

## Estimation of Heritability of Growth Parameters among Siblings of *Tilapia Guineensis* from Hierarchical Breeding Programme

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### Abstract

*As prelude to future selection of *Tilapia guineensis* for fast growth, size attributable to heritable and non-heritable factors were investigated. A hierarchical breeding design was employed to produce full and half-sib progenies. Variation in offspring size was investigated. Heritability was estimated on half-sib families. Variation in total length (CV=10.2%) and body weight (CV=22.5%) were observed. Analysis further showed that environment and genetics accounted for 44.7% and 55.3% of the variability in total length respectively. Conversely, environment and genetic accounted for 96.7% and 3.3% of the variability in body weight respectively. Heritability of total length was moderate (0.35), while heritability of body weight was very low (0.03). Parental effect on total length was significant ( $P < 0.01$ ). Parental effect on body weight was not significant ( $P > 0.05$ ). Dam contribution to variability was higher due to additional maternal effect. Heritability of size attributable to sire was higher suggesting emphasis on size of male. The study confirmed variation in size that should warrant growth enhancement of *T. guineensis* by selection. However, selection for increase in total length will be more effective than selection for increase in body weight since body weight is much more strongly influenced by environment than total length.*

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**Keywords:** *Environment, Genetic, growth, Heritability, Parental effect, Phenotypic variation and *Tilapia guineensis*.*

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### Introduction

Aquaculture is the technology of raising organisms in a confined water body that can be easily manipulated to achieve desired objective. The organism may be plant or animal. Scope of aquaculture therefore, covers the cultivation of wide spectra of brackish, fresh and marine water dwelling organisms in diverse confined enclosure systems such as earthen pond, tanks, cage, raceway and pen: which could be operated with static, running/flow through or recirculation water at different levels of intensification termed extensive, semi-intensive and intensive methods. On the basis of species combination, the culture could be described as monoculture, polyculture and integrated culture types of aquaculture. Aquaculture in Africa is barely significant. The continent as a whole contributed 0.9% (404,571 t) to the world aquaculture production in 2000 (FAO, 2003). The production increased to 1.8% only by 2008 (FAO, 2010). Ambali and Malekano (2004) observed that genetic improvement of *Tilapia* in Africa is imperative for increased aquaculture production in the continent. Genetic improvement could be

approached through promotion of such method as selective breeding (Tave 1995), hybridization (MCAndrew *et al.* 1993) or by chromosome manipulation and gene transfer (Purdom 1993). Of all the improvement options, selection appear to offer the greatest opportunity in African region, where *Tilapia* originate and where improvement of *Tilapia* needs to be achieved without causing significant genetic deterioration of the wild population. Selective breeding was employed to improve skin colour, body conformation, fillet yield, growth rate and cool tolerance in *Oreochromis niloticus* (Fitzsimmons, 2000). Gupta *et al* (2001) reported that Genetically Improved Farmed Tilapia (GIFT) strain of *O. niloticus* was generated through selective breeding. Improvement through selection is achievable if variation exists. The phenotype to change must exhibit variance. If there is no variation or minimal variation exists, application of selection as improvement option will be unnecessary (Tave 1995). Selection makes sense only when level of variation in the trait of interest is reasonable. The reasonable variation could originate from genotype or interaction between genotype and environment. Hence, the exercise is a lot easier when the contributory sources of the variation are known. Also for planning a selection scheme, good estimates of genetic parameters of heritability are needed. Wang and Li (2007) reported that use of data generated elsewhere on genetic parameters and environmental correlates in designing selective breeding programme may not be suitable in a new environment. They recommended specific parameters for specific environment because of genotype-environmental interaction. The interaction may be important in phenotypic variation of quantitative trait such as growth. Moreover, one caveat to the application of variance analysis in aquaculture is the qualification that estimates of genetic and environmental variances only apply to the population from which the estimates were derived (Lutz 2000). The present report tends to elucidate heritability of growth parameters, variation in growth and sources of the variation to warrant growth enhancement programme for *Tilapia guineensis* in Niger Delta, Nigeria.

