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A Quantitative Genetic Analysis of Six Phenotypes in *Oreochromis niloticus* in Different Olds

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Abstract
Heritability estimates were determined for six phenotypes in *Oreochromis niloticus* for 180, 210 and 300 days old: body weight (BW), total length (TL), standard length (SL), body height (BH), caudal tail height (CTH) and head length (HL). Heritability estimates were calculated by half-sib analysis from an experiment that contained 3 paternal half-sib families and 11 full-sib families. Heritabilities ranged from 0.00-0.88. These results suggest that because heritabilities of BW, TL, SL, BH, CTH and HL for sires in *Oreochromis niloticus* for 180 and 210 days old are low, family selection or progeny testing can proposed for selection. But, therefore heritabilities of all traits both male and female for 300 days old are high, selection will propose for are mass selection.
Keywords: *Oreochromis niloticus*, Heritability, Hierarchial Classification

INTRODUCTION

Cichlidae family generally wide spreading in the different region of Africa continent are hot climate fish grown in the tropic and sub-tropic climates. Various tilapia species i.e. *O. niloticus, O. aureus, T. zilli, T. rendalli* were imported to Fresh Water Research Station of Faculty of Fisheries, Çukurova University from Israel. Among the tilapiines, the *Oreochromis niloticus*, is the most important cultured fish species because of its good growth in freshwater[1]. To increase fish production, stocking ratte, poly-culture, feeding, feeding rate, hybridization studies, sex transformation, sex steroids, carcass studies and cage breeding studies were done[2-6]. But also genetic analyses of phenotypes and quantification of their heritabilities are necessary because heritabilities are needed parameter to design breeding program of this species. Heritabilities are important because they quantify the proportionate amount of additive genetic variance, quantify the potential for future selection, give an indication of previous selection and help explain variation that is seen within and among population. So the heritability has to be estimated in order to design breeding programs of fishing as well as the other animal breeding plans. It also plays a major important role in deciding the types of selection and mating. In order to determine using selection type and mating method, this parameter is needed to know.

The objective of this study was to determine heritabilities of 6 phenotype for 180, 210, 300 and 330 days old of *Oreochromis niloticus.*

MATERIALS AND METHODS

O. nilotica measured in this experiment were produced and grown at the Fresh Water Research. Phenotypes analyzed in this were: body weight, total length, standard length, body height, caudal tail height and, head length. Heritability estimates and standard errors were determined from the expansion of the variance of the phenotypic variation using variance analysis, hierarchical classification as describe by Kirpichnikov[7]. The experimental design used in this study was a nested, completely randomized design which contained in different number off-spring per dam, two or three dams per sire and three sires as given in Fig 1[7].

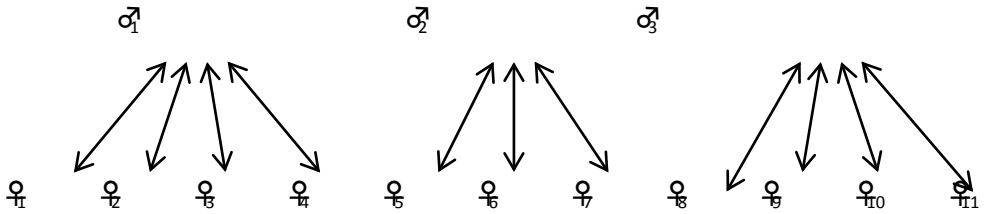


Figure 1. Shemes of crosses for determination of heritability using the variance analysis, hierarchial complex.

In this experiment, progeny from each family were grown in 80x40x60 cm the plastic cages placed in tanks of 455x75x90 cm size. Environmental conditions in the spawning and nursery cages were maintained similar for all the treatments. Therefore, the temperature, the density of light and the photoperiod differences among the cages were minimal, and the phenotypes of the fish should not have been affected by condition in spawning or nursery cages.

Estimates of variance components were optained from the statistical model:

$$Y_{ijk} = \mu + S_i + D_{ij} + W_{ijk}\ ;\ i=1,2,3;\ j=1,2,\ldots,d_i \quad (d_1=4,\ d_2=3,\ d_3=4) \qquad (1)$$

Where Yijk is the record [body weight(g), total length(cm), standard length(cm), body height(cm), caudal tail height (cm), head length(cm)] of the k-th progeny of the j-th dam mated to the i-th sire; μ is common mean; Si is the effect of the i-th sire ; D ij is the effect of the j-th dam mated to the i-th sire and Wijk is the uncontrolled environmental and genetic deviation of the progenies . The whole effects are assumed to be random, normal and independent with the means equal to zero and have variances such that S ~N (0, σ^2_s), D ~N (0, σ^2_d) and W ~N (0, σ^2_w)[8-9]. Variance components used to calculate heritability estimates were determined by analysis of variance; hierarchical classification of SAS system10. The analysis of variance (ANOVA) was constructed and the formulas for n1, n2 and n3 were given by Becker[9] and Akar[11] employing them were estimated.

