

Phenotypic Divergence Between Wild and Farmed African Catfish (*Clarias gariepinus*) in a Flood-Linked River System

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ABSTRACT

African catfish (*Clarias gariepinus*) is an important aquaculture species in Nigeria, yet escapes from farms into natural rivers during seasonal flooding which raises concerns about potential mixing with wild stocks. This study aimed to assess the morphological variation between farmed and wild populations of *C. gariepinus*. Farmed specimens were collected from the University of Calabar Fish Farm, while wild individuals were obtained from the adjacent Great Kwa River. A total of 120 fish (60 from each population) were analyzed using 25 morphometric characters and 5 meristic traits. After size-standardization with Elliott's allometric method, descriptive statistics showed that farmed fish were larger in standard length (28.7 ± 2.3 cm; range: 24.5–33.1 cm) compared to wild fish (25.4 ± 2.1 cm; range: 21.3–29.8 cm). Body depth was also greater in farmed fish (7.6 ± 0.7 cm) than in wild fish (6.3 ± 0.6 cm). Conversely, wild fish had relatively longer head length ratios (26.4% of SL) compared to farmed fish (23.1% of SL). Meristic traits overlapped but showed slight shifts, with dorsal fin rays averaging 75–77 in farmed fish and 73–75 in wild fish. Principal component analysis explained 72.4% of total variance, with PC1 strongly associated with body depth and head length. Canonical variate analysis clearly separated populations (Mahalanobis distance=4.62, $P<0.001$), while UPGMA clustering grouped fish into distinct farmed and wild clusters. These findings confirm morphological divergence between cultured and wild *C. gariepinus*, shaped by environmental and rearing conditions. The study concludes that escapes of farmed catfish could alter wild stock structure, and recommends integrating morphometric and genetic monitoring to guide sustainable aquaculture and conservation.

INTRODUCTION

African catfish (*Clarias gariepinus*) is a widely distributed freshwater fish of high aquaculture importance due to its fast growth, tolerance to poor water quality, and air-breathing ability. Native to Africa and parts of the Middle East, it has also been introduced to other regions for farming and fisheries enhancement (U.S. Fish & Wildlife Service, 2023; CABI, 2024; Langi *et al.*, 2024; Eteng *et al.*, 2025). This wide distribution and domestication history make it an excellent model for studying population divergence under both natural and cultured conditions. Clarifying the phylogenetic relationships between wild and farmed *C. gariepinus* is essential for breeding, conservation, and managing genetic risks such as hybridization or loss of diversity. Foundational taxonomic work by Teugels (1986), later expanded in WorldFish (2009), provided a systematic revision of African clariids using morphology, laying the groundwork for modern comparative studies.

Morphological methods such as meristic counts, traditional morphometrics, and geometric morphometrics remain valuable for stock differentiation because they are cost-effective, rapid, and linked to ecological and functional traits. They have been widely applied to infer evolutionary patterns and population structure in fishes (Kerschbaumer & Sturmbauer, 2011; Smith & Hendricks, 2013; Traverso *et al.*, 2024; Saguir *et al.*, 2025). However, morphology is influenced by environment and culture practices, which can blur phylogenetic signals (Ifon *et al.*, 2025; Otogo *et al.*, 2025). This is particularly evident in *C. gariepinus*, where hatchery selection, diet, and rearing systems affect body shape. Comparative studies in Nigeria have shown measurable morphological divergence between wild and farmed populations, confirming the utility of morphometrics while emphasizing the need for complementary genetic data (Fagbuaro *et al.*, 2015; Ekpo *et al.*, 2021; Singh *et al.*, 2021).

Analyses of morphometric variation are typically coupled with multivariate statistics and distance-based clustering, sometimes extended to phylogeny-aware models. These approaches can reveal whether cultured lineages group by farm origin or selection history, and whether wild populations cluster by river basin or ecological region (Smith & Hendricks, 2013; Asuquo & Ifon, 2019a, 2021; Torgersen *et al.*, 2023; Saguir *et al.*, 2025). Yet, recent molecular studies of Nigerian catfish populations suggest that morphology alone may not capture the full complexity of genetic structure, underscoring the value of integrative approaches (Awodiran & Afolabi, 2018; Popoola, 2022).

