Comparative Morphometric Analysis of a Salinity-Tolerant Nile Tilapia (*Oreochromis niloticus*) Local Strain (*Salina*) and Its Parental Strains

Yohanes Pamungkas Bawono^[D], Kiki Mariya Dewi^[D]*, Ekky Ilham Romadhona^[D], Handang Widantara^[D], Wisnu Sujatmiko^[D], Ratu Siti Aliah^[D], Sutanti Sutanti^[D], Annisa Fitri Larassagita^[D], Muhamad Kholik Firmansyah^[D], Novi Megawati^[D], Aslia Aslia^[D], Arif Rahmat Ardiansyah^[D], Iding Chaidir^[D], Dedy Yaniharto^[D]

¹Research Center for Fishery, National Research and Innovation Agency, Cibinong, West Java 16912, Indonesia.

*Corresponding author: kiki002@brin.go.id

Abstract

This study focuses on the morphology of the Nile tilapia local strain (Salina), a salinity-tolerant tilapia hybrid strain developed by crossbreeding between female Nile tilapia Red NIFI with male Nile tilapia Sultana. The research aimed to analyse the morphometric characteristics of the Salina strain to understand species adaptation to suboptimal environmental conditions compared with the parental groups. A total of 60 Nile tilapia fish, ten female and ten male samples from each strain (Salina, Sultana, and red NIFI), were measured for their total length (TL), standard length (SL), head length (HL), body width (WID), dorsal fin length (DL), caudal fin length (CL), pectoral fin length (PL), caudal peduncle depth (CPD), eye diameter (ED), snout length (SNL), and body weight (BW). Each measurement parameter was then normalized by comparing it with the standard length (SL). The data were analysed using MS Excel 2019 and R v4.5.1 for all statistical analysis including MANOVA, Canonical Variance Analysis, Principal Component Analysis, and Hierarchical Clustering Analysis. Condition factor (K) and length-weight relationship (LWR) were calculated to investigate growth conditions and allometric growth patterns, respectively. Based on the findings, the six tilapia populations exhibit overlapping morphological traits, except for female Salina with slight differences in morphological variations. This implies its potential unique traits acquired from crossbreeding between two different strains. Meanwhile, male Salina showed morphometric traits closely aligned with its male parent, the Sultana strain. The condition factor across all populations indicates favourable growth conditions, although the negative allometric growth pattern suggests that length increases more rapidly than body weight, implying an adaptive trade-off in suboptimal environments.

Keywords: adaptation, crossing, morphometric, tilapia, populations

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INTRODUCTION

Aquaculture is one of the most promising sectors within Indonesia's fisheries industry (16.96 million tons in 2023), surpassing the capture fisheries outputs and establishing aquaculture as the primary contributor to the national fish supply. Although annual production varies, the aquaculture sector has sustained a healthy average growth rate of 2.65% from 2019 to 2023. Indonesia's aquaculture industry is marked by its species diversity, encompassing fish, shrimp, and seaweed, which underscores its adaptability and growing economic importance (MMAF, 2024).

Nile tilapia (Oreochromis niloticus) is a major aquaculture commodity in Indonesia. In 2023, national tilapia production of Nile tilapia reached 1.36 million tons- the second-highest aquaculture product after seaweed (Albani et al., 2023; Gustiano et al., 2023; MMAF, 2024). Originally native to Africa, Nile tilapia has been successfully introduced tropical subtropical regions worldwide (Shuai and Li, 2022). The species is favoured for its rapid growth, high fecundity, and adaptability to suboptimal environmental conditions (Kurniawan et al., 2023; Munguti et al., 2022). Its euryhaline nature allows it to thrive in a wide range of salinity levels, making it suitable for brackish



water culture. Furthermore, Nile tilapia can grow and reproduce in salinities from 0 to 20 parts per thousand (ppt), and can tolerate salinities up to 35 ppt (Diego *et al.*, 2023; Nurchayati *et al.*, 2021).

Several strains of Nile tilapia are cultured in Indonesia, each with specific enhancements or adaptations. These strains include the Bogor Enhanced Strain Tilapia (BEST), the Genetically Supermale Enhanced Indonesian Tilapia (GESIT), the Salinity Resistant Improvement from Sukamandi (Srikandi), Nila Ras Wanayasa (NIRWANA), Jatimbulan, the superior Salabintana (Sultana), and the National Inland Fish Institute (Red NIFI) (Faqih et al., 2015; Nugroho et al., 2024; Taukhid et al., 2024). Among these advancements, the Saline-Tolerant Indonesian Tilapia (Salina) represents significant milestone in selective breeding. This strain was officially released by the Ministry of Marine Affairs and Fisheries in March 2014, according to Decree Number 22/KEPMEN-KP/2014 (Dewi et al., 2018).

The Salina strain (O. niloticus) developed through crossbreeding between female Red NIFI (O. mossambicus x O. niloticus) and male Sultana (O. niloticus) (Figure 1), both were from a certified Main Center of Freshwater Aquaculture (MCFA) Sukabumi, West Java, Indonesia (Aliah, 2017). This center obtained the Indonesian Good Aquaculture **Practices** (IndoGAP) certificate that the fish seed produced is of high quality. IndoGAP is a set of guidelines and procedures for breeding fish, including broodstock management, spawning, egg hatching, and larval/seed maintenance in a controlled environment, by applying technologies that meet technical, management, food safety, and environmental criteria and requirements.

The *Salina* strain spawning is conducted in a brackish environment, ensuring the hybrid Salina fry is highly adaptable to such conditions. Fish crossbreeding occurs naturally or artificially between different species and strains to produce superior new strains. The *Salina* strain exhibits notable characteristics, including high tolerance to salinity levels exceeding 20 ppt, high survival rates, a low feed conversion ratio (FCR), and a strong resistance to pathogenic bacteria from

Streptococcus species. These conditions emphasize the Salina strain as a highly promising candidate for revitalizing aquaculture systems, particularly in inactive shrimp ponds and freshwater ponds affected by saline intrusion due to rising sea levels. By leveraging the resilience and adaptability of the *Salina* strain, these ponds may overcome salinity-related challenges to resume sustainable operations, contributing to food security and local economies (Dewi *et al.*, 2018; Setyawan *et al.*, 2022).

