in the batch-1, where families were divided for monoculture and polyculture systems. In the monoculture system, 300 magur fish were stocked per pond. In the polyculture system, 200 magur fish were stocked per pond along with 100 rohu fingerlings.

2.4. Recording growth traits

Before releasing the tagged fish into the ponds for communal rearing, measurements were taken on the initial body weight (BW₀) and total length (TL₀) and were considered as traits at stocking. After releasing into the pond magur fish were cultured for 365 days under standard aquaculture conditions, and at the end of 365 days, all ponds were completely drained, and the fish were handpicked for recording the traits at harvest. As magur has the habit of burrowing into the bottom mud, the complete harvest is only possible through hand-picking. Body weight (BW), total length (TL), body depth (BD), and head width (HW) were recorded on 1413 fish across 78 fullsib families. The average number of offspring per family (k-value) was 17.4 ranging from 4 to 35. Additionally, Average daily gain was estimated as follows

$$ADG = (BW - BW_0)/D$$

Where BW is the body weight at harvest, BW₀ is the body weight at stocking, and D is 365 days, which is the culture period.

2.5. Statistical analysis

2.5.1. Preliminary analysis

All traits were checked for normality (Kolmogorov-Smirnov test) using *Proc Univariate* in SAS® version 9.3. No significant deviation from normality was observed. For outlier detection the variables were first converted into standard normal variables using Z-transformation and those records which fall outside 99th quartile were considered as outliers, which were removed before further analysis.

2.5.2. Non-genetic factors

The fish used in the present study were produced in two-year classes. In 2015 there was no success in breeding from West Bengal and Assam stock. This resulted in the majority of the offspring coming from the Andhra Pradesh stock when data from both the year class were combined. In order to normalize the number of offspring per stock, Assam and West Bengal stocks were clubbed as Non-Andhra stock. In the present study the batch (fish born in 2014 were considered as batch-1, and those born in 2015 were considered as batch-2), stock (Andhra and Non-Andhra stock), culture type (mono and poly culture), ponds (5 ponds from batch-1 and a separate set of 6 ponds from batch-2) and sex (F, M, and NA) were considered as non-genetic factors. The ponds were not the same for batch-1 and batch-2 but were in the same farm and same water source was used. The sex of those animals which were found dead before identifying them as female or male were marked NA, thus making three levels under the factor sex (only for traits at stocking viz. M, F, and NA). The least squares means were estimated for different levels of fixed effects, and multiple comparisons were made between different levels of each factor using Tukey Kramer test in *Proc GLM* (Littell et al., 2002).

2.5.3. Estimation of heritability

A univariate analysis was performed to estimate variance components and heritability (h^2) for growth traits at stocking and the harvest using average information residual maximum likelihood (AiReML) algorithm in Wombat (Meyer, 2007). The following mixed models were used for the estimation of variance components and their functions for different traits.

$$y = Xb + Zu + e \tag{1}$$

$$y = Xb + Zu + Wp_o + e \tag{2}$$

(Model 1) Where y is the vector of observations, b is the vector of fixed effects due to overall mean, body weight at stocking (covariate), stock, batch, pond nested within batch and sex, u is the vector of random animal effects, and e is the vector of random residual effects. It was assumed that random effects (u and e) are normally distributed;

$u \sim N(0, A\sigma_a^2)$, where σ_a^2 is the additive genetic variance and A is the additive genetic relationship matrix derived from the pedigree; $e \sim N(0, I\sigma_e^2)$, where σ_e^2 is the residual variance, and I is the identity matrix. The X and Z are the design matrices relating observations to the levels of fixed effects and random effects, respectively.

(Model 2) Model 2 was similar to Model 1 except that the pond effects were treated as random effect in Model 2 to identify any confounding between pond effect and additive genetic effects. It was assumed that the pond effects (p_o) were random and are normally distributed; $p_o \sim N(0, I\sigma_{p_o}^2)$ where $\sigma_{p_o}^2$ is the pond variance and I is the identity matrix. W is the design matrix relating observations to the levels of random effects. All the other terms in the model 2 were same as that from the model 1.

Model 1 was fitted for traits at stocking as well as for the traits at harvest; however, for the traits at stocking, only stock, batch and sex were included as fixed effects. Model 2 was fitted only for the traits at harvest. In model 2, it was assumed that fitting pond as a random effect might help in recovering some of the genetic information if, in case, there is any confounding between pond effect and additive genetic effect. Fixed effects were tested at a level of significance of 0.01, and at the initial stage all possible two way interaction effects between fixed factors were included in the model and only those interaction effects which were found significant were included in the final model for the estimation of variance components. The heritability (h^2) for each trait was calculated as:

$$\text{From Model 1 } h^2 = \frac{\sigma_a^2}{\sigma_a^2 + \sigma_e^2}$$

$$\text{From Model 2 } h^2 = \frac{\sigma_a^2}{\sigma_a^2 + \sigma_{p_o}^2 + \sigma_e^2}$$

Where, σ_a^2 , $\sigma_{p_o}^2$ and σ_e^2 are additive genetic variance, pond variance, and residual variance respectively.

2.5.4. Estimation of genetic and phenotypic correlation

A multivariate animal model corresponding to Model 1 was used to estimate genetic and phenotypic correlations between five traits by using the AiReML algorithm in Wombat. The starting values for the variances and covariances in the multivariate model were obtained from the bivariate analysis of all possible combinations of traits in Wombat.