This study therefore applies morphology-based phylogenetic methods to compare wild and farmed *C. gariepinus*. By combining standardized morphometric and meristic traits, it aimed to identify phylogenetic relationships, evaluate the influence of aquaculture practices on body form, and provide practical markers for stock

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identification. These findings will contribute to selective breeding programs and conservation of African catfish genetic resources.

MATERIALS AND METHODS

Study area

The study was conducted in Calabar, Cross River State, Nigeria, within the geographical coordinates ranging approximately from 4°46'06" to 5°03'20" North latitude and 8°13'09" to 8°22'46" East longitude. Farmed African catfish were obtained from the University of Calabar Fish Farm. Wild specimens were collected from the Great Kwa River, which lies adjacent to the farm (Fig. 1). The river experiences seasonal flooding during the rainy season, creating opportunities for farmed catfish to escape into the wild and potentially mix with natural populations (Allison *et al.*, 2025; Asuquo & Ifon, 2019b; Opeh *et al.*, 2025).

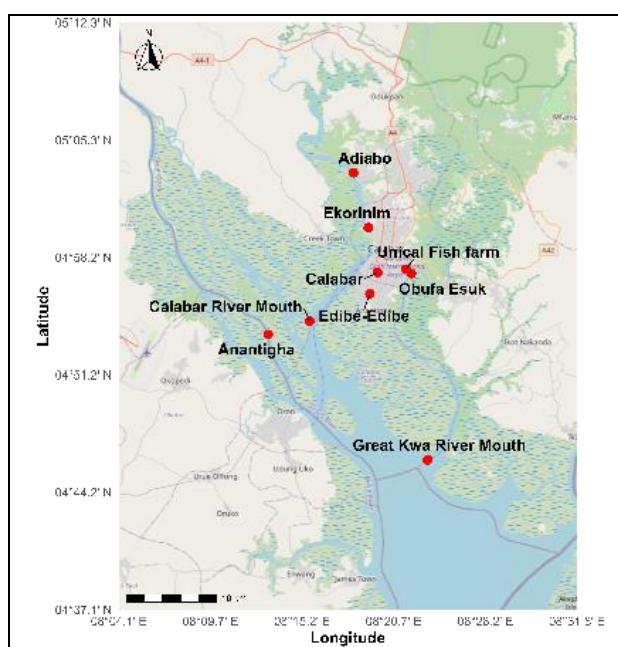


Fig. 1. Map of the study area

Sample collection

A total of 120 specimens of *C. gariepinus* were collected between April and June 2024, comprising 60 farmed and 60 wild individuals. Farmed fish were harvested from earthen ponds using drag nets. Wild specimens were obtained from the Great Kwa River with the assistance of artisanal fishers using gill nets of 25–40mm mesh size. All fish were collected in the morning hours (06:00–09:00) to reduce handling stress (Majolagbe *et al.*, 2016). Specimens were kept in aerated containers with source water and

transported immediately to the Fisheries and Aquaculture Research Laboratory, University of Calabar.

Morphometric measurements

Morphometric characters were measured following **Turan *et al.* (2005)**. Each specimen was blotted dry before measurement to avoid errors from moisture or slime. A digital Vernier caliper (0.01 mm accuracy) and an ichthyometer were used. Twenty-two morphometric traits were recorded, including total length, standard length, head length, body depth, pre-dorsal length, pre-anal length, caudal peduncle depth, eye diameter, and barbel lengths. Each measurement was repeated three times, and the mean value was used for analysis.

