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Research Article

Evaluation of the Hereditable Characteristics of F_1 Generation of Parent Stock *Oreochromis niloticus* (5-red Thailand and 1- black Ghana breed)

***Ndana, T. Kedigi, Isah, M. C., Alhassan, M. N., Aliyu, D. A., and Rani, A. A.**

Department of Biological Sciences, Ibrahim Badamasi Babangida University, Lapai, Nigeria
****Corresponding Author's email*: kedigi@ibbu.edu.ng; Phone: +2347039104271**

ABSTRACT

This study evaluates the hereditable characteristic of F1 Generation of *Oreochromis niloticus* from a mixed parent stock population of 5-red improved Thailand local breed Tilapia and 1-black local Ghana breed. Parent stocks were obtained from the National Institute for Freshwater Fisheries Research (NIFFR), New Bussa. Morphometric and meristic features such as head length, standard length, body depth, as well as meristic features, such as fin ray and the scale counts, were used to analyze the heritable genetic characteristic in the F_1 generation. A controlled breeding strategy to track the offspring at different phases of development. The results revealed head length (03.00±0.05 - 05.00±0.01), standard length (03.00±0.05 - 05.00±0.01), body depth (03.00±0.05 - 05.00±0.01) as well as meristic features, such as fin ray (25.00±0.00 - 26.00±0.00, 15.00±0.00 - 16.00±0.00, 11.00±0.00 - 16.00±0.00) for Dorsal Fin ray, Hard ray and soft ray respectively. For the scale counts, Scale in Lateral Line recorded between 25 and 34 rays, while Scale below Lateral Line recorded 10 to 12 rays. Strong genetic control and low heritability were observed as a result of 99% of the F_1 generations being red, taking the characteristics of the Improved Thailand breed. These findings have significant implications for selective breeding strategies in tilapia aquaculture that aim to improve production efficiency and sustainability.

Keywords: Genetic heritability; F_1 generation; *Oreochromis niloticus*; Morphometric traits; Meristic counts

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INTRODUCTION

Tilapia ranks among the most farmed freshwater species globally, celebrated for its rapid growth, nutritional value, and resilience in diverse environmental conditions (FAO, 2021). Despite its prominence in aquaculture, challenges such as limited genetic variability and low heritability of economically important traits constrain the effectiveness of selective breeding programs (Mair and Little, 2021). A detailed understanding of the genetic basis of both morphometric (quantitative body measurements) and meristic (discrete, countable features) traits is essential for the improvement of tilapia strains (El-Sayed, 2020). Recent African studies have documented moderate heritability for growth traits but low variation in many morphometric and meristic characteristics (Adeyemi *et al.*, 2017; Oduro *et al.*, 2019).

Measurements of body length, depth, head length, fin length, and eye diameter are the most commonly used morphological characters in fish morphometry. These measurements provide a lot of important information that is typically described as total, fork, and standard length. Morphometry is a type of quantitative analysis in which the shape and size of the entire body and parts are physically measured. Morphometric measurements are widely used to assess the variation between populations of various fish species (Howe, 2002, Khalid *et al.* 2023).

Additionally, fish morphometric measures, offer valuable data for evaluating the fish population (Turan *et al.*, 2004). Fish morphological differences have been found to be more variable within the species than those of many other animals (Khalid *et al.*, 2023)

This study focuses on evaluating the genetic heritability of essential phenotypic traits in the F_1 generations (mixed population of improved Thailand – red and 1-black Ghana improved tilapia parent stocks) of *Oreochromis niloticus*. By examining these traits, the research aims to provide insights that can guide future breeding strategies and contribute to the sustainable genetic improvement of tilapia in African aquaculture systems (Eke and Olayemi, 2021).

MATERIALS AND METHODS

Study Site and Design

The experiment was conducted in the Department of Biological Sciences Garden at Ibrahim Badamasi Babangida University, Lapai, Niger State, Nigeria. A GP rubber tank pond was used for the study due its cheap and easy handling of fish and other factors, such as its optimum rearing conditions — including easy water control, temperature control, and adequate solar exposure —which are critical for consistent tilapia production (FAO, 2021). Before stocking, the pond was thoroughly cleaned, disinfected, and set up with routine environmental parameter monitoring.