Before the analyzing the data we adjusted them by defining the additive corrections factors about general mean for the birth date of each progeny[8]. The variances of σ^2_w, σ^2_d and σ^2_s were calculated according to the model which is given in equation (1) for the estimation of the heritabilities with standard errors for sires and dams. The ANOVA was done by using SPSS[12] and SAS[10] package programs. The variance of components ($\hat{\sigma}^2_d$, $\hat{\sigma}^2_s$ and $\hat{\sigma}^2_w$) and the heritabilities with respect to the traits were not defined as nonnegative. However, it is impossible[9,13] but we accept them as zero[14,15].

The heritability is defined as the ratio of genetic variance (σ^2_G) to phenotypic variance (σ^2_P)[16] :

$$h^2 = \frac{\sigma^2_G}{\sigma^2_P} \qquad (2)$$

All components of phenotypic variance could not be estimated within the aim of this study, so that we assumed epistatic variance and maternal variance were zero[17]. Once those assumptions were made, then:

$$\sigma^2_s = \frac{1}{4}V_A \qquad (3)$$

$$\sigma^2_d = \frac{1}{4}V_A + \frac{1}{4}V_D \qquad (4)$$

$$\sigma^2_w = \frac{1}{2}V_A + \frac{3}{4}V_D + V_E \qquad (5)$$

$$\sigma^2_p = \sigma^2_d + \sigma^2_s + \sigma^2_w \text{ or}$$

$$\sigma^2_p = V_A + V_D + V_E \qquad (6)$$

Where VA is the additive genetic variance; VD is the dominance genetic variance; VE is the environmental variance components of phenotypic variance (σ^2_p).

The heritability of sire and dam can be defined, respectively, as follows:

$$h_s^2 = \frac{V_A}{\sigma_p^2} \quad (7)$$

and

$$h_d^2 = \frac{V_A + V_D}{\sigma_p^2}. \quad (8)$$

σ_w^2, σ_d^2, σ_s^2 and σ_p^2 are estimated by $\hat{\sigma}_w^2$, $\hat{\sigma}_d^2$, $\hat{\sigma}_s^2$ and $\hat{\sigma}_p^2$, respectively.

RESULTS AND DISCUSSION

The ANOVA and the estimation of variance components for all traits according to model (1) are found.

The additive genetic variance (VA), the dominance genetic variance (VD) and the environmental variance (VE) are computed by using six decimal points and the formulas (3), (4), (5) and (6) which are presented in Table 1.

The heritabilities with the errors with all respect to traits are evaluated by using the values in Table 1 which are give in Table 2.

Heritabilities significantly different (p=0.05) from zero $\left(h^2 \pm 1.96\,[SE]\right)$ are marked with an asterisk.

The heritability of sires is generally lower than the heritability of dams for 180 days *Oreochromis niloticus* (*Table 2*). The heritability of caudal tail height for sire is not nonnegative such that it is regarded as zero. The heritabilities of other traits change from between 0.00 to 0.19 for sires and between 0.63 and 0.89 for dams. The heritability of sires is also lower than the heritability of dams for 210 days. The heritability of caudal tail height for sire is not also nonnegative such that it is accepted as zero[13] and the heritabilities of other traits are between 0.04 and 0.10 for sires but the heritability of dams change between 0.20 and 0.70. The lowest value of heritability of the traits for sires is 0.13 and the highest value is 0.31 for 300 days old of male. The heritability of caudal tail height for dams is not nonnegative such that it is regarded as zero and other traits are between 0.22 and 0.35. The heritability of caudal tail height for sire is not nonnegative for 300 days old of female such that we accept it as zero and the heritability of other traits are between 0.21 and 0.36 and the heritability of traits for dams change from 0.39 to 0.49 (*Table 2*). The heritability (h^2) estimates of fish in these studies are comparable with estimates of earlier studies in fish.