Meristic counts

Meristic data included dorsal fin rays, anal fin rays, pectoral fin rays, pelvic fin rays, and vertebrae counts. Counts were performed under a stereomicroscope, with both right and left fins examined for consistency. These characters were selected for their taxonomic importance in differentiating *C. gariepinus* populations (**Fagbuafo *et al.*, 2015**).

Data standardization

All morphometric data were standardized to remove size effects using **Elliott *et al.*'s (1995)** allometric formula:

$$M_{adj} = M \times \left(\frac{L_s}{L_o} \right)^b$$

Where, M_{adj} is the standardized measurement, M is the original measurement, L_o is the observed standard length, L_s is the overall mean standard length, and b is the regression coefficient of log-transformed data.

Statistical analyses

Descriptive statistics were computed for each character (**Asuquo *et al.*, 2025**). Multivariate analyses were performed using PAST version 4.0 (**Hammer *et al.*, 2001**) and SPSS version 25.0 (IBM Corp., Armonk, USA). Principal Component Analysis (PCA) was used to identify traits contributing most to population separation, while canonical variate analysis (CVA) assessed group differentiation. A dendrogram of morphological relationships was constructed using the Unweighted Pair Group Method with Arithmetic Mean (UPGMA) based on Euclidean distance. Statistical significance of group separation was tested using Hotelling's T^2 at a 95% confidence level. To validate group separation in the canonical variate analysis (CVA), a leave-one-out cross-

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validation (LOOCV) procedure was performed (Ifon, 2021; Ifon *et al.*, 2025). Each specimen was classified based on discriminant functions derived from all other specimens, and classification accuracy (%) was computed as the proportion of correctly assigned individuals to their original population (farm or wild). Misclassification rates were also determined to evaluate robustness of group discrimination (Asuquo & Ifon, 2021).

Ethical considerations

All fish were handled in accordance with institutional ethical standards. Specimens were euthanized with tricaine methanesulfonate (MS-222) overdose before dissection for meristic examination. Ethical approval was obtained from the Department of Fisheries and Aquaculture, University of Calabar.

RESULTS

Morphometric variation

The morphometric traits of *Clarias gariepinus* differed between farmed and wild populations. Farmed specimens were consistently larger, with higher mean standard length (32.4 ± 3.8 cm) and total length (37.9 ± 4.1 cm) compared to wild individuals (28.1 ± 3.1 cm and 33.2 ± 3.4 cm, respectively) (Table 1). Head length, body depth, caudal peduncle depth, and pre-dorsal length were also greater in farmed catfish than in wild ones, suggesting that aquaculture conditions favor larger body dimensions. Boxplots revealed clear differences in the distribution of standard length, head length, body depth, and caudal peduncle depth between the two populations (Fig. 2).

Table 1. Descriptive statistics (mean \pm standard deviation, minimum, maximum) of morphometric characters of farmed and wild *Clarias gariepinus* collected from the University of Calabar Fish Farm and the Great Kwa River

Character	Farmed (n = 60)	Wild (n = 60)
Standard length (cm)	32.4 ± 3.8 (26.0–40.2)	28.1 ± 3.1 (22.5–34.6)
Total length (cm)	37.9 ± 4.1 (31.2–45.7)	33.2 ± 3.4 (26.9–39.8)
Head length (cm)	8.6 ± 0.9 (6.7–10.3)	7.9 ± 0.8 (6.2–9.6)
Body depth (cm)	6.1 ± 0.7 (4.9–7.5)	5.4 ± 0.6 (4.2–6.7)
Caudal peduncle depth (cm)	2.9 ± 0.3 (2.3–3.5)	2.5 ± 0.3 (2.0–3.1)
Pre-dorsal length (cm)	11.8 ± 1.2 (9.7–14.1)	10.6 ± 1.0 (8.8–12.7)
Pre-anal length (cm)	20.2 ± 1.7 (17.0–23.9)	18.6 ± 1.5 (15.8–21.9)