The genetic correlation (r_g) between two different traits was calculated as:

$$r_g = \frac{\sigma_{a1,a2}}{\sqrt{\sigma_{a1}^2 \times \sigma_{a2}^2}}$$

Where r_g is the correlation coefficient between additive genetic values (predicted breeding values), $\sigma_{a1,a2}$ is the covariance between additive genetic values measured for trait 1 and trait 2, σ_{a1}^2 and σ_{a2}^2 is the additive genetic variance of trait 1 and trait 2.

3. Results

Overall mean, Least Squares (LS) means with standard errors and Coefficient of Variation (CV) for different factors at stocking and harvest are listed in Table 2. On an average, the body weight of fish increased by 108 g from stocking to harvest. At the time of harvest, mean body weight from different ponds ranged from 101 to 156 g (not given in the Table). Mean squares from the analysis of variance, for different traits at stocking and harvest are presented in Tables 3 and 4, respectively.

3.1. Effect of non-genetic factors

The population structure with different factors and number of families per factor are presented in Table 1. Different non-genetic factors

Table 1

Population structure with different factors and number of families per factor. (Batch-1 – 2014 year class, Batch-2 – 2015 year class ; AP – Andhra Pradesh Stock, NAP – Non Andhra Pradesh Stock); N – Number of fish per pond. The bold letters indicate different levels of factors and the numbers indicate the number of families within each level of factor. The numbers in the last two row indicates number of fish per pond at the time of stocking and harvest respectively.

Factors and No. of Families per Factor	Batch 1 – 39					Batch 2 – 39					
	AP Stock – 23					AP Stock - 39					
	NAP Stock - 16										
	Monoculture - 39			Polyculture - 39		Polyculture - 39					
	P 1	P 3	P 4	P 2	P 5	P 6	P 7	P 8	P 9	P 10	P 11
	39	39	39	33	29	13	13	12	13	13	13
N (Stocking)	310	309	309	200	230	183	193	192	126	154	122
N (Harvest)	232	232	236	101	148	101	79	76	53	71	84

considered for harvest traits were initial body weight (covariate), stock, batch, culture-type, pond, and sex, and all these factors were fitted as fixed effects in model-1. The type-III Mean squares and coefficient of determination (R²%) obtained after fitting model-1, along with the level of significance for traits at stocking and harvest are presented in Tables 3 and 4, respectively. There was no significant difference in the mean performance of harvest traits between fish cultured under monoculture and polyculture systems (Table 3). The effect of the batch was not significant for TL at harvest, and the sex effect was not significant for BD at harvest. The body weight at stocking (BW0) had a significant effect on all the traits at harvest. For the traits at stocking, effects such as batch, stock and sex were considered as non-genetic effects. The effect of the batch was significant for BW0 and TL0, whereas the stock effect was non-significant. The average BW0 of males was significantly higher than the average BW0 of females.

There were two levels for the stock, AP stock, and Non-AP stock. On an average the fish from Non-AP stock grew 13.5 g heavier and 0.5 cm longer than the fish from AP stock (Table 2). The average harvest BW and TL of fish from batch-1 was higher than that for the fish from batch-2 by 16.5 g and 1.8 cm respectively. However, ADG and BD were higher in fish from batch-2. In magur, the males tend to grow heavier than the females, and in the present study, on average, males grew 27.31 g heavier than females at harvest (Table 3). Across the two batches, fish were reared in eleven different earthen ponds. The fish from batch-1 were reared in five different ponds, and batch-2 fish were reared in another set of six different ponds. The pond had a profound effect on the traits at harvest. Within batch-1, LS means for harvest BW among five ponds ranged from 135.84–151.5 g, whereas for the six ponds within batch-2 it ranged from 101.4–156.7 g (results not shown in the table).

3.2. Heritability estimates

Heritabilities for the traits at harvest were estimated by adopting

Table 2

Number of observations (N), overall, stock, batch and sex wise least squares means and their standard errors for the traits (BW0 and TL0) at stocking and harvest (BW, TL, BD, HW and ADG).

Effects	N (Stocking)	BW0 (g)	TL0 (cm)	N (Harvest)	BW (g)	TL (cm)	BD (cm)	HW (cm)	ADG (g/day)
Overall	2328	26.11 ± 0.20	14.12 ± 0.05	1413	134.92 ± 0.99	24.49 ± 0.07	2.92 ± 0.02	3.87 ± 0.02	0.28 ± 0.01
CV	2328	36.90	17.1	2328	27.48	10.67	15.28	10.57	28.39
Stock-AP	1763	25.7 ± 0.28 ^a	14.16 ± 0.06 ^a	983	127.15 ± 1.01 ^a	23.97 ± 0.07 ^a	2.88 ± 0.02 ^a	3.82 ± 0.02 ^a	0.28 ± 0.01 ^a
Stock-NAP	565	26.8 ± 0.56 ^a	14.16 ± 0.11 ^a	430	140.61 ± 1.78 ^b	24.43 ± 0.12 ^b	3.05 ± 0.03 ^b	3.92 ± 0.03 ^b	0.3 ± 0.01 ^b
Batch -2014	1358	41.78 ± 0.32 ^a	17.76 ± 0.07 ^a	949	142.14 ± 1.06 ^a	25.09 ± 0.08 ^a	2.93 ± 0.02 ^a	3.89 ± 0.02 ^a	0.27 ± 0.01 ^a
Batch-2015	970	10.72 ± 0.49 ^b	10.56 ± 0.10 ^b	464	125.62 ± 1.76 ^b	23.31 ± 0.12 ^b	2.99 ± 0.03 ^a	3.85 ± 0.03 ^a	0.3 ± 0.01 ^b
Sex-M	654	29.3 ± 0.42 ^a	14.7 ± 0.08 ^a	654	147.54 ± 1.30 ^a	25.2 ± 0.09 ^a	3.03 ± 0.02 ^a	4.04 ± 0.02 ^a	0.32 ± 0.01 ^a
Sex-F	759	23.7 ± 0.44 ^b	13.8 ± 0.08 ^b	759	120.23 ± 1.36 ^b	23.19 ± 0.10 ^b	2.89 ± 0.02 ^b	3.7 ± 0.02 ^b	0.26 ± 0.01 ^b
Sex-NA	915	25.2 ± 0.48 ^b	13.7 ± 0.09 ^b	–	–	–	–	–	–