Fish morphometrics is a critical technique used in ichthyology to quantitatively assess the physical dimensions of fish, such as the length, height, and other key body measurements. These measurements are essential for identifying and comparing morphological variations both within between species and or populations. Morphometric analysis plays a vital role in understanding phenotypic variation and adaptive traits, providing insights into environmental factors response (Tripathy, 2020). Moreover, morphometric analysis also contribute to broader ecological and evolutionary studies by revealing patterns in fish morphological divergence. Numerous studies have extensively documented the morphometric characterization of various Nile tilapia species across diverse environmental conditions (Kosai et al., 2014; Ndiwa et al., 2016; Kwikiriza et al., 2023; Engdaw, 2023).

However, a notable gap persists in the literature regarding the morphometric properties of saline-tolerant Nile tilapia strains. To address this gap, this study investigates the morphology and morphometric characteristics of the hybrid Salina strain, developed from a crossbreeding between female Red NIFI (O. mossambicus x O. and male Sultana tilapia. niloticus) establishing baseline data on the morphology of these hybrids, the study aims to provide insights on their adaptability and potential applications in aquaculture. Additionally, comparative analysis the hybrid offspring and their parental strains are expected to yield valuable contributions to fisheries biology, offering insightful information effects of hybridization on fish morphology, especially in suboptimal environments.

MATERIALS AND METHODS

Ethical Approval

This study did not involve animal experimentation. Fish were obtained from routine aquaculture production at the Regional Technical Implementation Unit in Karawang, West Java, Indonesia. All individuals used were already harvested and frozen before morphometric analysis. According to institutional and national regulations, ethical approval was not required for studies involving post-mortem morphometric measurements of fish.

Study Period and Location

All fish in this study were collected at the Regional Technical Implementation Unit in Karawang, West Java, Indonesia (6°04'06.4"S and 107°25'06.7"E). This study was performed from 2011 to 2012.

Fish Rearing Location and Conditions

The 3 tilapia strains: *Red NIFI*, *Sultana*, and *Salina* were reared in different earthen ponds, with males and females separated by $3x5m^2$ hapas within each pond. All reared fish were fed with uniform commercial feed (32% protein content) twice a day (*at satiation*). During the rearing period, water quality was measured periodically. Water quality records showed similar trends in all ponds: temperature 27.8–32.7 °C, salinity 5–10 ppt, pH 7.16–8.92, dissolved oxygen 6.65–8.54 mg/l, turbidity 3.29–4.35 NTU, and Ammonia (NH₃) 0.18–0.73 mg/l. These values are considered normal and suitable for aquaculture performance.

Sample Collection and Morphometric Measurement

The fish samples were obtained in frozen form from a routine harvest at the Regional Technical Implementation Unit in Karawang, West Java, Indonesia. Within each pond, females (10 samples) and males (10 samples) from each strain of *Red NIFI*, *Sultana*, and *Salina* in different ponds were collected randomly. Fish collected in this study were more than 6 months old and considered in the adult stage (Ariyanto,

2002). With a total of 60 fish, only a single trained individual was assigned to take morphometric measurements using a Mitutoyo Vernier Caliper with a precision of 0.01 cm, while the body weight was determined using a calibrated digital scale with an precision of 0.01 g. The fish total length (TL), standard length (SL), head length (HL), body width (WID), dorsal fin length (DL), caudal fin length (CL), pectoral fin length (PL), caudal peduncle depth (CPD), eye diameter (ED), snout length (SNL), and body weight (BW) were used for morphometrics data (Figure 2).

Data Analysis

Each measurement parameter was then normalized by comparing it with the standard length (SL) before any statistical processing as displayed in Table 1 to ensure consistency across all measurements. This approach enabled fairer group comparisons, ensuring morphometric differences reflected biological variation rather than age, growth, or environmental influences (Ramli, 2016). The data was processed and analysed using MS Excel 2019 and R v4.5.1 for all statistical analysis. The normalized data were checked for normality and homogeneity assumptions with Shapiro-Wilk and Levene's test, respectively. Multivariate Analysis of Variance (MANOVA) performed was incorporating strain, sex, and their interaction as using factors, and all 10 standardized morphometric traits as dependent variables. To evaluate effects, pond we conducted PERMANOVA with permutations restricted within pond blocks (Red NIFI in pond 1, Sultana in pond 2, and Salina in pond 3).

Following the multivariate results, we conducted univariate ANOVAs with Tukey's post-hoc tests to identify which specific traits contributed most to the observed difference. Partial eta squared (η_P^2) was used to investigate the effect sizes of *strain*, *sex*, and *strain*×*sex* using Cohen's benchmark for interpretation. Principal component analysis (PCA), canonical variance analysis (CVA), and hierarchical clustering analysis (HCA) were employed to evaluate variation, relationship, and correlation



between fish populations among multiple morphometric traits.

The length-weight relationship (LWR) of the samples was analysed to assess growth patterns and overall body condition, using the established standard allometric equation:

$$W = a L^b \dots (1)$$

Where W represents the body weight in grams, L denotes the total length in centimetres, while a and b are the intercept and slope of the regression function, respectively (Le Cren, 1951). This relationship provides insights into growth dynamics and body proportionality, indicating the association of length and weight within the population. Piecewise regression was also investigated as a comparative LWR analysis model in this study (De Robertis and Williams, 2008) which formulated in the equation:

$$log_e(W) = log_e(a_i) + b_i log_e(L) + \varepsilon \dots (2)$$

Where i is an index of the fish group, e is the error term, W, L, a, and b are terms of the allometric equation defined before. Additionally, the condition factor (K), which serves as an indicator of the fish's well-being and robustness, was calculated using the formula:

$$K = 100 \times (W/L^3)$$
....(3)

Where W is the body weight in grams and L is the total length of the fish in centimetres (Htun-Han, 1978). The condition factor allows for a comparative analysis of fish health across different size classes and environmental conditions, offering valuable data for understanding fish physiological state across the populations. The p-value < 0.05 is considered significant in all analysis.

RESULTS AND DISCUSSION

Morphometric Characteristics of Tilapia Populations

In this study, eleven primary morphometric traits, specifically head length (HL), pectoral fin

length (PL), body weight (BW), body width (WID), total length (TL), standard length (SL), dorsal fin length (DL), and caudal fin length (CL), caudal peduncle depth (CPD), eye diameter (ED), and snout length (SNL). This selection was based on the premise that primary morphometric characteristics include total length (TL) and body weight (BW), as these traits are adequate for assessing fish condition and estimating biomass (Zhang *et al.*, 2024). Targeting these traits enables efficient analysis while preserving accuracy of condition and biomass estimates, supporting practical implementation in fisheries biology.