Stocking and Monitoring

A mixed population of improved local tilapia containing 5 – red Thailand breed and 1 – black Ghana breed, were purchased from the National Institute for Freshwater Fisheries Research (NIFFR), New Bussa, to determine the genetic hereditable characteristics of the F_1 offspring using morphometric and meristic features in the F_1 generation of *Oreochromis niloticus*. The population was introduced into the GP tank pond. Fish were fed using factory-processed feed (blue crown 2mm) for 4 – 8 months. Health, growth, and survival were monitored and recorded throughout the study period (Mair and Little, 2021).

Experimental Design for Crossing Thailand Red (5) × Ghana Black (1) Nile Tilapia

The following assumptions were made to integrate genetic principles with morphometric/meristic analysis to predict and analyze hereditable features in the F1 generation from this cross:

Genetic Assumptions & F1 Color Prediction

The color inheritance model assumes that, for the sake of simplicity, black (Ghana) is recessive (r) and red (Thailand) is dominant (R).

In the event where Ghana Blacks are homozygous (rr) and Thailand Reds are homozygous (RR):

Every F_1 offspring has the black gene and is phenotypically red.

If the reds of Thailand are heterozygous (Rr):

50% red (Rr) and 50% black (rr) are the F1 offspring, notable were the red results of the F_1 generation. The coloration of tilapia may be influenced by polygenic traits or environmental conditions (such as feeding and water quality).

Heritability Data Collection

Table 1. Evaluation of Traits in F_1

Parameter Type	Measurable Traits	Tools
Morphometric	Body weight, total length, head depth	Digital calipers, weighing scales
Meristic	Dorsal fin spines (XVII–XVIII), anal fin rays	Magnifying lens
Color	Visual classification	Magnifying lens

The morphometric traits of the parent stock and F1 were measured using a transparent plastic meter rule, a digital Vernier caliper, and electronic weighing scales. The measured parameters include: Head Length (HL), Standard Length (SL), Total Length (TL), Body Depth (BD), Head Width (HW), Snout Length (SNL), Eye Diameter (ED), Interorbital Width (IW), and Mouth Width (MW). Other parameters measured include: Dorsal Fin Base Length (DFBL), Anal Fin Base Length (AFBL), Caudal Fin Length (CFL), Pelvic Fin Length (PFL), and Pectoral Fin Length (PEFL).

Additionally, meristic traits recorded are: Dorsal Fin Rays (DFR), Hard and Soft Rays (HR and SR), Anal Fin Rays (AFR), Pelvic Fin Rays (PFR), Pectoral Fin Rays (PEFR), Caudal Fin Rays (CFR), Scale counts along the Lateral Line (SLL) and Below the Lateral Line (SBL), Vertebral Count (VC), and Branchiostegal Rays (BR).

Measurements were taken at key developmental stages (post-fingerling, juvenile, and adult) to capture growth dynamics (Joshi *et al.*, 2020).

Heritability Estimation

The heritable characters were estimated from both the parent stock and F_1 generations from the generated data, and reference was made to predictable lineage history.

Quantitative Genetics:

Calculate **narrow-sense heritability** (h^2) for traits like growth rate: $h^2 = \frac{V_A}{V_P}$ *Where* V_A = *additive genetic variance and* V_P = *phenotypic variance.* (Khalid *et al.*, 2023)

For body weight, expect moderate heritability ($h^2 = 0.3$– 0.5) based on tilapia studies.

Analysis of variance (ANOVA) statistical tools was employed to partition phenotypic variance into genetic and environmental components, thus enabling estimation of heritability for each trait (Khaw *et al.*, 2019; Sanchez *et al.*, 2020).

RESULTS

Morphometric Measurements

Data revealed from the mixed population of the parent stock (5 – red improved Thailand breed and 1 – black improved Ghana breed) that several morphometric traits—such as head width, snout length, and eye diameter—exhibited minimal variation in the F$_1$ generation compared to the parental stock (Table 2). For instance, while differences were noted between the parental groups, the F$_1$ offspring showed consistent measurements for these key traits. This uniformity suggests that these morphometric characteristics are under strong genetic control (Adeyemi *et al.*, 2017; Xie *et al.*, 2021).

Meristic Count

The meristic traits in the F$_1$ generation showed no variation, indicating strong genetic regularity (Table 3). This suggests that these traits are under strict genetic control, with little or no influence from environmental factors.

Meristic traits—including fin ray and scale counts—showed no variation within the F$_1$ generation, indicating high genetic uniformity.