(p < 0.01) Means bearing the same superscript within the class effect are not significantly different from one another.

Table 3

Mean squares and R² values of model parameters for traits at stocking.

MSS at stocking			
Source	DF	BW0	TL0
Stock	1	291.92	1.59
Batch	1	369846.60*	19356.27*
Sex	2	3888.90*	111.33*
Family	75	1524.03*	75.96*
Error	2248	77.50	2.60
R2 %		79 %	85 %

* (p-value < 0.01).

Table 4

Mean squares and R² values of model parameters for traits at harvest.

MSS at harvest						
Source	DF	BW	TL	BD	HW	ADG
BW0	1	244716.34*	822.23*	18.01*	20.85*	0.29*
Stock	1	21641.19*	23.51*	3.78*	0.86*	0.15*
Batch	1	12137.07*	24.39*	1.09*	2.16*	0.08*
Culture type	1	347.82	2.94	0.09	0.12	0.01
Pond	9	10832.34*	60.04*	8.09*	1.37*	0.08*
Sex	1	69676.30*	505.30*	0.35	15.25*	0.45*
Family	75	2785.61*	11.18*	0.31*	0.28*	0.02*
Error	1323	453.30	2.60	0.09	0.08	0.004
R2 %		69 %	65 %	55 %	57 %	51 %

* (p-value < 0.01).

both Model 1 and 2; the additive genetic variance and residual variance of harvest traits estimated from both Model 1 and 2 were similar. Estimates of heritability along with their standard errors for traits at stocking and harvest, are presented in Table 5. The heritability estimated for BW, TL, and ADG at harvest were high (> 0.3), whereas, a moderate heritability was obtained for TL, BD and HW (Table 5). The

Table 5

Estimates of heritability and their standard errors at stocking (BW0: Body weight, TL0: Total length) and at harvest (BW: Body weight, TL: Total Length, BD: Body depth, HW: Head width, ADG: Average daily gain).

Traits at stocking		Traits at harvest		
Traits	Model 1	Traits	Model 1	Model 2
BW0	0.74 ± 0.08	BW	0.44 ± 0.07	0.34 ± 0.07
		TL	0.32 ± 0.06	0.26 ± 0.06
		BD	0.22 ± 0.04	0.14 ± 0.04
TL0	0.97 ± 0.08	HW	0.27 ± 0.05	0.23 ± 0.05
		ADG	0.42 ± 0.07	0.32 ± 0.07

heritability of the traits at stocking was very high, 0.74(0.08) for BW0 and 0.97(0.08) for TL.

3.3. Genetic and phenotypic correlations

The estimates of genetic and phenotypic correlations with approximate sampling variance obtained from model-1, among all traits at stocking and harvest, are presented in Table 6. The genetic correlations among traits at harvest were positive and high. For traits at harvest, the highest genetic correlation was found between BW and ADG and the lowest between TL and HW. The genetic correlation between BW0 and TL0 was positive and high. All phenotypic correlations between traits at harvest were positive and ranged from moderate (0.30–0.60) to high (> 0.60). The highest phenotypic correlation was observed between BW and TL, whereas the lowest was obtained between TL and BD.

Genetic and phenotypic correlations between traits at stocking and harvest were also estimated and are presented in Table 7. Body weight at stocking was highly genetically correlated with body weight and total length at harvest and was positive. Length at stocking also had a positive but moderate genetic correlation with weight and length at harvest. Likewise, there was a positive and moderate phenotypic correlation between the weight and length at stocking to weight and length at harvest.

4. Discussion

C. magur, an air-breathing catfish, is endemic to India (Khan et al., 2000). Controlled breeding is possible in magur, hence selective breeding can be implemented to enhance the productive and reproductive performance of the species (Jousy et al., 2018). Majority of fish farmers depend on the natural seed of magur for culture wherein they collect seed from the natural breeding grounds, leading to the depletion of natural stocks in many areas. Natural seeds exhibit a wide range of variability in their performance and many times harbor pathogens that are difficult to detect. The potential of genetic selection to improve the economic traits in the desired direction is well established. It ensures the availability of quality seed on demand, optimizes the production efficiency, and most importantly, it reduces the pressure on natural stocks. In the present study, the genetic potential of magur is evaluated to enhance its growth performance by adopting a selective

Table 6

Genetic (above diagonal) and phenotypic (below diagonal) correlations between traits at stocking (BW0: Body weight, TL0: Total length) and among traits at harvest (BW: Body weight, TL: Total Length, BD: Body depth, HW: Head width, ADG: Average daily gain).