The sample size of 10 males and 10 females per strain was determined based on practical constraints, including available resources, labor, time, and costs. While we recognize that larger sample sizes generally increase statistical power and the ability to detect small effect sizes, our study prioritized balanced sampling across all strains to enable fair comparisons. Random sampling within each strain was applied to ensure that every individual in the population had an equal chance of being selected, thereby reducing selection bias and increasing representativeness. Although the modest sample size may limit the precision of certain estimates and the detection of subtle morphometric differences, it remains sufficient for detecting moderate to large differences in multivariate morphometric traits, as supported by similar sample sizes in previous tilapia morphometric studies. Future research with larger cohorts and replicated trials would be valuable to confirm and extend these findings. To minimize measurement error, all instruments were regularly calibrated prior to data collection, with particular attention to the digital scale, which was calibrated before each use. Morphometric measurements were conducted by a single trained individual to avoid inter-observer variability. In addition, a subset of samples was randomly remeasured to assess and ensure data precision and consistency.

One-way ANOVA revealed significant standardized morphometric differences among the populations (Table 1). Tukey HSD tests showed that female *Salina* had the lowest TL:SL and CL:SL values, indicating smaller overall



body size and caudal development than both male Salina and the parental (male Sultana, female Red NIFI) and nonparental groups. This smaller body form, also reflected in raw (unstandardized) measurements as shown in Table 2, suggests slower somatic growth, which in aquaculture, which may be influenced by environmental mismatches. According to the official released document by Ministry of Fisheries and Marine Affairs (Keputusan Menteri Kelautan dan Perikanan Republik Indonesia Nomor 22/KEPMEN-KP/2014), the Salina strain exhibits optimal growth at salinity levels of 20-25 ppt. Therefore, the lower salinity of 5–10 ppt in the present study, coupled with quite fluctuated water quality conditions in the pond and exposure unpredictable factors like rain, likely constrained their growth performance. Male Salina, while shorter (lower TL:SL) and lighter (lower BW:SL) than male Sultana and male Red NIFI, exhibited proportionally longer dorsal fins (DL:SL), larger heads (HL:SL), and deeper bodies (WID:SL), indicating possible shifts in growth allocation under suboptimal salinity. In contrast, male Red NIFI consistently displayed the largest body proportions among groups, reflecting strong growth potential under pond culture and suggesting suitability for production traits prioritized in aquaculture, such as rapid biomass gain and higher market yield. The smaller body proportions observed in Salina compared to its parental lines may have implications for reproductive performance. In many fish species, fecundity increases with standard length and body weight because larger individuals possess greater energy reserves and larger body cavities for oocyte production (Jonsson and Jonsson, 1999). For example, Hasan et al. (2020) reported that 55.1% of fecundity variation in Clupisoma garua catfish could be explained by variation in standard length, with fecundity rising significantly alongside body size. Given this potential relationship, the reduced body size in Salina may limit egg production, representing a potential size-fecundity trade-off. Whether this trade-off arises primarily from hybridization effects or from environmental constraints is unclear, as Salina in this study were

reared at 5–10 ppt salinity which is lower than the 20–25 ppt range previously associated with optimal growth.

The findings of this study align with previous research that has indicated significant differences in morphometric traits among various tilapia strains. Allaman et al., (2013) and Regala et al., (2018) emphasized that tilapia strains can exhibit morphological characteristics, distinct highlighting the inherent variability within the species. Similarly, this study also demonstrates significant differences in certain morphological traits among the tilapia strains examined. The observed variation in morphological traits occurs between different strains observed. As mentioned by Ramli (2016), such variation occurs between different strains and within hybrids of the same or different parental strains, suggesting that genetic diversity plays a crucial role in shaping the physical characteristics of tilapia and leading to a wide range of morphometric outcomes. Moreover, this study also align with Wahidah et (2023),who reported morphological differences between male and female tilapia were influenced by genetic and environmental factors, contributing to the differences in body shape and size between the males and females.

Environment Effects and Strain \times Sex Interaction Analysis

The environment might affect the fish morphometric traits, especially when different tilapia strains are being reared in different ponds as in this study design. While rearing conditions aimed to minimize environmental variation, we acknowledge that strain and pond effects were confounded in this study, and thus environmental influences could not be entirely ruled out. To partially address this, we performed permutation-based MANOVA with permutations restricted within the pond to control for pondlevel variation. These approaches provide valid tests for sex and strain \times sex, while we interpret the strain main effect cautiously as potentially reflecting both genetic and pond influences.

Based on PERMANOVA results, $Strain \times sex$ effects remained high (R² = 0.868, p-value < 0.05), suggesting that morphological

differentiation was not solely driven by pondlevel differences. With this evidence, we have reasonable means to focus on *strain x sex* interaction analysis.

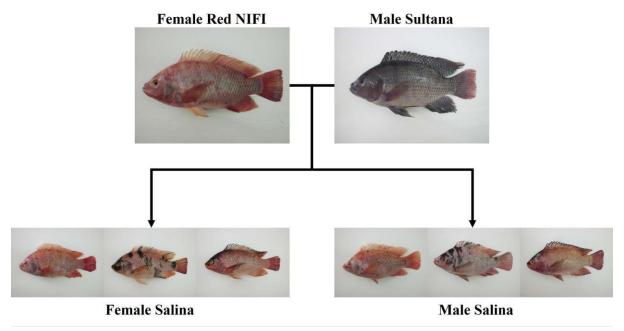


Figure 1. Crossbreeding diagram of *Salina* strain from its parental group: female *Red NIFI* (*O. mossambicus x O. niloticus*) and male *Sultana* (Author's documentation).

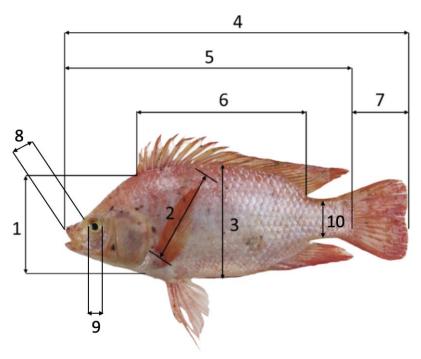


Figure 2. Measurements of the morphometric characteristics of examined *O. niloticus*: 1. head length (HL), 2. pectoral fin length (PL), 3. body width (WID), 4. total length (TL), 5. standard length (SL), 6. dorsal fin length (DL), 7. caudal fin length (CL), 8. snout length (SNL), 9. eye diameter (ED), and 10. caudal peduncle depth (CPD) (Author's documentation).