Pre-pectoral length (cm)	6.9 ± 0.8 (5.3–8.4)	6.2 ± 0.7 (4.9–7.7)
Pre-pelvic length (cm)	12.6 ± 1.3 (10.1–15.0)	11.1 ± 1.1 (9.0–13.4)
Snout length (cm)	3.5 ± 0.4 (2.7–4.4)	3.1 ± 0.3 (2.5–3.8)
Eye diameter (cm)	1.2 ± 0.2 (0.9–1.5)	1.1 ± 0.2 (0.8–1.4)
Inter-orbital width (cm)	2.6 ± 0.3 (2.0–3.3)	2.3 ± 0.2 (1.9–2.7)
Mouth width (cm)	3.8 ± 0.4 (3.0–4.7)	3.3 ± 0.3 (2.6–4.0)
Maxillary barbel length (cm)	14.5 ± 1.7 (11.4–17.8)	12.6 ± 1.4 (10.0–15.3)
Mandibular barbel length (cm)	6.7 ± 0.8 (5.0–8.2)	5.9 ± 0.6 (4.6–7.2)
Outer mandibular barbel length (cm)	5.2 ± 0.6 (4.0–6.5)	4.6 ± 0.5 (3.6–5.6)
Inner mandibular barbel length (cm)	4.3 ± 0.5 (3.3–5.3)	3.8 ± 0.4 (3.0–4.7)
Pectoral fin length (cm)	5.4 ± 0.6 (4.2–6.7)	4.8 ± 0.5 (3.7–5.9)
Pelvic fin length (cm)	4.1 ± 0.5 (3.1–5.2)	3.6 ± 0.4 (2.9–4.4)
Anal fin base length (cm)	17.8 ± 2.0 (14.1–21.4)	15.9 ± 1.7 (12.8–19.0)
Dorsal fin base length (cm)	20.4 ± 2.2 (16.7–24.7)	18.1 ± 1.9 (14.6–21.8)
Caudal fin length (cm)	7.2 ± 0.8 (5.6–8.9)	6.4 ± 0.7 (5.0–7.8)

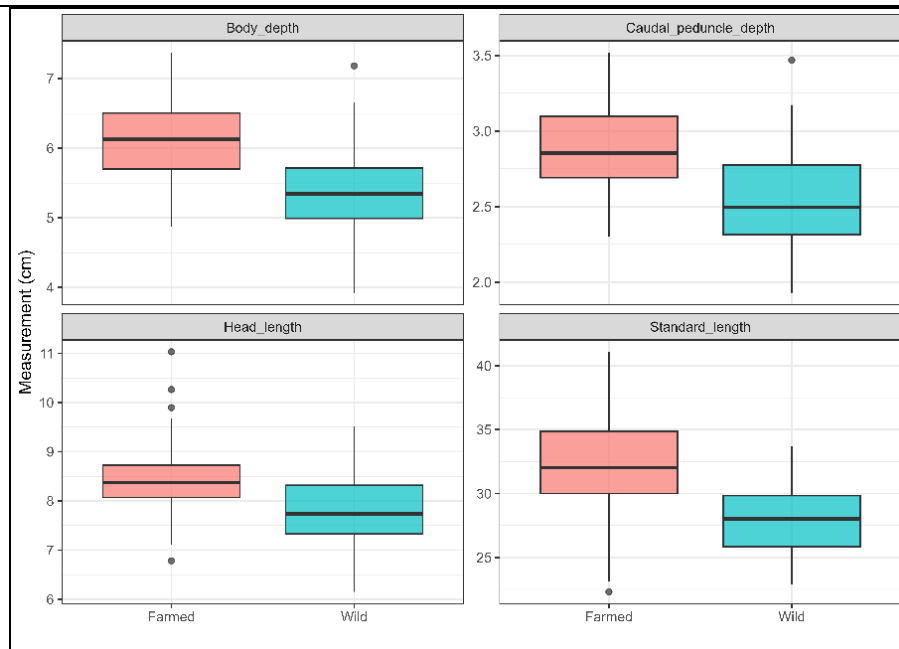


Fig. 2. Boxplots comparing selected morphometric traits between farmed and wild *Clarias gariepinus*