### Materials and methods

Second filial generation of *Tilapia guineensis* were used to produce sufficient full and half sib progenies. The first filial generation from which the parents that yielded the second filial generation resulted was generated from communal spawning of 18 wild parents stocked in 1:1 sex ratio. The reproduction exercise was conducted in an indoor hatchery. Hierarchical breeding design was employed during the hatchery propagation. Three males (M1, M2 and M3) were individually paired to F1, F2 and F3 females in that order to produce three full sib families in the first instance (Set A families). The same males were paired to another set of females (F4, F5 and F6) to produce another set of three full sib families (Set B families). The pairing that produced the full sib families and their half sib relations were M1F1, M2F2, M3F3, M1F4, M2F5 and M3F6. The resultant six families were treated uniformly in terms of food and ambient water condition during the study. Prior to the pairing, total length (cm) and body weight (g) of couples were individually taken. Hatchlings were nursed with shell free *Artemia* after complete re-absorption of yolk from day 5 post hatch. Thirty larvae were sampled from each family on day 7 post hatch for total length and body weight measurement. Heritability and parental (sire and dam) effects on heritability of total length and body weight were estimated on half-sib families following the method described for hierarchical crosses in Falconer (1989) and as applied in fish by Kirpichnikov (1981). Heritable (Genetic) and non-heritable (Environmental) components of

the phenotypic variation were estimated employing expansion of Analysis of variance as documented in Kirpichnikov, (1981) and various components of the variation were extracted using the formula:  $V_T = V_G + V_E$  as described in Tave, (1995) Where  $V_T$  = Total variance,  $V_G$  = Genetic variance and  $V_E$  = Environmental variance. During the study, fish were maintained in clean water. Water quality temperature,  $P^H$ , salinity, and dissolved oxygen were monitored using digital metres. Ammonia and Nitrite were also monitored using LaMotte Salt water Aquaculture test kit (Model AQ-4/AQ – 5).

### Results and discussion

Intra class variation in offspring total length and body weight were observed within narrow limits of  $6.93 \pm 0.20 - 7.40 \pm 0.17$  and  $3.45 \pm 0.13 - 3.81 \pm 0.15$  (mean  $\pm$  standard deviation from the mean) respectively. Coefficients of variation of the phenotypes were 10.2% and 22.5% in that order (Table 1).

**Table 1: Intra-class variations in offspring size**

Family	M1F1	M1F4	M2F2	M2F5	M3F3	M3F6
Sample size	30	30	30	30	30	30
Mean Length	6.93	7.07	7.01	7.15	7.16	7.40
StdM (TL)	0.2	0.17	0.19	0.14	0.18	0.17
CV in fry total length (CV)	= 10.2%					
Mean Weight						
	3.46	3.45	3.66	3.81	3.64	3.77
StdM (BW)	0.14	0.16	0.13	0.15	0.17	0.15
CV in fry body weight (CV)	= 22.5%					

StdM = Standard deviation from mean; TL = Total Length; BD = Body weight; CV = Coefficient of variation

The higher coefficient of variation in body weight could be as a result of stronger environmental influence on weight than on length. Zhu (1997) reported that developmental character (such as weight or length) is not necessarily the result of genetic variation only, but are controlled by genes differently expressed at any time and by interaction of the genes with the environment (Zhu, 1997). The coefficients of variation of the traits recorded here for *T. guineensis* followed similar trend as reported for body weight (23.6%) and total length (7.4%) for Channel catfish (El-Ibiary and John, 1978).

Table 2 showcase correlations of parent-offspring parameters, genetic effects and heritabilities. The coefficient of correlation of total length ( $r = 0.99$ ) was strong as well as the correlation coefficient of body weight ( $r = 0.98$ ; Table 2). The slightly stronger correlation coefficient of the total length suggests higher inheritance of the trait than the body weight. Griffiths *et al* (1993) reported that resemblances of biological relatives that are associated with gene are captured as positive correlation between the relatives if they share common environment with nonrelatives.