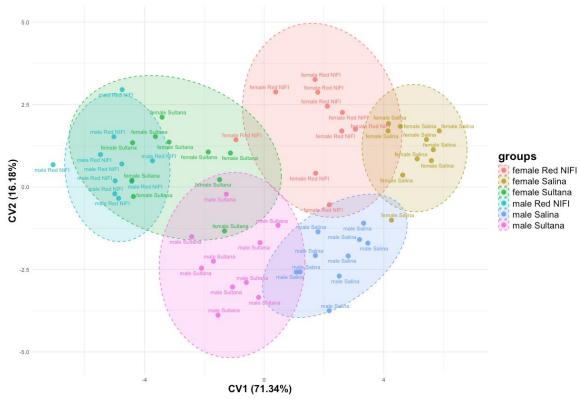


Figure 3. Canonical Variates Analysis of the 6 tilapia populations shows clustering separation between males and females in each strain with CV1 contributing 71.34% and CV2 contributing 16.18% to the variance.

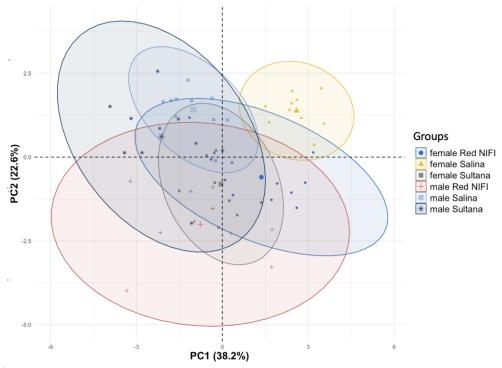


Figure 4. Principal component analysis of the 6 tilapia populations shows overlapping between most of the groups and a distinguished separation of female *Salina*, with PC1 contributing 38.2% and PC2 contributing 22.6% to the variance.

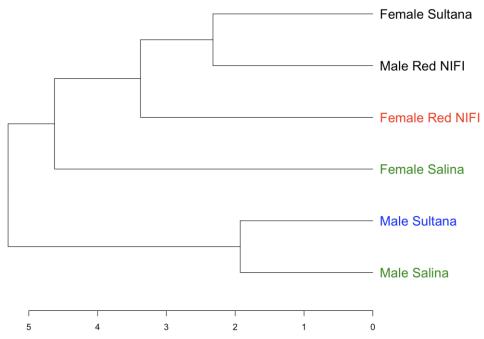


Figure 5. A cluster dendrogram of six tilapia groups based on multi-morphometric traits. Distance metrics and branches show separation between male *Salina* and female *Salina*. Both are closely related to its parental group, where male *Sultana* clustered with male *Salina*, while female *Red NIFI* has a closer distance to female *Salina*.

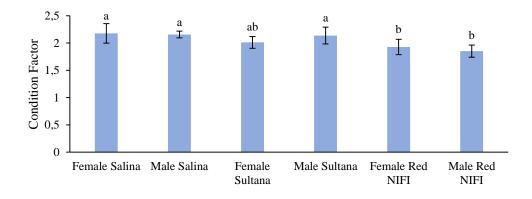


Figure 6. Condition factors (K) of the 6 tilapia groups. Error bars represent standard errors from the total sample, with statistical differences indicated by different letters (p < 0.05).

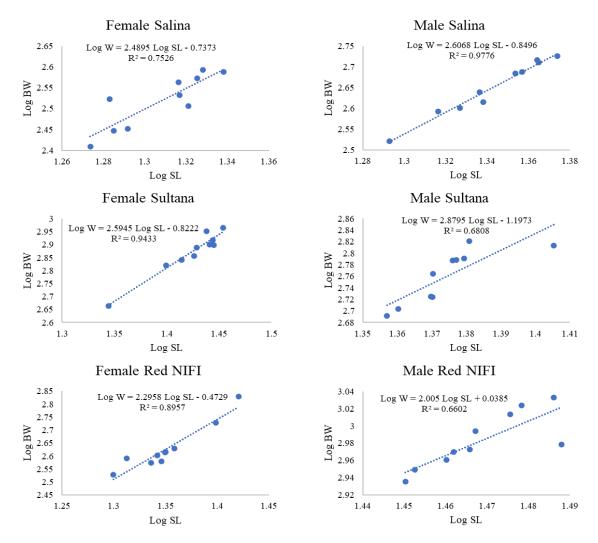


Figure 7. Length-weight relationship (LWR) among the tilapia populations using standard Le Cren's allometric model. R² is a coefficient of determination that represents the proportion of variance in the body weight (BW) that can be explained by the standard length (SL).

Based on MANOVA results, there is an interaction between strain x sex (p < 0.05), suggesting that morphological differences among strains vary by sex and vice versa. Further, twoway ANOVA (Table 3) revealed strong strain x sex interactions for standardized BW:SL, ED:SL, CL:SL, and PL:SL ($\eta_p^2 > 0.14$; p < 0.05). Adding evidence that morphological traits differ between sexes, and vice versa, that sex differences are strain-dependent, particularly on mentioned variables. Moreover, based on partial η^2 , sex parameters have significantly large effects on several traits such as BW:SL, WID:SL, CL:SL, SNL:SL, TL:SL, HL:SL, CPD:SL, and DL:SL. This implies that sexual dimorphism exists in the populations, hence sex may strongly influence variation in weight and body size of the studied

tilapia populations. Canonical Variates Analysis (Figure 3) visualizes how the males and females in each strain are separated by morphometrical profiles with CV1 contributing 71.34% and CV2 contributing 16.18% to the variances.

Morphometric Relationships between *Salina* Strain and Its Parental Groups

The application of Principal Component Analysis (PCA) in fish morphometric analysis serves as a powerful tool for evaluating the variation and relationships among multiple morphometric traits. By reducing the dimensionality of the dataset, PCA highlights the primary axes of variation while preserving essential patterns, thus facilitating the interpretation of complex trait interdependencies

(Laskar et al., 2013). In this study, PCA was employed to analyze ten distinct morphometric traits, resulting in the extraction of seven principal components. Each component represents a variation aspect present in the original dataset. Notably, the first two principal components (PC1 and PC2) accounted for a substantial portion of the variance, with PC1 contributing 38.17% and PC2 contributing 22.62%, culminating in a combined total of 60.79% of the observed variation (Table 4). Based on PCA loadings, variables of standardized CL:SL, CPD:SL, TL:SL, WID:SL, and HL:SL are most contributed to PC1. Therefore, PC1 represents general body size and caudal propulsion capacity, which may be linked to swimming performance, predator avoidance, or sexual display. Meanwhile, variables of standardized ED:SL, BW:SL, HL:SL, WID:SL, and TL:SL are the main contributors to PC2. This component represents head-sensory morphology which may be related to visual adaptations against water turbidity and light intensity. In addition, eye size might be related to schooling coordination, social cue detection or allometric growth. PC2 also represents body condition related to health and sexual maturity. The cumulative variance explained by the first four components exceeded 60%, indicating that these components retained the critical morphometric information from the original variables, consistent with the thresholds established in previous studies (Yu et al., 1998).