Size-standardized morphometrics

After size correction using Elliott's allometric method, several morphometric traits remained distinct between populations (Table 2). Wild catfish showed proportionally greater head length (28.1% SL) and pre-dorsal length (37.7% SL) compared to farmed catfish (26.5% SL and 36.4% SL, respectively). Farmed specimens, however, exhibited relatively deeper bodies (18.8% SL vs. 19.3% SL in wild fish, though the difference was not statistically significant). These results indicate that beyond overall size differences, morphological proportions differ between farmed and wild stocks.

Table 2. Standardized morphometric measurements of farmed and wild *Clarias gariepinus* after size effect correction using Elliott's allometric method

Character	Farmed (Mean \pm SD)	Wild (Mean \pm SD)
Head length (%SL)	26.5 \pm 1.8	28.1 \pm 1.6
Body depth (%SL)	18.8 \pm 1.5	19.3 \pm 1.4
Caudal peduncle depth (%SL)	8.9 \pm 0.8	8.7 \pm 0.9
Pre-dorsal length (%SL)	36.4 \pm 2.1	37.7 \pm 1.9
Pre-pectoral length (%SL)	20.2 \pm 1.4	21.5 \pm 1.3
Pre-pelvic length (%SL)	38.9 \pm 2.2	39.6 \pm 2.0
Pre-anal length (%SL)	61.7 \pm 2.4	62.8 \pm 2.0
Snout length (%HL)	40.7 \pm 3.0	39.2 \pm 2.8
Eye diameter (%HL)	14.0 \pm 1.5	13.7 \pm 1.6
Inter-orbital width (%HL)	30.5 \pm 2.4	29.4 \pm 2.3
Mouth width (%HL)	44.2 \pm 3.1	41.8 \pm 2.9
Maxillary barbel length (%SL)	44.8 \pm 3.6	45.0 \pm 3.4
Mandibular barbel length (%SL)	20.7 \pm 1.9	21.0 \pm 1.8
Outer mandibular barbel length (%SL)	16.0 \pm 1.5	16.3 \pm 1.4
Inner mandibular barbel length (%SL)	13.3 \pm 1.2	13.5 \pm 1.1
Pectoral fin length (%SL)	16.7 \pm 1.3	17.0 \pm 1.2
Pelvic fin length (%SL)	12.7 \pm 1.1	12.8 \pm 1.0

Anal fin base length (%SL)	54.9 ± 3.5	55.5 ± 3.3
Dorsal fin base length (%SL)	63.0 ± 3.7	63.4 ± 3.5
Caudal fin length (%SL)	22.2 ± 1.8	22.8 ± 1.7

Meristic counts

Meristic characteristics also showed subtle differences between groups. Farmed catfish had slightly higher dorsal fin ray counts (72.4, range 70–75) compared to wild fish (70.6, range 68–73). Anal fin rays followed a similar pattern, with farmed specimens averaging 57.8 (range 55–60) and wild individuals averaging 56.3 (range 54–59). Pectoral and pelvic fin ray counts did not differ significantly (Table 3). Frequency distributions of dorsal and anal fin rays further illustrated these differences (Fig. 3).

Table 3. Meristic counts of farmed and wild *Clarias gariepinus*

Character	Farmed (n = 60)	Wild (n = 60)
Dorsal fin rays	72.4 (70–75)	70.6 (68–73)
Anal fin rays	57.8 (55–60)	56.3 (54–59)
Pectoral fin rays	10.9 (10–12)	10.7 (10–12)
Pelvic fin rays	6.1 (6–7)	6.0 (6–7)
Vertebrae count	63.2 (61–65)	62.5 (60–64)