Table 2: Morphometric Measurements of the Parent Stocks and the Offsprings

PARAMETER	P1	P2	F$_1$1	F$_1$2
HL	5.00±0.30^{c}	3.00±0.50^{b}	1.50±0.20^{a}	1.40±0.30^{a}
SL	0.38±0.01^{b}	0.27±0.03^{a}	0.30±0.03a^{b}	0.34±0.05a^{b}
TL	0.31±0.02^{b}	0.21±0.03^{a}	0.25±0.03^{ab}	0.25±0.04^{ab}
BD	0.83±0.01^{b}	0.59±0.04^{a}	1.15±0.03^{d}	1.08±0.02^{c}
HW	2.52±0.23^{a}	2.25±0.47^{a}	3.25±0.98^{a}	3.47±1.79^{a}
SNL	2.52±0.23^{a}	1.81±0.25^{a}	3.25±0.98^{a}	2.34±1.20^{a}
ED	5.26±1.34^{a}	3.44±1.39^{a}	3.25±0.98^{a}	3.47±1.79^{a}
IW	3.95±0.70^{b}	3.11±1.65^{ab}	1.00±0.00^{a}	1.08±0.02^{a}
MW	5.26±1.34^{b}	5.26±1.34^{b}	2.21±0.36^{ab}	2.15±0.54^{a}
DFBL	4.73±1.06^{c}	3.44±1.39^{bc}	1.37±0.07^{ab}	1.08±0.02^{a}
AFBL	1.67±0.07^{b}	1.52±0.13^{b}	1.15±0.03^{a}	1.42±0.14^{b}
CFL	1.51±0.05^{c}	1.11±0.02^{b}	1.00±0.00^{a}	1.08±0.02^{b}
PFL	1.25±0.05^{ab}	1.02±0.27^{a}	1.51±0.11^{b}	1.39±0.16^{ab}
PEFL	0.50±0.05^{a}	0.50±0.03^{a}	2.61±0.67^{b}	2.61±0.67^{b}

Values are presented as Mean ± standard deviation. Values with the same superscript letters are not significantly different at $P<0.05$.

Head Length (HL); Standard Length (SL); Total Length (TL); Body Depth (BD); Head Width (HW); Snout Length (SNL); Eye Diameter (ED); Inter-orbital Width (IW); Mouth Width (MW); Dorsal Fin Base Length (DFBL); Anal Fin Base Length (AFBL); Caudal Fin Length (CFL); Pelvic Fin Lenth (PFL); Pectoral Fin Length (PEFL).

Table 3: Meristic Counts of Parent Stock (P1&P2) and the Offsprings

Parameter	P$_1$	P$_2$	F$_1$1	F$_1$2
DFR	26.00±0.00	25.00±0.00	26.00±0.00	26.00±0.00
HR	15.00±0.00	15.00±0.00	15.00±0.00	15.00±0.00
SR	11.00±0.00	10.00±0.00	11.00±0.00	11.00±0.00
AFR	9.00±0.00	8.00±0.00	8.00±0.00	7.00±0.00
HR	2.00±0.00	3.00±0.00	2.00±0.00	3.00±0.00
SR	7.00±0.00	6.00±0.00	6.00±0.00	7.00±0.00
PFR	9.00±0.00	7.00±0.00	9.00±0.00	9.00±0.00
PEFR	8.00±0.00	8.00±0.00	6.00±0.00	7.00±0.00
CFR	17.00±0.00	17.00±0.00	16.00±0.00	14.00±0.00
SLL	34.00±0.00	32.00±0.00	28.00±0.00	25.00±0.00
SBL	12.00±0.00	11.00±0.00	12.00±0.00	11.00±0.00
VC	30.00±0.00	30.00±0.00	30.00±0.00	29.00±0.00
BR	7.00±0.00	6.00±0.00	6.00±0.00	6.00±0.00

The meristic traits in the parent and F$_1$ generation shows no variation (standard deviation=0), indicating strong genetic uniformity.

Dorsal Fin Ray (DFR); Hard Ray (HR); Soft Ray (SR); Anal Fin Ray (AFR); Pelvic Fin Ray (PFR); Pectoral Fin Ray (PEFL); Caudal Fin Ray (CFR); Scale in Lateral line (SLL); Scale Below the Lateral Line (SBLL); Vertebrate Count (VC); Branchiostegal Rays (BR).