In this study, Principal Component Analysis (PCA) revealed considerable overlapping across all clusters, with the notable exception of the female Salina (Figure 4). This distinction suggests notable differences in morphometric traits in female Salina implying unique morphometric traits. However, no significant separation was observed between the male Salina group and its parental lines, especially this group overlapping closely with male Sultana. The lack of distinct separation between male Salina and male Sultana implies a considerable overlap in their morphometric characteristics, suggesting that the male Salina's traits closely resemble those of their parental lines. This could be attributed to the specific breeding history of these

strains, as the Salina strain is a hybrid of male Sultana and female Red NIFI, and may have inherited distinct traits from both parental lines (Kwikiriza et al., 2023). The overlapping clusters observed in the PCA further reinforce the likelihood that the majority of the fish sampled originate from a common genetic pool, which aligns with the theory that shared environmental pressures or genetic backgrounds can lead to similar physical traits (Le Moan et al., 2021). However, the clear distinction seen in the female Salina underscores the presence of significant morphometric variation, likely driven by their unique genetic backgrounds or selective breeding This distinctiveness could have practices. important implications for understanding the genetic diversity and potential breeding strategies of these populations.

Hierarchical cluster analysis (HCA) plays a pivotal role in fish morphometric research, particularly in identifying similarities and differences in morphological characteristics across various populations. This method provides a visual representation of relationships through dendrograms, which depict clusters of individuals or groups based on their morphological traits (Ondang et al., 2019). HCA not only facilitates the identification of distinct morphological groups but also serves as an essential tool in taxonomy, stock structure analysis, evolutionary studies (Rasheeq et al., 2023). By organizing individuals into hierarchical clusters, researchers can observe patterns that may otherwise remain hidden, offering insights into the biological and ecological significance of these groupings.

In the present study, HCA revealed the formation of two distinct clusters as shown in the dendrogram Figure 5. The first cluster comprised the male *Sultana* and the male *Salina*, while the second cluster included the female *Salina*, the female *Red NIFI*, the male *Red NIFI*, and the female Sultana. In the second cluster, female *Red NIFI* and female *Salina* are separated from the nonparental group of male *Red NIFI* and the female *Sultana*. This dendrogram, along with the PCA results, highlights a statistical similarity distance on real biological inheritance between

Salina and its parental strain. It also implies potential maternal effects between female Red NIFI and female Salina. Not to mention that both male and female Salina exhibit a red body color with small portions of dark spots scattered on their body, which is another implication of maternal dominance in Salina strain, since female Red NIFI exhibit a red body color (Figure 1). Maternal effects can significantly influence traits in tilapia, including body weight, body depth, and fillet weight. These effects arise from the maternal transmission of mRNA transcripts, cytoplasmic elements, and mitochondrial DNA (mtDNA), all of which play crucial roles in early development. Because mtDNA is inherited exclusively from the female, the interaction between mitochondrial and nuclear genomes is known as mitonuclear coevolution, which shapes phenotypic traits such as metabolic rate, growth, and morphology (Quéméneur et al., 2022). Another mechanism is that maternal gene expression can shape offspring phenotype through egg composition, hormone deposition, and the early developmental environment, independent of direct DNA inheritance (Joshi et al., 2020). Another study suggests the larger or better-conditioned females often produce larger eggs with greater yolk reserves, enhancing early larval growth and influencing body shape and size during the juvenile stage (Koenigbauer and Höök, 2023).

The complementary nature of PCA and HCA in this analysis highlights the complexity of the morphometric relationships among the different tilapia groups. While PCA offers a broad, multivariate perspective on trait similarities and differences, HCA provides a more granular view, delineating specific clusters that represent inherent groupings within the data. integration of both methods allows for a more comprehensive understanding of morphometric variation, which is essential for interpreting the biological and ecological implications of these findings (Silva, 2003). In this study, the PCA revealed substantial morphological overlap among most populations. Notably, male Salina overlapped more extensively with male Sultana than with female Red NIFI. This pattern is

consistent with the HCA, which clustered male Salina and male Sultana within the same branch, whereas the female Red NIFI formed. These results suggest that male Salina morphologically resembles its male parent more strongly. In contrast, female Salina, while still overlapping with both parental populations in the PCA, exhibited the most distinguishable cluster separation among all groups. The HCA placed female Salina closer to female Red NIFI and distinctly apart from male Sultana, indicating that female Salina inherits more morphological similarity from its female parent and shows more differentiated morphometric traits compared to male Salina. Taken together, the concordance between PCA and HCA highlights that male and female hybrids express different parental resemblance patterns, reflecting potential sexlinked influences on morphological inheritance. Such detailed analysis is crucial in fisheries research, as it informs conservation strategies, breeding programs, and the management of fish stocks.

Condition Factor and Length-Weight Relationship Correlation

The condition factor is a widely recognized and essential indicator in fisheries science, frequently employed to evaluate the health status, body condition, and growth performance of fish populations in various environments. examining the weight-to-length ratio, the condition factor provides insight into how well individual fish are thriving, often reflecting underlying biological and ecological conditions. In this study, the condition factor (K) differed among the populations observed (p < 0.05), as shown in Figure 6. Both male and female Salina groups demonstrated higher condition factors compared to the male and female Red NIFI groups, although no significant differences were found when compared to male and female Sultana populations. Importantly, all the populations exhibited condition factors greater than 1, which is a key indicator of fish health and overall wellbeing during culture (Jisr et al., 2018). Numerous factors impact the condition factor, with intrinsic aspects such as sex and developmental stage