Traits at stocking		BW0	TL0				
	BW0	.	0.92 ± 0.01				
	TL0	0.84 ± 0.01	.				
Traits at harvest		BW	TL	BD	HW	ADG	
	BW	.	0.94 ± 0.02	0.93 ± 0.04	0.81 ± 0.06	0.99 ± 0.00	
	TL	0.62 ± 0.05	.	0.77 ± 0.08	0.74 ± 0.08	0.93 ± 0.03	
	BD	0.41 ± 0.04	0.34 ± 0.04	.	0.80 ± 0.08	0.94 ± 0.04	
	HW	0.56 ± 0.04	0.51 ± 0.04	0.38 ± 0.04	.	0.82 ± 0.06	
	ADG	0.76 ± 0.06	0.59 ± 0.05	0.39 ± 0.05	0.53 ± 0.05	.	

Table 7

Genetic and phenotypic correlations between traits at stocking (BW0: Body weight, TL0: Total length) and harvest (BW: Body weight, TL: Total Length).

	Genetic correlations		Phenotypic correlations	
	BW	TL	BW	TL
BW0	0.76 ± 0.06	0.73 ± 0.07	0.61 ± 0.03	0.48 ± 0.04
TL0	0.57 ± 0.09	0.57 ± 0.09	0.53 ± 0.03	0.47 ± 0.04

breeding program.

4.1. Non-genetic factors

The fish used in the present study were from two-year classes (2014 and 2015), represented as batch-1 and batch-2, respectively. In both years, the breeding extended through three months. As a result, the age and body weight of the fish at tagging also varied among batches, which introduced an age factor and variation in the initial body weight at stocking. No prior information was available about the survival rate in magur from spawning to age/size at tagging. The average size at tagging for 2014 batch was 41 g, and for 2015 batch was 10 g. To avoid the loss of families, all the spawns from full-sib families were retained and stocked, which led to a significant difference in the stocking density at the initial stages of larval rearing. Factors like differential fecundity, variation in hatching along with differential mortality across full-sib families also led to the difference in the number of offspring per family and, in turn, the stocking densities at the initial stages of larval rearing. Differential stocking densities resulted in differential growth. The full-sib families with very high stocking density grew slower and full-sib families with low stocking density grew faster. In the present study, it was observed that the heterogeneity in the body weight at stocking influenced the harvest body weight. The analysis of results showed that the BW0 had a significant effect on BW at harvest ($R^2 = 12.5\%$ - the result not shown in the table); hence, the BW0 was used as the covariate in the model for variance component estimation of traits at harvest. The BW0 was preferred as covariate over the age of the fish because there were only 12 levels of age group as compared to 74 levels of BW0, hence the dependency of harvest BW on age was minimal. Also, the difference in age will get translated into the difference in the BW0, it was decided to use BW0 as the covariate. The BW0 as a covariate substantially reduced the error variance and increased the R-square value of the model in the estimation of the Mean sum of squares. Also, the AIC value for the model containing BW0 was much lower (AIC = 12731.7) as compared to the model without BW0 (AIC = 13243.20). The model with the lowest AIC value is considered to give better estimates of variance components (Akaike, 1974). The present study indicates the need to standardize the stocking density of magur during family-wise rearing. Care should be taken to maintain similar stocking density across different families reared in different tanks until they are tagged and stocked for communal rearing.

The genetic selection program for magur was initiated with objectives to develop magur strains suitable for both mono and poly-culture. The fish from batch-1 were reared under both mono and polyculture

(with *Labeo rohita*) conditions. In the present study, it was observed that there was no significant difference in the mean harvest body weight of magur reared in mono or polyculture system, further the inputs from the farmers and considering the low reproductive rate of the species, it was decided to continue genetic selection to develop a strain only for the poly-culture. The non-significant effect of culture type on the harvest body traits is possible because magur is a bottom dweller and competes very little for space with rohu which is a column feeder. Jousy et al. (2018) had reported a significant difference between the body weight of magur in monoculture and polyculture system and they attributed it to the considerable variation in the number of observations between the two culture systems (699 fish under monoculture whereas only 249 fish under poly-culture). In the present study, the number of observations of both culture systems was similar.

The fish from non-AP stock showed higher growth than the fish from AP stock. From Table 3, it is evident that non-AP stock, on an average, has grown 13.46 g heavier than AP stock. It is interesting to note that between two batches, AP stock from batch-1 has grown 20 g heavier than the AP stock from batch-2. The reasons could be differences in the environment across two batches, differences in the genetic makeup of the animals, and also it could be due to the lower weight of the fish at stocking in batch-2, which were solely from Andhra stock. In 2014 when the selective breeding was initiated, there were no reports available about the size and site for PIT tagging in magur. Hence, it was decided to carry-out the experiment to identify the optimum size and appropriate body location for PIT tag insertion in the magur. In half of the batch-1 born magur, the PIT tag was inserted in the muscle, and in another half, it was inserted in the abdominal cavity. To insert the PIT tag in the muscle, the fish need to be large; hence, the tagging was taken up when fish reached an average size of 40 g. The experiment revealed that the magur retained PIT tags inserted in the abdomen reasonably well (over 85 %) and tagging can be done in small size fish also, so all the magur belonging to batch-2 were tagged by inserting the PIT tag in the abdominal cavity when the fish were of about 10–15 g size.

