GENETIC AND PHENOTYPIC PARAMETERS OF WEIGHT AND LENGTH TRAITS OF THE NILE TILAPIA *OREOCHROMIS NILOTICUS* (LINNAEUS)

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ABSTRACT

Heritability of and genetic correlation of two traits, weight and length,. measured in *Oreochromis niloticus* (1150 records) were estimated using MTDFREML programme. The model included fixed effect of line (four lines: Giza (G), Fouky (F), Mariut (M) and Nag Hamady (N)). Besides, the model included the effects of individual (fish), sire and dam as random effects. The results of h^2 for the two traits were 0.99, 0.87, respectively. The genetic correlation between the two tested traits was 0.91. Ignoring line effect, the same previous model was used to estimate heritability and genetic correlation for the two studied traits for each line. Line N recorded the best estimate of h^2 for weight (1.0), whilst line M had the highest estimate of h^2 for length (0.97). The estimated genetic correlation (0.98) for line M was higher than that of the other experimental lines.

INTRODUCTION

Tilapia is the most important cultured fish species in Egypt, and one of the most important fish in tropical aquaculture that serves as a model organism in many laboratories (Focken *et al.*, 2001). Although serious operations of tilapia domestication probably started in the 1950s' and 1960s with groups working in several countries, tilapia is at an early stage of domestication (Fitzsimmons, 1997; Kocher, 1997). However, during these operations, the genetic resources of tilapia have been poorly managed. Genetic problems associated with loss of pure species through mismanagement of interspecific hybridization were early emphasized and discussed by McAndrew and Majumdar (1983). The latter authors showed that one popular commercial strain contained genes from as many as four species. It is not unusual that tilapias in exotic locations can quickly spread and impact native fish populations.Today, finding of pure

strains of *Oreochromis niloticus* is becoming more difficult even in Egypt which is Nile tilapia homeland.

Prior to breeding programmes, the breeding goals must be defined, which means, specifying selection traits and their importance in the selection process. Elnady *et al.* (2000) suggested that weight and length are the most important traits that should be used in genetic improvement for marketing weights in Nile tilapia. Growth performance was mostly overlooked, as an economically important trait of its own (Yapi-Gnaori, 1996). The most important traits to express the growth performance are the weight and length. Rutten *et al.* (2004) used body weight and length to predict fillet weight in Nile tilapia. They observed significant variations in body measurements among Nile tilapias differing in their origins and highlighted the possibility of predicting fillet yield based on body measurements. Body weight and length are easy to be measured in fish without injuring the offspring and are considered the best indicators for selection index of Nile tilapia (Elnady *et al.*, 2000). Considerable interest exists among animal breeders and geneticists in the estimation of heritability and genetic correlation for the prediction of possible genetic improvement and changes in traits under consideration (Roman and Wilcox, 2000). Estimation of these parameters can be affected by many factors among which the magnitude of the parameters and the algorithm for the estimation.

The objectives of this study were to estimate the heritability of weight and length and to estimate genetic and phenotypic correlations for two traits (weight and length) in four lines of *Oreochromis niloticus* which were obtained from different geographical locations in Egypt.

MATERIAL AND METHODS

The present study was carried out in the Aquaculture Closed Systems project of the Faculty of Agriculture, Ain Shams University, during spring and summer of 2002. Four lines of *O. niloticus*, Giza (G), Mariut (M), Fouky (F), and Nag-Hamady (N) were used in testing genetic parameters of weight and length in the early growing stages. The broodstock of Giza line was obtained from middle East farm, a private fish farm at Giza, Mariut line came from Mariut fish farm which belongs to the General Authority for Fish Resources Development. Fouky line was obtained from Fouky farm, an intensive fish farm near to Cairo, whereas the Nag-Hamady line was acquired from Nag-Hamady hatchery, a governmental fish hatchery that belongs to the General Authority for-

Fish Resources Development. Four breeding groups of the above origins, each of which consisted of ten breeding groups were employed in the present study. Each breeding group consisted of one male and four females and was held in a square fiberglass tank (125 x 125 cm). The experimental tanks were a part of a large recycling water system with a total volume of approximately 270 m^3. Brood fish were regularly checked for eggs or yolk-sac fry every ten days. Fertilized eggs and yolk-sac larvae were robbed from the females' mouth by shack their heads in a small water basin. The collected yolk-sac fry and eggs were incubated in hatching jars for few days. Upon hatching, the newly hatched fry of each progeny group were transferred to square fiberglass tanks (60 x 60 cm) which were joined to the main recycling system. Water quality was kept around the following criteria: temperature, 29 °C; Oxygen, >5 mg/l; pH, 7.2; total ammonia nitrogen, 0.05 mg/l or less; total alkalinity, 200 mg/l as calcium carbonate and total hardness, 250 mg/l as calcium carbonate. The fry were fed *ad libitum* with a commercial diet 40% protein six times a day. Fifty fry from individual groups were weighed (g) and measured (total length, cm) after 30 days. Data consisted of 1150 records belonging to 40 males and 160 females.