Table 1. Standardized morphometric traits of tilapia populations

Populations	TL:SL DL:SL	DF:SF	TS:TO	HL:SL	WID:SL	PL:SL	CPD:SL	ED:SL	SNL:SL	BW:SL
Female Salina 1.22±0.01 ^d 0.59±0.01 ^{ab} 0.23±0.01 ^c 0.39±0.01 ^b 0.40±0.01 ^{bc} 0.32±0.04 ^c 0.15±0.00 ^a 0.06±0.01 ^{ab} 0.12±0.00 ^d 16.33±1.7 ^c	1.22±0.01 ^d	0.59±0.01ab	0.23±0.01°	0.39±0.01b	0.40±0.01bc	0.32±0.04€	0.15±0.00a	0.06±0.01 ^{ab}	0.12±0.00d	16.33±1.7°
Male Salina 1.25±0.01 ^c 0.61±0.02 ^a 0.26±0.01 ^b	1.25±0.01°	0.61±0.02 ^a	0.26±0.01 ^b	0.41±0.01 ²	0.43±0.012	0.36 ± 0.02^{ab}	0.16±0.01³	0.06 ± 0.00^{ab}	0.12 ± 0.01^{bc}	20.37±1.92 ^d
Female Sultana 1.26±0.01 ^{abc} 0.60±0.01 ^a	1.26 ± 0.01^{abc}	0.60±0.01	0.26±0.01 ^b	0.39 ± 0.01^{b}	0.40 ± 0.01^{bc}	0.39±0.02	0.15 ± 0.00^{a}	0.06 ± 0.01	0.12 ± 0.01^{cd}	28.20±3.37°
Male Sultana 1.27±0.012b 0.60±0.012	1.27±0.01 ^{ab}	0.60±0.01₃	0.28±0.01 ^a	0.41 ± 0.02^{3}	0.43 ± 0.02^{a}	0.38 ± 0.03 ²	0.16±0.01	0.06±0.01₃	0.13 ± 0.01^{ab}	24.41±2.02°
Female Red NIFI 1.25±0.01 bc 0.58±0.01b	1.25±0.01bc	0.58 ± 0.01^{b}	0.26±0.01b	0.38 ± 0.02^{b}	0.39±0.02	0.35±0.04abc	0.15±0.01	0.06 ± 0.00^{ab}	0.12 ± 0.01^{cd}	19.12±2.63de
Male Red NIFI 1.27±0.02 ^a 0.6±0.01 ^{ab}	1.27±0.02	0.6±0.01ab	0.27 ± 0.02^{ab}	0.39 ± 0.02^{b}	0.41±0.01 ^b	0.38 ± 0.02^{bc}	0.16±0.01ab	0.05±0.01€	0.14±0.012	32.73±1.74 ^a
F	18.82	5.21	20.12	10.03	20.14	8.52	3.33	4.58	9.64	70.81
Ь	0	0.001	0	0	0	0	0.01	0.002	0	0

Statistically significant differences (p < 0.05) indicated by different letters.

Table 2. Morphometric measurements of tilapia populations before standardized with SL along with standard deviations

	Total	Standard	Standard Dorsal Fin Caudal Fin	Caudal Fin	Head	Body	Pectoral	Caudal	Eye	Snout	Rody Wolaht
Populations	Length (TL)	Length (SL)	Length (DL)	Length (CL)	Length (HL)	Width (WID)	Fin Length (PL)	Depth (CPD)	Diameter (ED)	Length (SNL)	(BW)
Female Salina	24.81±1.22	20.35±1.04	12.1±0.65	4.64±0.29	7.94±0.46	8.24±0.49	6.42±0.93	3.10±0.14	1.22±0.08	2.35±0.13	24.81±1.22 20.35±1.04 12.1±0.65 4.64±0.29 7.94±0.46 8.24±0.49 6.42±0.93 3.10±0.14 1.22±0.08 2.35±0.13 333.43±47.74
Male Salina	27.49±1.39	27.49±1.39 22.03±1.26 13.4±0.95	13.4 ± 0.95	5.75±0.31	9.09 ± 0.43	9.63±0.58	7.91±0.61	3.54 ± 0.20	1.31 ± 0.12	2.75±0.29	9.09±0.43 9.63±0.58 7.91±0.61 3.54±0.20 1.31±0.12 2.75±0.29 450.95±66.51
Female Sultana	33.38±2.26	33.38±2.26 26.57±1.86 15.9±0.97	15.9±0.97	6.97±0.39	10.34±0.79	10.74±0.74	10.34±0.79 10.74±0.74 10.3±0.9		1.47±3.22	3.22 ± 0.34	4.09±0.28 1.47±3.22 3.22±0.34 754.46±131.92
Male Sultana Female Red NIFI	30.03±0.94 28.16±2.32	30.03±0.94 23.7±0.74 14.28±0.45 28.16±2.32 22.53±1.91 13.1±1.29	14.28±0.45 13.1±1.29	6.61±0.44 5.89±0.55	9.8±0.31 8.6±0.67	10.28±0.42 8.71±0.73	9.08±0.67 7.89±0.7	3.79±0.18 3.44±0.30	1.52±0.15 1.33±0.11	3.09±0.20 2.74±0.31	9.8±0.31 10.28±0.42 9.08±0.67 3.79±0.18 1.52±0.15 3.09±0.20 579.52±61.12 8.6±0.67 8.71±0.73 7.89±0.7 3.44±0.30 1.33±0.11 2.74±0.31 434.61±99.31
Male Red NIFI	37.36±1.32	37.36±1.32 29.43±0.89 17.57±0.51	17.57±0.51	7.88±0.57	11.42±0.56	11.94±0.45	11.42±0.56 11.94±0.45 9.67±0.74	4.62±0.33	1.53 ± 0.18	3.98±0.31	3.98±0.31 964.05±72.27
Average	30.2±4.45	30.2±4.45 24.1±3.33 14.4±2.03	14.4±2.03	6.29±1.11	9.53±1.27	9.92±1.37	8.54±1.49	3.76±0.55	1.40±0.19	3.02 ± 0.58	6.29±1.11 9.53±1.27 9.92±1.37 8.54±1.49 3.76±0.55 1.40±0.19 3.02±0.58 586.17±231.03

Table 3. Summary of effect sizes of 3 Tilapia's strain and sex parameters on standardized traits based on ANOVA p-values and partial η^2 (interpreted using Cohen's benchmarks)