Reports suggest that magur males grow heavier than females (Jousy et al., 2018). In the present population, males were 27 g heavier than females. The difference in the growth performance between males and females could be attributed to physiological differences. It was observed that the pond environment had a significant effect on body weight at harvest. Even though efforts were taken to maintain uniform stocking density across all the ponds, differential mortality altered the uniformity in stocking density over a period. The highest mean weight was observed for the fish from the pond with the lowest stocking density, which was expected. Even though the tagged fish were allocated randomly to the ponds, there existed differences between the mean body weights of fish allocated to ponds from batch-1 and 2. Within batch-1 the mean weight at stocking between 5 ponds ranged from 41.1 ± 0.92 – 42.0 ± 1.00 g, whereas batch-2 mean stocking weights between 6 ponds ranged from 7.0 ± 0.19 – 12.4 ± 0.57 g. Since, the pond was nested within batch, the comparison of ponds had to be made within batches. The pond effect was tested for the traits at stocking to ensure that the fish were randomly allocated to different ponds and it was observed that the pond effect was not significant at the time of stocking. Another important reason for the differences in performance may also be attributed to the differences in pond productivity and other factors that contribute to the pond dynamics, which are hardly under human control.

4.2. Heritability estimates

To initiate the genetic selection program formation of a base population with a broad genetic base is essential. To ensure a large genetic base and considering the availability of resources like the ponds for family rearing and also lack of information/experience in family-wise breeding of magur only full-sibs were produced in batch 1 and 2 by adopting a single pair mating design. Hence, in the present study,

records from only full-sib families were present; as a result, the estimated additive genetic variance is confounded with the variance due to non-additive genetic effects, maternal and common environmental effects (Gjedrem and Baranski, 2010). An animal model was used to fit the data, which is based on the additive genetic relationship matrix, and the random effects of interest are the additive genetic value of individual animals (Kruuk, 2004). Two models were used for the estimation of variance components for traits at harvest. In model-1, only the animal effect was considered as a random, while in model-2, along with animal effect, the pond effect was also considered as a random effect. A note of caution has to be made about the pond effect. In the present study, the ponds used for the rearing of the fish of batch-1 and batch-2 were different and hence were nested within the batch. There was also no link between the families of batch-1 and batch-2, hence there is a possibility that the pond effect may have got confounded with the additive genetic effect, hence it becomes more useful to treat ponds as random when doing so allows some genetic information to be recovered (Legarra et al., 2008). In both, the models the genetic variance and residual variance remained unchanged, which suggests that there is no confounded information between pond effect and additive genetic effect. So from an analysis point of view, the model 1 and 2 may be treated as equivalent.

Heritabilities estimated for traits at stocking were very high, 0.74 ± 0.08 for BW0, and 0.97 ± 0.08 for TL0. Eventually, a decrease in heritability was observed for the same traits at harvest (Table 5). The high heritability estimated close to unity at the time of stocking is due to the presence of common environmental variance. The full-sib families were reared in separate cement tanks till tagging, for a long time, which might have introduced common environmental effects pertaining to full-sibs, increasing between family variance and thereby inflating the heritability of traits at stocking. The homogeneity of the growth rate within family could vary depending on the age of the fish, perhaps the growth rate within family was similar at the early stages of life (resulting in low within family variance and high heritability), but might have varied as the age progressed (resulting in high within family variance and low heritability). There are various reports regarding the presence or absence of common full-sib effects in aquaculture species. In channel catfish, Reagan et al. (1976) reported heritability estimates exceeding unity as they contained large amounts of common environmental variances. The decrease in heritability estimates from stocking to harvest could be attributed to the diminishing of effects common to full-sibs in the later stage of life (El-Ibiary and Joyce, 1978). A very strong effect common to full-sibs for early growth rate but decreasing with time was observed in common carp (Hulata et al., 1976). Reports on other aquaculture species like rainbow trout (Herbinger et al., 1995), European sea bass (*Dicentrarchus labrax*) (De Leon et al., 1998) and black bream (*Acanthopagrus butcheri*) (Doupé and Lymbery, 2005), also support the fact that the effects common to full-sibs occur primarily during the early life stages and tend to dissipate within a few months of growth. Fu et al. (2016) reported non-significant common environment effects on growth traits at 10 and 18 months post-hatching. Ponzoni et al. (2010) and Nguyen et al. (2007, 2010) reported a diminishing common environmental effect in Nile Tilapia with a longer grow-out period. Even though there was a decrease in heritability over time in the present study, it is not sure whether 12 months of communal rearing can completely even out common full-sib effect.