Statistical analysis

MTDFREML Algorithm (Boldman *et al.*, 1993) was used to estimate the heritability and covariance components of the two tested traits using the following linear animal model:

$$Y = X\beta + ZU + e,$$

where:

Y	is the vector of observations;
X	is the incidence matrix for fixed effects
β	is the vector of an overall mean and line (4 lines);
Z	is the incidence matrix for random effects
U	is the vector of direct genetic effects of fish;
e	is a vector of random errors normally and independently distributed with zero mean and variance $\sigma_e^2 I$

$$E \begin{bmatrix} Y \\ U \\ e \end{bmatrix} = \begin{pmatrix} xb + Z\,E(u) + E(e) \\ E(u) \\ E(e) \end{pmatrix}$$

$$= \begin{pmatrix} Xb \\ 0 \\ 0 \end{pmatrix}$$

$$V \begin{bmatrix} Y \\ U \\ e \end{bmatrix} = \begin{pmatrix} V & ZG+S & ZS+R \\ G\acute{Z}+\acute{S} & G & S \\ \acute{S}\acute{Z}+\acute{R} & \acute{S} & R \end{pmatrix} \qquad \begin{array}{l} \text{Notice that:} \\ V=ZG\acute{Z}+R+ZS+\acute{S}\acute{Z} \end{array}$$

G   is the additive genetic variance $= A \sigma_a{}^2 I$;

R.   is the residual variance $= I \sigma_e{}^2$;

S   is the covariance between u, e assumed to be Zero

Where A is the relationship matrix.

MTDFREML programme was also used to calculate heritability, covariance components and genetic correlation estimates of the two studied traits using the same previous model for each line, so that the effect of line was ignored from the previous model.

RESULTS AND DISCUSSION

Means, Standard deviations and Coefficients of variations for weight and length traits

Means, standard deviations (SD) and coefficient of variations (CV%) of the two examined traits, weight and length obtained from a MTDFREML programme are presented in Table 1. Coefficients of variations were high for body weight, whilst those of body length were lower. Similar trends were observed for the different experimental lines (Table 2). These results are in agreement with that reported by Gjedrem (1983). The latter author advocated the usefulness of using coefficients of variations for judging the magnitude of variance.

Variance components, Heritabilities and Genetic correlations

Table (3) shows the estimates of genetic, environmental and phenotypic variance and covariance components of the two studied traits (weight and length) that were obtained from the MTDFREML programme. The results of Table 3 indicate that the genetic variances of the two traits are high when compared with that of the phenotypic ones, indicating that initiating a selective breeding programme is justifiable.

The estimates of heritabilities obtained from MTDFREML programme for the two traits, weight and length, were 0.99, 0.87,

respectively (Table 4). Table 5 shows that the genetic correlation between weight and length is 0.91, which is considered high. Heritability estimates close to 1 indicated that the questioned trait could be effectively and quickly changed by selection. Several authors reported that the genetic correlation between body weight and length in salmonids is close to unity (Refstie and Steine, 1978; Gunnes and Gjedrem, 1978 and 1981; Refstie, 1980). These authors recommended the use of traits with high heritability when measuring growth rate, although body weight must be considered as the prime breeding objective. The high heritability estimates for weight and length obtained in the present study possibly provide evidence that these traits are controlled by additive genes (Behrends et al., 1996). Similarly, the results obtained by Elnady et al. (2000) indicated that these two characters were the best indicators for selection index in Nile tilapia.

Table (5) shows the estimates of h^2 and genetic correlation for weight and length traits obtained from MTDFREML programme for each experimental line. Line N gave the highest estimate of h^2 for weight (1.00), whereas line M showed the best estimate of h^2 for length (0.97). The highest estimate of genetic correlation was observed for line M, whilst the worst estimates of h^2 and genetic correlation were estimated for line F.

Working with Nile tilapia, selection should be performed indirectly for standard length and directly for body weight to obtain better improvement in body weight, since these characters have high heritabilities and revealed a high positive genetic correlation between them. Elnady et al. (2000) came to the same conclusion.

Conclusion

The two studied traits (weight and length) are heritable and apparently controlled by additive genes, so they could be improved by selection. Furthermore, the genetic correlation between these two traits is positive and considered high. Improving one of them leads to step up the other trait. This conclusion is applicable for all the experimental lines under the conditions of this study.

REFERENCES

Behrends, L.L.; Kingsley, J.B. and Bulls, M.J. (1996). Cold tolerance in maternal mouthbrooding tilapia: Heritability estimates and correlated growth responses at suboptimal temperatures, In: Pullin, R.S.V.; Lazard, J.; Legendre, M.; Amon Kothias, J.B. and

D. Pauly (eds.) The Third International Symposium on Tilapia in. Aquaculture. ICLARM Conference Proceedings, 1996, pp.257-265.

Boldman, K.G.; Kriese, L.A.; Van Vleck, L.D. and Kachman, S.D. (1993). A manual for use of MTDFREML. A set of programs to obtain estimates of variances and covariances (DRAFT). U.S. Department of Agriculture, Agricultural Research Service, 114 pp.