DISCUSSION

The morphometric measurement

Certain features of the morphometric measurements among the F_1 generation of tilapia were not significantly different. These characteristics, which remained constant across the population, include eye diameter, snout length, and head width. The negligible variations imply that these characteristics are largely heritable and genetically regulated, with little impact from environmental influences. (Adeyemi *et al.*, 2017; Yosef *et al.*, 2018; Xi *et al.* 2021; Eke and Olayemi, 2021).

For the first parent, the Head length (HL) was represented by HLa, and for the second parent, by HLb. Both members of the F_1 generation have head lengths that are represented by the symbol HLa, meaning that they have the same pattern or measurement.

Measurements of the two parental groups' standard lengths (HL) were represented by the letters SLb for the first parent and SLa for the second. Both individuals in the F_1 generation have head lengths that are represented by the symbol F_1b, meaning that they have the same standard length measurement or pattern without any differences.

Measurements of total length (TL): TLb and TLa, respectively, were used to represent the total length of the two parental groups. The superscripts "ab" in the F_1 generation (offspring of the two parental groups) stand for the combined genetic contributions of both parents.

Body depth (BD) measurements: The body depth of the two parental groups was denoted as BDb for the first parent and BDa for the second parent. In the F_1 generation, the individuals exhibit different body depth represented F_1d and F_1c, indicating that there is variation in body depth among the F_1 offspring.

Measurements of head width (HW): The first parent's and second parent's HWa were both the same, and the head width of the two parental groups was indicated as such. Both people in the F_1 generation have head lengths indicated by F_1a, meaning that they have the same head width measurement or pattern without any differences.

Measurements of Snout Length (SNL): The first parent's and second parent's snout lengths were indicated as SNLa and SNLa, respectively; both individuals display the same SNL. Both individuals in the F_1 generation display the identical snout lengths, denoted by F_1a, meaning that they have the same measurement or pattern of snout length without any differences.

Measurements of eye diameter (ED): The first parent's and second parent's eye diameters were designated as EDa and EDa, respectively; both individuals display the same eye diameter. Both members of the F_1 generation have the same eye diameter, or F_1a, which means that their head width measurements or patterns are identical.

Measurements of Interrorbital Width (IW): IWb for the first parent and IWab for the second parent were used to represent the two parental groups' IWs. There is no variation in the interrobital width of the F_1 offspring, as the individuals in the F_1 generation display the identical interrobital width as indicated by F_1a.

Mouth width (MW) measurements: Both individuals have the same mouth width, which is represented by the numbers MWb for the first parent and MWb for the second parent. Both people in the F_1 generation display varied mouth widths, as indicated by their MW^{ab} and MWa values, suggesting that their mouth width measurements or patterns vary.

Measurements of Dorsal Fin Base Length (DFBL): the first parent's dorsal fin base length is DFBLc, whereas the second parent's is DFBLbc. Both individuals display varying dorsal fin base lengths. Both individuals in the F_1 generation have varied dorsal fin base lengths, denoted by DFBLab and DFBLa, which suggests that their measurements or patterns vary.

Measurements of Anal Fin Base Length (AFBL): The first parent's and second parent's anal fin base lengths are represented by the letters AFBLb and AFBLb, respectively; both individuals have the same anal fin base length. Both individuals in the F_1 generation, designated F_1a and F_1b, respectively, have varying anal fin base lengths, suggesting that they share a variance in anal fin base length or pattern.

Caudal Fin Length (CFL) measurements: the first parent's CFLc and the second parent's CFLb are the caudal fin lengths of the two parental groups; the caudal fin lengths of the two individuals differ. Both individuals in the F_1 generation, denoted by the letters CFLc and CFLb, have distinct caudal fin lengths, which suggests that their measurements or patterns vary.

Pelvic Fin Length (PFL) measurements: the first parent's pelvic fin length is indicated by PFLab, whereas the second parent's is PFLa. Both individuals have varying pelvic fin lengths. Both individuals in the F_1 generation have varied pelvic fin lengths, denoted by PFLb and PFLab, which suggests that their measurements or patterns vary. Pectoral Fin Length (PEFL) measurements: The pectoral fin length of the two parental groups is denoted as PEFLa for the first parent and PEFLa for the second parent, both individuals exhibit the same pectoral fin length. In the F_1 generation, both individuals exhibit the same pectoral fin length represented F_1b, indicating that they share the same pectoral fin length measurement or pattern with variation between the parent and F_1 generation.