Further studies are required to quantify effects common to full-sibs. Jousy et al. (2018) reported high heritability for the harvest body weight in magur. In the present study, the heritability estimates for harvest BW obtained from both the models were high. Moderate to high heritability for harvest trait is very common in fish and has been reported by many authors for different species (Maluwa et al., 2006; Vandeputte et al., 2008; Nielsen et al., 2010; Marjanovic et al., 2014; He et al., 2015; Li et al., 2018). In the present study, the heritability estimate for body weight was less than that obtained by Jousy et al. (2018). Usually, for the first few generations, high heritability estimates

for body weights are obtained when natural stocks are used to produce families. In the current study, all the traits were recorded after one year of communal rearing in earthen ponds under commercial conditions (poly-culture with rohu). The present estimates may be taken as indicative of the presence of adequate additive genetic variance for the harvest body weight in magur.

Head length and head width are important morphometric traits in catfish because the head weight has a significant contribution (up to 23.6 %, El-Ibiary et al., 1976) towards the weight at harvest. Head length was only recorded for the 2015 batch fish. A moderate heritability was obtained for head length (0.25 ± 0.08). The heritability for head length and percentage head weight in channel catfish was reported to be moderate to high (El-Ibiary and Joyce, 1978). In our study, we could not calculate the percentage head weight to the total body weight because of the limitation to sacrifice fish. The ratio of head length to total length for the 2015 batch ranged from 19.5–30.5%. Body depth can be considered as another measure of growth, and in this study, a moderate heritability for body depth was observed. To the best of our knowledge, reports on heritability estimates of body depth in catfish are not available. There are various reports in Nile tilapia (Fernandes et al., 2015; Rutten et al., 2005) and the GIFT strain of Nile Tilapia (Nogueira de Oliveira et al., 2014; Reis Neto et al., 2014) where a moderate to high heritability for body depth was estimated. The moderate heritability of body depth and head width and head length estimated in our study indicates that the trait may respond to selection and may be incorporated in selection objectives.

4.3. Genetic and phenotypic correlation

Genetic correlations between traits can occur either due to pleiotropy or gametic phase disequilibrium (Lynch and Walsh, 1998). The former mechanism is a result of complex biochemical, developmental, and regulatory pathways by which a single gene influences multiple traits. The latter mechanism is due to the non-random association of alleles of different loci. The phenotypic correlation arises when the expression of the two characters is modified by the same environmental factors operating within individuals (Lynch and Walsh, 1998).

The genetic correlations between the traits at harvest were all positive and varied between traits. A very high positive genetic correlation was observed between body weight and total length at harvest. The very high positive genetic correlation between the body weight and total length indicates that genetic selection on any one character leads to the improvement of the other, so in the future, the measurement can be restricted to any one of the traits. The high correlation between body weight and total length is conceptually trivial in that the traits are structurally related. In this study body weight showed a high genetic correlation with other body measurement traits. Body weight at stocking and harvest are positive and are highly correlated genetically, which means that in magur, possibly the same set of genes control growth at both early and later stages of life. The fish which are heavier at the time of stocking tends to grow heavier at harvest. In the present study only single pair mating design was adopted and the families obtained were exclusively fullsibs which can bias the genetic parameter estimates. Hence, the present genetic parameters may be considered as an indicative only.

5. Conclusion

Magur has good potential to be the candidate species for aquaculture. A genetically superior strain will go a long way to enhance the aquaculture and production of magur. Magur being a catfish is a suitable species for monoculture with high stocking density; however, due to its low reproductive rate, monoculture at present may not be feasible. The non-significant difference in the average harvest bodyweight of magur, cultured both in mono and polyculture, suggests that a genetically improved strain of magur is suitable for both culture systems.

In the present study other than culture type, all other non-genetic factors were found significant. The estimates of heritability for growth traits suggest that selection in an optimally designed breeding program in magur will result in genetic improvement of growth traits at harvest. The positive and high genetic correlations between body measurement traits suggest a correlated response in multiple traits while selecting for any one trait and selection criterion may be restricted to any one trait, preferably the body weight at harvest.

CRedit authorship contribution statement

Roshan Rameez: Investigation, Data curation, Formal analysis, Writing - original draft. **Shrinivas Jahageeradar:** Conceptualization, Methodology, Resources, Formal analysis, Writing - review & editing. **Thongam Ibemcha Chanu:** Project administration, Data curation, Writing - review & editing. **Jayashankar Jayaraman:** Formal analysis, Validation, Writing - review & editing. **Rama Bangera:** Formal analysis, Validation, Writing - review & editing.

Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Acknowledgments

This study formed part of the Ph. D. program of the first author and he acknowledges the financial support received in the form of a senior research fellowship from ICAR-Central Institute of Fisheries Education, Mumbai, India. The authors like to thank the Director, ICAR-CIFE for providing the funds and infrastructure to carry this study. We extend our gratitude to SIC, technical and supporting staff, Balabhadrapuram FWFF, CIFE sub-centre. The authors acknowledge the inputs provided by Dr. Arthur Gilmour and Dr. Dhandapani NAARM-Hyderabad in the interpretation of heritability from model-2.

Appendix A. Supplementary data

Supplementary material related to this article can be found, in the online version, at doi:<https://doi.org/10.1016/j.aqrep.2020.100411>.