Effect	Traits	<i>p</i> -value	η_p^2
strain	BW:SL	2.22E-16	0.737
strain:sex	BW:SL	6.92E-16	0.726
sex	BW:SL	2.44E-10	0.527
sex	WID:SL	4.59E-10	0.516
strain	TL:SL	3.78E-09	0.512
strain	CL:SL	1.18E-08	0.491
strain	WID:SL	2.95E-07	0.427
sex	CL:SL	1.8E-07	0.399
sex	SNL:SL	3.85E-07	0.382
sex	TL:SL	5.18E-07	0.375
strain	PL:SL	6.72E-06	0.357
sex	HL:SL	5.44E-06	0.320
strain	HL:SL	0.000297	0.260
strain:sex	ED:SL	0.000738	0.234
sex	CPD:SL	0.00039	0.210
strain	SNL:SL	0.002576	0.198
strain:sex	CL:SL	0.003434	0.190
strain:sex	PL:SL	0.004006	0.185
strain	DL:SL	0.004783	0.180
sex	DL:SL	0.001323	0.175
strain	ED:SL	0.050172	0.105
strain:sex	HL:SL	0.065534	0.096
strain:sex	TL:SL	0.096441	0.083
strain:sex	WID:SL	0.242386	0.051
strain:sex	DL:SL	0.258895	0.049
strain:sex	SNL:SL	0.484492	0.026
strain	CPD:SL	0.54491	0.022
strain:sex	CPD:SL	0.577618	0.020
sex	PL:SL	0.522109	0.008
sex	ED:SL	0.916752	0.000

Statistical significance expressed by p < 0.05, while stronger effect on traits expressed by higher η_p^2 .

Table 4. PCA summary on 10 standardized morphometric traits of 60 samples within 6 populations

	PC1	PC2
% Variance	38.17%	22.62%
Standard deviation	1.9537	1.5039
Variable	Loadings	
TL:SL	-0.3900894	-0.3330611
DL:SL	-0.1774408	0.24706297
CL:SL	-0.4086349	-0.2381186
HL:SL	-0.3609769	0.39050834
WID:SL	-0.3629046	0.36461521
PL:SL	-0.2701067	0.02182457
CPD:SL	-0.3973716	0.17385839



ED:SL	-0.05006277	0.44217524
SNL:SL	-0.3061702	-0.2589871
BW:SL	-0.2454592	-0.4388535

The dimension axis of PC1 explains the most variance, following the dimension PC2. Higher loading value indicates that the variable has a stronger contribution to the principal component.

Table 5. Length-Weight model performance comparison for standard (Le Cren) and piecewise regression approaches across 6 tilapia populations

Population	Model	RMSE	Max Abs Bias	AIC*
Female Salina	Le Cren	22.38	14.11	-18.86
	Piecewise	21.57	11.98	-15.88
Male Salina	Le Cren	9.44	5.40	-42.14
	Piecewise	8.93	4.12	-39.58
Male Red NIFI	Le Cren	41.28	10.54	-29.42
	Piecewise	10.47	2.42	-51.66
Female Red NIFI	Le Cren	28.57	10.98	-21.39
	Piecewise	13.09	6.76	-29.06
Male Sultana	Le Cren	34.86	9.26	-22.81
	Piecewise	17.67	5.99	-30.91
Female Sultana	Le Cren	36.73	9.32	-27.84
	Piecewise	34.83	9.95	-24.75

^{*}indicates that for model selection, the lower the value means better fit model.

Values for RMSE (root mean square error) and Max Abs Bias are in grams. AIC is Akaike's Information Criterion.

Table 6. Length-weight relationship of each tilapia population calculated using the standard model (Le Cren, 1951)

Population	n	Standard Length (SL)	Body Weight (BW)	а	b
Female Salina	10	20.35±1.04	333.43±47.74	-0.7373	2.4895
Male Salina	10	22.03±1.26	450.95±66.51	-0.8496	2.6068
Female Sultana	10	26.57±1.86	754.46±131.92	-0.8222	2.5945
Male Sultana	10	23.70 ± 0.74	579.52±61.12	-1.1973	2.8795
Female Red NIFI	10	22.53±1.91	434.61±99.31	-0.4729	2.2958
Male Red NIFI	10	29.43±0.89	964.05±72.27	0.0385	2.0050

If the *b* value = 3.00, this indicates isometric growth, b < 3.00 indicates a negative allometric growth, *b* value > 3.00 suggests a positive allometric growth.

playing key roles, while external environmental factors, including water quality, temperature, and food availability. Consequently, K measurements offer valuable data for assessing habitat quality and guiding fishery management efforts to sustain population health (Adeogun *et al.*, 2016; Reyes, 2024). Moreover, post hoc analysis confirmed

that male and female *Salina* strains had significantly higher condition factors than their *Red NIFI* counterparts, indicating that genetic strain plays a role in growth performance. These results are consistent with findings from Gunadi *et al.* (2021), who reported variability in K values among tilapia strains in Indonesia. Furthermore,



environmental factors such as sex and geographical location have been identified as significant factors to variations in K values, complexity reinforcing the of growth performance evaluation in aquaculture systems (Oyebola et al., 2022). In aquaculture context, the condition factor is a crucial parameter that reflects the physiological and nutritional status of fish. A higher K value generally indicates better growth performance and exhibits better feed conversion ratios (FCR) (Barylo et al., 2021).

The length-weight relationship (LWR) in fish biology is a crucial parameter for understanding growth dynamics by correlating length and weight (Jisr et al., 2018). In this study, we compared the performance of 2 known models: standard Le Cren and Piecewise regression for LWR analysis of 6 tilapia populations as shown in Table 5. The Piecewise regression model occasionally yielded slightly lower Root Mean Square Error (RMSE) and bias values than the standard allometric model (Le Cren), particularly in male *Red NIFI* and female Red NIFI. However, these improvements were not consistent across all populations, and the associated AIC differences were modest in several cases (e.g., female Salina and female Sultana). Applying the standard Le Cren model uniformly offers important advantages: it maintains a simple, biologically interpretable form through a single exponent (b) that captures the length-weight scaling, facilitates direct comparison among populations, and avoids the risk of overfitting to population-specific irregularities that may reflect sampling variation rather than true biological shifts. As for interpretation, the b value of the LWR equal to 3 indicates isometric growth, where weight and length increase proportionally. The b value less than 3 indicates negative allometric growth, meaning weight increases more slowly than length, which is typical of organisms that become slimmer as they grow. Conversely, the b value greater than 3 suggests positive allometric growth, where weight increases more rapidly than length (Asmamaw et al., 2019; Jisr et al., 2018). Given its broad acceptance in fisheries science as a benchmark for length-weight analysis, the

standard Le Cren model provides a coherent and comparable framework for interpreting growth patterns across diverse populations in this study.