In the F_1 generation of Nile tilapia, studies on the heritability of morphometric and meristic features indicate that there is little genetic variation in these traits. This finding is important because it affects breeding plans that try to increase particular body counts and metrics that may not react well to selection because of low heredity (Nguyen *et al.*, 2010; Oduro *et al.*, 2019; Abdulrahman *et al.*, 2020). When chosen from a small genetic pool, morphometric traits—which are quantifiable body dimensions like length, height, and fin size—usually show little variation between generations. This is frequently because stabilizing selection pressures favor the best physical forms for survival in caged environments (El-Sayed, 2020). According to studies, some morphometric features, like body depth and standard length, have low heritability values (0.05–0.15), indicating that they are less sensitive to selective breeding. According to research by Rutten *et al.* (2005), tilapia's low heritability values indicate a lack of genetic diversity in these traits, which may be caused by canalization, a process that preserves particular phenotypes with little variation between generations. Because of this, achieving notable changes in morphometric features through selective breeding alone is difficult.

The meristic counts

Strong genetic regularity was indicated by the F_1 generation's meristic characteristics, which displayed no variance. This implies that environmental influences have little to no effect on these features, which are strictly controlled by genetics. The population-wide stability of these traits illustrates how meristic qualities in tilapia are heritable. The invariability confirms that these countable traits are strictly regulated by genetic factors and are minimally influenced by environmental conditions (Ponzoni and Yáñez, 2020; Oduro *et al.*, 2019).

The absence of variability indicates that the meristic qualities (such as the number of fin rays and the vertebral column) are highly heritable and unaffected by external variables. These traits are frequently defined during early developmental stages. This may indicate that the genes causing these characteristics are either fixed or extremely well-preserved among the population.

Meristic traits include countable characteristics, including the number of scales or fin rays; Nile tilapia F_1 generations also show little genetic variation. Recent studies have shown heritability estimates as low as 0.05 to 0.10, indicating that these traits frequently exhibit little response to selecting pressure (Bentsen *et al.*, 2012). The developmental stability of meristic features, which are heavily influenced by both genetic and environmental factors, is probably the reason for their low heritability. As a result, there is little variation among these counts.

Breeding programs should concentrate on qualities with higher genetic variation, like growth rate, disease resistance, and feed efficiency, which have been shown to have more substantial heritable components, given the low heritability of both morphometric and meristic traits (Khaw *et al.*, 2016; Oduro *et al.*, 2019; Abdulrahman *et al.*, 2020). In order to prevent genetic drift or decreased adaptability in farmed populations, morphometric and meristic features may be preserved within natural variation verges, as they do not significantly change under selection (Ponzoni *et al.*, 2011; Oduro *et al.*, 2019; Abdulrahman *et al.*, 2020).

The genetic control of aquaculture breeding stocks is also responsible for the low level of genetic diversity shown in these characteristics. Long-term inbreeding in confined breeding programs frequently narrows the genetic base, which may lessen the heritability of traits that could otherwise show diversity in wild populations, according to Bentsen *et al.* (2012).

Moreover, the absence of variation in meristic counts underscores the strong genetic control over these traits. Several African researchers have reported similar findings, noting that meristic traits in Nile tilapia are highly conserved, which may limit the response to selective breeding (Oduro *et al.*, 2019; Abdulrahman *et al.*, 2020). These results imply that while some economically important traits (such as growth rate) may be improved through selective breeding, traits with low heritability like the morphometric and meristic characteristics studied here may require alternative approaches—such as the incorporation of genomic selection—to enhance genetic diversity and performance (Khaw *et al.*, 2019; Sanchez *et al.*, 2020).

CONCLUSION

The study revealed that the F_1 generation of *Oreochromis niloticus* locally improved breeds (mixed populations that was obtained NIFFR, New Bussa – 5 – red Thailand breeds; and 1 black Ghana breed) exhibits strong genetic control over key morphometric and meristic traits, with minimal variation observed among offspring. This low heritability suggests that traditional selective breeding approaches may yield only modest improvements in these traits. This study can further be expanded to improve on the breeding initiatives targeted at enhancing aquaculture production while also adding to the expanding corpus of information on genetic heritability in tilapia. Selective breeding strategies can improve the genetic potential of commercial tilapia populations by determining which features are most consistently inherited.

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