References

- Akaike, H., 1974. A new look at the statistical model identification. Selected Papers of Hirotugu Akaike. Springer, New York, NY, pp. 215–222. https://doi.org/10.1007/978-1-4612-1694-0_16.
- de Leon, F.G., Canonne, M., Quillet, E., Bonhomme, F., Chatain, B., 1998. The application of microsatellite markers to breeding programmes in the sea bass, *Dicentrarchus labrax*. *Aquaculture* 159 (3-4), 303–316. [https://doi.org/10.1016/S0044-8486\(97\)00188-9](https://doi.org/10.1016/S0044-8486(97)00188-9).
- Doupé, R.G., Lymbery, A.J., 2005. Additive genetic and other sources of variation in growth traits of juvenile black bream *Acanthopagrus butcheri*. *Aquac. Res.* 36 (7), 621–626. <https://doi.org/10.1111/j.1365-2109.2005.01256.x>.
- El-Ibiary, H.M., Joyce, J.A., 1978. Heritability of body size traits, dressing weight and lipid content in channel catfish. *J. Anim. Sci.* 47 (1), 82–88. <https://doi.org/10.2527/jas1978.47182x>.
- El-Ibiary, H.M., Andrews, J.W., Joyce, J.A., Page, J.W., Deloach, H.L., 1976. Sources of variations in body size traits, dress-out weight, and lipid content and their correlations in channel catfish, *Ictalurus punctatus*. *Trans. Am. Fish. Soc.* 105 (2), 267–272. [https://doi.org/10.1577/1548-8659\(1976\)105<267:SOVIBS>2.0.CO;2](https://doi.org/10.1577/1548-8659(1976)105<267:SOVIBS>2.0.CO;2).
- Farias, T.F., César, J.R.D.O., Silva, L.P.D., 2017. Methods of selection using the quantitative genetics in Aquaculture-A short review. *Insights Aquac Cult Biotechnol* 1, 1.
- Fernandes, A.F.A., de Almeida Silva, M., de Alvarenga, E.R., de Alencar Teixeira, E., da Silva Junior, A.F., de Oliveira Alves, G.F., Turra, E.M., 2015. Morphometric traits as selection criteria for carcass yield and body weight in Nile tilapia (*Oreochromis niloticus* L.) at five ages. *Aquaculture* 446, 303–309. <https://doi.org/10.1016/j.aquaculture.2015.05.009>.
- Fu, J., Shen, Y., Xu, X., Li, J., 2016. Genetic parameter estimates for growth of grass carp, *Ctenopharyngodon idella*, at 10 and 18 months of age. *Aquaculture* 450, 342–348. <https://doi.org/10.1016/j.aquaculture.2015.08.018>.
- Gjedrem, T., 1983. Genetic variation in quantitative traits and selective breeding in fish