**Table 2: Parent-offspring correlations, Sources of variation and heritabilities of growth parameters in *T. guineensis***

Parameters	Total length	Body weight
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Components	Value	Percentage	Value	Percentage
Genetic variance (VG)	0.655	55.3	0.023	3.3
Environmental variance (VE)	0.53	44.7	0.67	96.7
Total variance (VT)	1.185	100	0.693	100
Statistical effect		P<0.01		P>0.05
Parent-offspring (r)		r=0.99 <sup>P&lt;0.01</sup>		r=0.98 <sup>P&lt;0.01</sup>
Variance due to dam (VD)	0.41	62.6	0.012	52.2
Variance due to sire (VS)	0.21	37.4	0.011	47.8
h <sup>2</sup> (Dam)	0.55	55	0.03	3
h <sup>2</sup> (Sire)	0.69	69	0.04	4
H <sup>2</sup>	0.35	35	0.03	3

H<sup>2</sup> = Broad heritability

h<sup>2</sup> = Narrow heritability

Genetic effect of the total length variability attributable to sire (paternal parent) and dam (maternal parent) was significant (P<0.01), while the genetic effect of the body weight attributable to sire and dam was not significant (P>0.05). Also, variance component attributable to genetic in offspring total length (55.3%) was higher than the variance component attributable to environment in offspring total length (44.7%). On the other hand, variance attributable to genetic in offspring body weight (3.3%) was much smaller than the variance attributable to environment (96.7%). The findings here inferred greater gene influence in observed changes in total length and greater environmental influence in changes that occurred in body weight. The statistical model used to analyse the data accounted for all the observed phenotypic variations. Griffiths *et al* (1993) noted that Mendelian genetic analysis is extremely difficult to apply in continuous phenotypic distributions, so statistics are employed instead. Wang and Li (2007) employed statistical model (mixed genetic model) in diallel cross of three variants of common carp to predict genetic merit (breeding values) and indicated that *Cyprinus carpio* var. colour was the best one for genetic improvement through direct selection in different environmental conditions.

Heritability of total length was moderate (0.35), while heritability of body weight was very low (0.03). This implies that the portion of the population variation in total length that is due to genetic variance is higher than the portion of the population variation in body weight that is due to genetic variance. The implication of this is that selection for increase in total length will be more effective for growth enhancement of *T. guineensis* than selection for increase in body weight. Tave, (1995) stated that heritability of  $\geq 0.25$  indicate that selection will produce good gain, while those  $\leq 0.15$  indicate that selection will be ineffective. The result therefore shows that application of mass selection or family selection will be effective in a programme based on total length, while mass selection will be ineffective if the selection will be based on increase in body weight. Tave, (1995) concluded that low heritability traits cannot be improved by mass selection. El-Ibiary and John (1978) reported that it is more profitable to enhance body depth or inter-orbital width of Channel catfish by family selection rather than mass selection as a result of low heritability value of the traits.

Overall contribution of dam to the total length and body weight variability (62.6% and 52.2%) were higher than the contribution of sire (37.4% and 47.8%), but the aspect of the variability that

is due to genetic (heritable) was higher from sire (0.69 and 0.04) than from dam (0.55 and 0.03) for total length and body weight respectively. The higher contribution of dam to overall variability could be due to additional maternal environment provided by dam to the developing embryo that remains influential during ontogenetic development of the larvae. Probst *et al* (2005) attributed higher proportion of variance in larval traits to dam since maternal contributions to progeny can be both genetic and due to extra-nuclear materials (maternal environment) and it is difficult to isolate the contribution of either of the two sources. Sperm contain virtually no extra-nuclear material (Rideout, 2004a). Therefore, paternally induced differences in total length and body weight variability were purely genetic in origin, hence heritability of total length and body weight from sire were higher than heritability of total length and body weight from dam.

The above findings suggest higher paternal influence and recommend emphasis on size of male during hatchery propagation. Bernado, (1996) reported that many aspect of parental phenotype may impact the offspring including condition and size. Panagiotaki and Geffen (1992) reported parental effect on larval standard length at hatch.

The study was conducted under relative uniform water quality condition of  $p^H$  6.8  $NH_3-N$  0.001  $NO_2-N$  0.001, Dissolved oxygen 4.8mg/l and temperature 28°C mean values which were within tolerable limits that support fish growth (Kutty, 1987).

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