Several other studies generated h^2's for body weight and length. Five studies calculated h^2 for body weight and length and found h^2's of similar magnitude as those calculated in this study. Charo-Karisa et al.[18] presented result of two generations of selections (G1 and G2) for growth of Nile tilapia and genetic parameter estimated separately for each year. Also, they showed that heritability

Table 1. Additive Genetic Variance (V_A), Dominance Genetic Variance (V_D), Environmental Variance (V_E) Components Expressed As a Percent of Total Variance For Body Weight (BW), Total Length (TL), Standard Length (SL), Body Height (BH), Caudal Tail Height (CTH) and Head Length (HL) for 180, 210 and 300 days old of *Oreochromis niloticus.*

Age (Days))		Traits	Variance Components		
			V_A	V_D	V_E
180		**BW**	7	70	23
		TL	6	83	11
		SL	3	84	13
		BH	19	65	16
		CTH	0[a]	73	37
		HL	10	55	35
210		**BW**	6	44	50
		TL	6	42	52
		SL	4	47	49
		BH	10	20	70
		CTH	0[a]	70	30
		HL	10	10	80
300	Male	**BW**	32	4	64
		TL	28	0[b]	72
		SL	22	8	70
		BH	28	0[b]	72
		CTH	27	0[b]	73
		HL	13	20	67
	Female	**BW**	34	5	61
		TL	21	23	56
		SL	23	17	60
		BH	37	4	59
		CTH	0[a]	50	50
		HL	35	7	58

[a]Assumed to be zero $\hat{\sigma}_s^2 < 0$ [b]Assumed to be zero $\hat{\sigma}_d^2 < \hat{\sigma}_s^2$

Table 2. Sires (h^2_s) and Dams (h^2_d) Heritability Estimates ± SE for Body Weight (BW), Total Length (TL), Standard Length (SL), Body Height (BH), Caudal Tail Height (CTH) and Head Length (HL) for 180, 210 and 300 days old in *Oreochromis niloticus*.

Age (Days)		Traits	Heritability ± SE(Standart error)	
			$h^2_s \pm SE$	$h^2_d \pm SE$
180		BW	0.07±0.23	0.76±0.37*
		TL	0.06±0.26	0.89±0.42*
		SL	0.03±0.23	0.87±0.41*
		BH	0.19±0.34	0.84±0.40*
		CTH	0.00±0.11	0.63±0.31*
		HL	0.10±0.23	0.65±0.32*
210		BW	0.06±0.17	0.49±0.25*
		TL	0.06±0.16	0.48±0.24
		SL	0.04±0.16	0.51±0.26*
		BH	0.10±0.15	0.29±0.16
		CTH	0.00±0.10	0.70±0.34*
		HL	0.10±0.13	0.20±0.13
300	male	BW	0.31±0.35	0.35±0.25
		TL	0.28±0.30	0.25±0.20*
		SL	0.22±0.27	0.30±0.23
		BH	0.28±0.29	0.22±0.19
		CTH	0.27±0.23	0.00±0.09
		HL	0.13±0.16	0.33±0.19
	female	BW	0.34±0.38	0.39±0.29
		TL	0.21±0.31	0.44±0.32
		SL	0.22±0.31	0.39±0.30
		BH	0.36±0.40	0.40±0.29
		CTH	0.00±0.18	0.49±0.35
		BB	0.34±0.39	0.42±0.30

estimates for body weight (BW) ranged from 0.38 to 0.60, and the survival ranged from 0.03 to 0.14. Tave and Smitherman[19] reported h^2 estimates of 0.04 for both 45 and 90-day body weights, 0.10 for 45 day length and 0.04 for 90 day length for *O. niloticus* which were reared in fertilized pools and received supplementary feed. Charo-Karisa et al.[20] investigated cold tolerance of juvenile Nile tilapia, *Oreochromis niloticus*, and obtained heritability estimates. They estimated the heritability of cold tolerance as 0.08±0.17 for cooling degree hours (CDH) and 0.09±0.19 for temperature at death (TAD) with an animal model. They indicated that fish body weight (BW) was a highly significant effect on cold tolerance (P <0.0001). Gjerde et al.[21] found zero heritability and higher common environmental effects (0.12) for survival in Atlantic cod, suggesting non-additive genetic common environmental effects. In Nile tilapia growed in ponds, Eknath et al.[22] reported similarly heritability (0.08) compared to the present study.

Consequently, the h^2 estimates in the present study indicate prospects for improvement of this trait by selection. The heritabilities of BW, TL, SL, BH, CTH and HL for sires are low, family selection or progeny testing could proposed to use for 180 and 210 days old *O. niloticus*. But, the heritability of all traits for dam is high, mass selection could propose to use for 180 and 210 days old *O. niloticus*. Selection will propose for all traits both male and female are mass selection.

Because heritabilities for sires are low, family selection for BW, TL, SL, BH, CTH and HL for 180 and 210 days old *Oreochromis niloticus* and because heritabilities are high, mass selection for these traits could prefer [23].

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