Elnady, M. A.; Obeida, A. M. and Hassanien, H. A. (2000). Estimates of heritabilities of some morphometric and blood traits in juvenile Nile tilapia from half-sib matings. Bulletin of Faculty of Agriculture, University of Cairo. 51(3): 283-292.

Fitzsimmons, S.K. (1997). Introduction to growth of Tilapia. New York, Northeast regional Agricultural Engineering Service (NRAES),. pp. 129-130.

Focken, U.; Groth, A.; Horstgen- Schwark, and K. Becker, G. (2001). Individual variability of growth, body composition and metabolic rates in clonal Tilapia (Oreochromis niloticus).Energy Metabolism in Animals. Proceedings of the 15th Symposium on Energy Metabolism in Animals, Snekkersten, Denmark, 11-16 September, pp 333-336.

GjeDrem, T. (1983). Genetic Variance in Quantitative Traits and Selective Breeding in Fish and Shellfish. Aquacul. 33:51-72.

Gunnes, K. and Gjedrem, T. (1978). Selection Experiments with Salmon. IV. Growth. of Atlantic salmon during two years in the sea. Aquacul. 15:19-23.

Kocher, T. D. (1997). Introduction to the genetics of tilapia. Procedings From the Fourth International Symposium on Tilapia in Aquaculture. Orlando, Florida, Nov. 9-12, 1997, pp 61-64.

McAndrew, B. J. and Majumdar, K. C. (1983). Tilapia stock identification using electrophoretic markers. Aquacul. 30:249-261.

Refstie , T. and Steine, T.A (1978). Selection experiments with salmon. III. Genetic and environmental sources of variation in length and weight of Atlantic salmon in the freshwater phase. Aquacul. *14*: 221-234.

Refstie, T. (1980). Genetic and Environmental Sources of Variation in Body Weight and Length of Rainbow Trout Fingerlings. Aquacul. *19*: 351-357.

Roman, R. M. and Wilcox, C. J. (2000). Bivariate animal model estimates of genetic, phenotypic and environmental correlations for production. Reproduction Science, *83*:829-835.

Rutten, M. J. M.; Bovenhuis, H. and Komen, H. (2004). Modeling fillet traits based on body measurements in three Nile tilapia strains (*Oreochromis niloticus* L.). Aquacul. *231*(1/4): 113-122.

Yapi-Gnaore, C.V. (1996). Estimation of additive and nonadditive genetic parameters in the growth of fry of three strains of *Oreochromis* spp., In: Pullin, R.S.V.; Lazard, J.; Legendre, M.; Amon Kothias, J.B. and D. Pauly (eds.), Manila, Philippines., International Center for Living Aquatic Resorces Management (ICLARM), (CIRAD-EMVT), pp 426-432.

Table 1. Means, standard deviations (SD) and coefficient of variation (CV) for weight and length traits of Nile tilapia using MTDFREM program.

Trait	Mean	SD	CV%
Weight, (g)	0.160	0.116	72.15
Length, (cm)	1.647	0.489	29.66

Table 2. Mean, standard deviation (SD) and coefficients of variations (CV%) for weight and length of Nile tilapia obtained from MTDFREML programme for each experimental line.

	TRAIT							
	Weight (g)				Length (cm)			
LINE	NO.	MEAN	SD	CV%	NO	MEAN	SD	CV%
Giza	310	0.167	0.671	40.19	300	1.756	0.418	23.82
Mariut	250	0.141	0.066	47.02	250	1.524	0.303	19.88
Fouky	250	0.107	0.045	41.80	250	1.490	0.248	16.62
Nag-Hamady	350	0.208	0.176	84.77	350	1.753	0.691	39.40

Table 3. Genetic and phenotypic variances (on the diagonal) and covariance's (off diagonal), estimates of weight and length obtained from MTDFREML programme.

Trait	Genetic variance and covariance	
	Weight	Length
Weight	0.008	0.032
Length	0.032	0.154
	Phenotypic variance and covariance	
Weight	0.008	0.031
Length	0.031	0.177

Table 4. Estimates of heritability (on the diagonal) and genetic correlation coefficient (off diagonal) of the weight, length and their standard errors using MTDFREML Programme.

Trait	Weight	Length
Weight	0.99 (0.112)	0.91 (0.034)
Length	0.91(0.034)	0.87 (0.122)

Table 5. Heritabilities (on the diagonal) and genetic correlation (off diagonal) estimates and their (standard errors) of the weight and length for the different experimental line obtained from MTDFREML programme.

LINE	TRAIT	
	WEIGHT	LENGTH
Giza	0.750	0.900
	(0.283)	(0.084)
	0.900	0.710
	(0.084)	(283)
Mariut	0.400	0.980
	(0.222)	(0.032)
	0.980	0.970
	(0.32)	(0.326)
Fouky	0.480	0.650
	(0.254)	(0.325)
	0.650	0.110
	(0.325)	(0.096)
Nag-Hamady	1.000	0.940
	(0.155)	(0.037)
	0.940	0.870
	(0.033)	(0.167)