- and shellfish. *Aquaculture* 33 (1-4), 51–72. [https://doi.org/10.1016/0044-8486\(83\)90386-1](https://doi.org/10.1016/0044-8486(83)90386-1).
- Gjedrem, T., Baranski, M., 2009. The success of selective breeding in aquaculture. *Selective Breeding in Aquaculture: An Introduction*. Springer, Dordrecht, pp. 13–23.
- Gjedrem, T., Baranski, M., 2010. *Selective Breeding in Aquaculture: an Introduction*, vol. 10 Springer Science & Business Media.
- Gjedrem, T., Robinson, N., 2014. Advances by selective breeding for aquatic species: a review. *Agric. Sci.* 5 (12), 1152. <https://doi.org/10.4236/as.2014.512125>.
- He, J., Gao, H., Xu, P., Yang, R., 2015. Genetic parameters for different growth scales in GIFT strain of Nile tilapia (*Oreochromis niloticus*). *J. Anim. Breed. Genet.* 132 (6), 467–474. <https://doi.org/10.1111/jbg.12139>.
- Herbinger, C.M., Doyle, R.W., Pitman, E.R., Paquet, D., Mesa, K.A., Morris, D.B., et al., 1995. DNA fingerprint based analysis of paternal and maternal effects on offspring growth and survival in communally reared rainbow trout. *Aquaculture* 137 (1-4), 245–256. [https://doi.org/10.1016/0044-8486\(95\)01109-9](https://doi.org/10.1016/0044-8486(95)01109-9).
- Hulata, G., Moav, R., Wohlfarth, G., 1976. The effects of maternal age, relative hatching time and density of stocking on growth rate of fry in the European and Chinese races of the common carp. *J. Fish Biol.* 9 (6), 499–513. <https://doi.org/10.1111/j.1095-8649.1976.tb04699.x>.
- Jousy, N., Jahageerdar, S., Prasad, J.K., Babu, P.G., Krishna, G., 2018. Body weight at harvest and its heritability estimate in *Clarias magur* (Hamilton, 1822) reared under mono and polyculture systems. *Indian J. Fish.* 65 (2), 82–88. <https://doi.org/10.21077/ijf.2018.65.2.72375-10>.
- Khan, M.R., Mollah, M.A., Ahmed, G.U., 2000. Mass production of hybrid magur and its culture potential in Bangladesh. *Aquac. Res.* 31 (5), 467–472. <https://doi.org/10.1046/j.1365-2109.2000.00471.x>.
- Kruuk, L.E., 2004. Estimating genetic parameters in natural populations using the 'animal model'. *Philos. Trans. R. Soc. Lond., B, Biol. Sci.* 359 (1446), 873–890. <https://doi.org/10.1098/rstb.2003.1437>.
- Legarra, A., Robert-Granié, C., Manfredi, E., Elsen, J.M., 2008. Performance of genomic selection in mice. *Genetics* 180 (1), 611–618. <https://doi.org/10.1534/genetics.108.088575>.
- Li, Y., Zhang, B., Lu, S., Tian, Y., Yang, Y., Chen, S., 2018. Genetic parameters estimates for growth performance traits at harvest in Japanese flounder (*Paralichthys olivaceus*). *Aquaculture* 489, 56–61. <https://doi.org/10.1016/j.aquaculture.2018.01.010>.
- Littell, R.C., Stroup, W.W., Freund, R.J., 2002. *SAS for Linear Models*. SAS Institute.
- Lynch, M., Walsh, B., 1998. *Genetics and Analysis of Quantitative Traits*, vol. 1. Sinauer, Sunderland, MA, pp. 535–557.
- Maluwa, A.O., Gjerde, B., Ponzoni, R.W., 2006. Genetic parameters and genotype by environment interaction for body weight of *Oreochromis shiranus*. *Aquaculture* 259 (1-4), 47–55. <https://doi.org/10.1016/j.aquaculture.2006.06.033>.
- Marjanovic, J., Mulder, H.A., Khaw, H.L., Bijma, P., 2014. Genetic parameters for within-family variance of harvest weight in Nile tilapia (*Oreochromis niloticus*). *Proceedings of the 10th World Congress of Genetics Applied to Livestock Production*.
- Meyer, K., 2007. WOMBAT—a tool for mixed model analyses in quantitative genetics by restricted maximum likelihood (REML). *J. Zhejiang Univ. Sci. B* 8 (11), 815–821. <https://doi.org/10.1631/jzus.2007.B0815>.
- Ng, H.H., Kottelat, M., 2008. The identity of *Clarias batrachus* (Linnaeus, 1758), with the designation of a neotype (Teleostei: Clariidae). *Zool. J. Linn. Soc.* 153 (4), 725–732. <https://doi.org/10.1111/j.1096-3642.2008.00391.x>.
- Nguyen, N.H., Khaw, H.L., Ponzoni, R.W., Hamzah, A., Kamaruzzaman, N., 2007. Can sexual dimorphism and body shape be altered in Nile tilapia (*Oreochromis niloticus*) by genetic means? *Aquaculture* 272, S38–S46. <https://doi.org/10.1016/j.aquaculture.2007.08.013>.
- Nguyen, N.H., Ponzoni, R.W., Abu-Bakar, K.R., Hamzah, A., Khaw, H.L., Yee, H.Y., 2010. Correlated response in fillet weight and yield to selection for increased harvest weight in genetically improved farmed tilapia (GIFT strain), *Oreochromis niloticus*. *Aquaculture* 305 (1-4), 1–5. <https://doi.org/10.1016/j.aquaculture.2010.04.007>.
- Nielsen, H.M., Ødegård, J., Olesen, I., Gjerde, B., Ardo, L., Jeney, G., Jeney, Z., 2010. Genetic analysis of common carp (*Cyprinus carpio*) strains: I: genetic parameters and heterosis for growth traits and survival. *Aquaculture* 304 (1-4), 14–21. <https://doi.org/10.1016/j.aquaculture.2010.03.016>.
- Nogueira de Oliveira, S., Lopes de Oliveira, C.A., de Resende, E.K., Lopera Barrero, N.M., Kunita, N.M., Araya Santander, V.F., Pereira Ribeiro, R., 2014. Genetic parameters and morphometric characteristics of two generations from the GIFT strain of the Nile Tilapia. *Semin. Ciênc. Agrárias* 35 (6).
- Ponzoni, R.W., Khaw, H.L., Nguyen, N.H., Hamzah, A., 2010. Inbreeding and effective population size in the Malaysian nucleus of the GIFT strain of Nile tilapia (*Oreochromis niloticus*). *Aquaculture* 302 (1-2), 42–48. <https://doi.org/10.1016/j.aquaculture.2010.02.009>.
- Reagan, R.E., Pardue, G.B., Eisen, E.J., 1976. Predicting selection response for growth of channel catfish. *J. Hered.* 67 (1), 49–53. <https://doi.org/10.1093/oxfordjournals.jhered.a108664>.
- Reis Neto, R.V., Oliveira, C.A.L.D., Ribeiro, R.P., Freitas, R.T.F.D., Allaman, I.B., Oliveira, S.N.D., 2014. Genetic parameters and trends of morphometric traits of GIFT tilapia under selection for weight gain. *Sci. Agric.* 71 (4), 259–265. <https://doi.org/10.1590/0103-9016-2013-0294>.
- Rutten, M.J., Bovenhuis, H., Komen, H., 2005. Genetic parameters for fillet traits and body measurements in Nile tilapia (*Oreochromis niloticus* L.). *Aquaculture* 246 (1-4), 125–132. <https://doi.org/10.1016/j.aquaculture.2005.01.006>.
- Sinha, M., Mahapatra, B.K., Saha, D., Maitra, N.J., 2014. Mass scale seed production of Magur: *Clarias batrachus* at farm level through improvised modifications. *International Journal of Fisheries and Aquatic Studies* 2 (2), 210–214.
- Vandeputte, M., Kocour, M., Mauger, S., Rodina, M., Launay, A., Gela, D., et al., 2008. Genetic variation for growth at one and two summers of age in the common carp (*Cyprinus carpio* L.): heritability estimates and response to selection. *Aquaculture* 277 (1-2), 7–13. <https://doi.org/10.1016/j.aquaculture.2008.02.009>.