We found that all the populations have a b value lower than 3 indicating all the populations have negative allometric growth (Table 6 and Figure 7). The male *Sultana* groups have *a b* value indicating more 3 (2.8795), proportional length and weight compared to other populations. The lowest b value was found in male Red NIFI (2,005), suggesting this strain possesses the slimmest body type among the groups. Both male and female Salina have b values greater than both male and female Red NIFI, meaning the Salina strain has a more proportional body compared to the Red NIFI strain. This suggests that Salina has a genetic that adaptation favours their balanced development, including greater adaptability to both freshwater and brackish water environments, which allows efficient energy utilization and steady growth, unlike the Red NIFI strain, which may exhibit less balanced development in terms of the length-weight growth. Environmental factors, including water quality and feeding inputs, can also influence growth patterns, contributing to the observed differences in LWR across strains. Variations in parameters such as dissolved oxygen, temperature, pH, and nutrient availability directly affect metabolic efficiency, feed utilization, and overall physiological performance. Likewise, differences in feed nutrient composition, and feeding quality, can alter growth trajectories regimes influencing protein synthesis, lipid deposition, and energy allocation. These environmental interactions not only shape condition factors and morphometric traits but may also interact with genetic backgrounds, amplifying or masking inherent strain-specific growth potential (Kamble et al., 2024; Washim et al., 2022). In this study, we obtained the b values of the Length-Weight Relationship (LWR) ranging from 2.0050 to 2.8795, is consistent with the findings of previous reports indicating that b values for tilapia was between 2 and 4 (Diallo et al., 2022; Kamble et al., 2024; Wagaw et al., 2024). The negative allometry observed in this study indicates that body weight increases at a slower rate than body length. This pattern suggests a growth strategy in which energy is preferentially allocated to linear growth rather than mass accumulation, which may confer advantages such as improved swimming efficiency and reduced predation risk during early life stages (Xie et al., 2024). From a physiological perspective, negative allometry may reflect metabolic scaling, where lower maintenance energy requirements allow more resources to be directed toward reproductive output and survival under challenging environmental conditions. This pattern suggests that individuals with relatively smaller body sizes may possess adaptive advantages in environments with limited resources, as their reduced energetic demands enable greater allocation of nutrients and energy to essential functions such as gametogenesis, immune defense, and stress resilience. Consequently, negative allometry can be interpreted not only as a constraint of growth but also as an adaptive strategy that optimizes fitness and enhances long-term population persistence in fluctuating or resource-poor habitats (Wiff and Roa-Ureta, 2008; Pontzer and McGrosky, 2022).

The coefficient of determination, or Rsquared (R²), is a key metric in regression analysis that quantifies the proportion of variance in the dependent variable explained by the model's independent variables. It reflects the model's explanatory power, with values ranging from 0 to 1, where higher values denote a better fit of the model to the observed data (Chicco et al., 2021). In this study, the R² values for the length-weight relationship (LWR) ranged from 0.6602 to 0.9776. An R² value above 0.9 indicates a strong correlation between weight and length, demonstrating that length is highly accurate predictor of weight (Deekrachang et al., 2024). Specifically, R² value above 0.9 were observed in male Salina and female Sultana strains, suggesting particularly robust LWR. A slightly lower R² value of 0.8957 was found in female Red NIFI group, while female Salina group exhibited an R² value of 0.7526. Male *Sultana* and male *Red* NIFI had R² values below 0.7, indicating a weaker correlation between length and weight in these

groups. In biological research, an R² values above 0.7 are generally considered strong, values between 0.3 and 0.7 reflect a moderate correlation, and values below 0.3 reflect a weak correlation (Rusakov, 2023). These findings highlight the variability in LWR among different strains, which may be influenced by genetic factors, environmental conditions or strain-specific growth patterns.

CONCLUSION

The results revealed overlapping morphometric traits across most populations, with the exception of female Salina, which exhibited slight but distinct differences likely reflecting unique traits acquired from crossbreeding between two different strains. Male Salina, in contrast, showed morphometric traits closely aligned with its male parent, the Sultana strain. The condition factor across all populations indicated favourable growth conditions; however, the observed negative allometric growth pattern suggests that length increases more rapidly than body weight, potentially reflecting adaptive tradeoffs in suboptimal environments. While these findings provide important phenotypic insights relevant to breeding strategies, several limitations must be acknowledged. Each strain was reared in a separate pond, with males and females housed in hapas within the same pond. As such, strain and pond effects were confounded, preventing complete separation of genetic influences from environmental effects. Although pond was accounted for as a blocking factor in the statistical analysis, the absence of pond replication means that subtle environmental influences cannot be entirely excluded. Given its low cost, minimal equipment requirements, and proven reliability, the morphometric baseline established in the present study can serve as a practical reference for future applications, including strain certification, selective breeding programs targeting desirable growth and body shape traits, and ecological adaptation assessments to optimize aquaculture performance across different environments. Overall, this research provides the first morphological evidence on the hybridization



outcomes of Salina tilapia under suboptimal salinity, offering insight into their growth patterns, potential reproductive trade-offs, and the balance between hybrid vigor and parental resemblance. The findings also underscore the economic relevance of selective breeding strategies that enhance salinity resilience in tilapia. In hatchery operations, incorporating broodstock that demonstrate tolerance to suboptimal salinity conditions can improve fry survival, growth performance, and overall production stability. For farmers, the use of hybrids such as the Salina strain, particularly when reared in environments closer to their optimal salinity range which may reduce mortality, shorten grow-out periods, and lower feed conversion ratios, ultimately increasing profitability. Future research directions should incorporate replicated common-garden designs to better isolate genetic effects and strengthen evidence for potential maternal dominance effects observed in the Salina strain. In addition, integrating molecular approaches such as microsatellite analysis, mitochondrial DNA sequencing, and SNP genotyping will be essential to complement morphological data and more robustly characterize the genetic diversity and population structure of these tilapia strains.

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AUTHORS' CONTRIBUTIONS

YPB conceived and designed the study. KMD was responsible for fieldwork, fish sampling, and morphometric measurements. Data entry, validation, and statistical analyses were conducted by EIR, HW, WS, and RSA. SS, AFL,

MKF, and NM assisted with the literature review and data interpretation. AA, ARA, IC, and DY contributed to manuscript writing, formatting, and final editing. All authors have read, reviewed, and approved the final version of the manuscript.

COMPETING INTERESTS

The authors declare that they have no competing interests.

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