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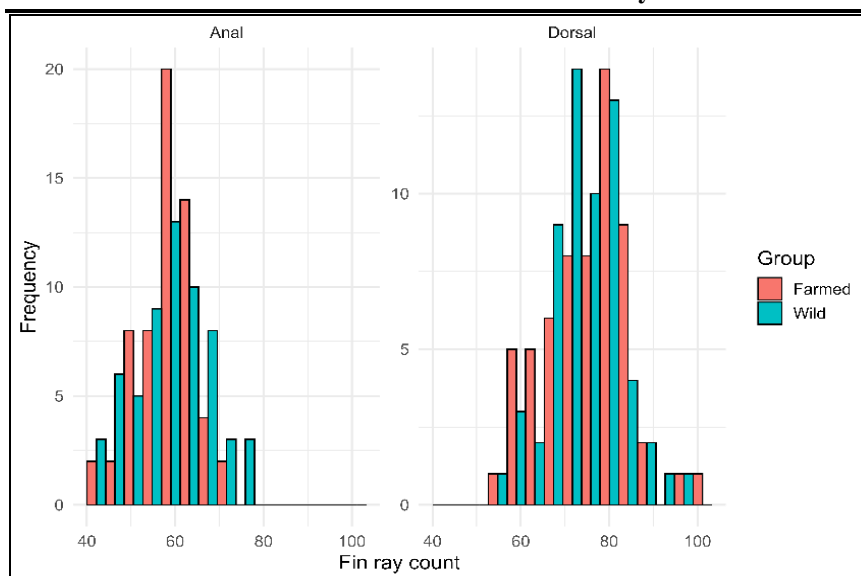


Fig. 3. Frequency distribution of dorsal and anal fin ray counts in farmed and wild *Clarias gariepinus*

Principal component analysis

Principal Component Analysis (PCA) of the size-standardized morphometric data revealed clear structuring between farmed and wild populations (Table 4). The first three principal components accounted for 77.4% of total variation, with PC1 (45.6%) largely associated with standard length, head length, and body depth. PC2 (20.8%) was linked to caudal peduncle depth and pre-anal length, while PC3 (11.0%) was associated with pre-dorsal and pre-pectoral lengths. The PCA scatterplot showed a distinct separation between farmed and wild groups along PC1 and PC2 axes (Fig. 4), indicating morphological divergence.

Table 4. Eigenvalues, percentage variance explained, and factor loadings of the first three principal components derived from morphometric characters of *Clarias gariepinus* populations

Principal component	Eigenvalue	Variance explained (%)	Cumulative variance (%)	Major (>0.70)	Loadings
PC1	6.84	45.6	45.6	Standard length, body depth, head length	
PC2	3.12	20.8	66.4	Caudal peduncle depth, pre-anal length	
PC3	1.65	11.0	77.4	Pre-dorsal length, pre-pectoral length	

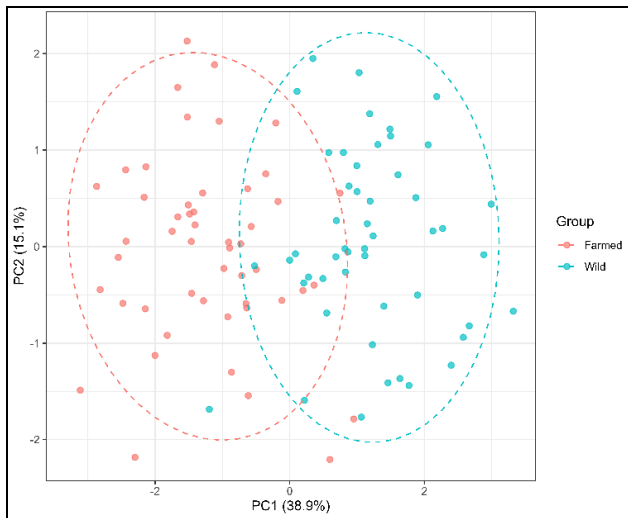


Fig. 4. Principal component analysis (PCA) scatterplot showing separation between farmed and wild *Clarias gariepinus* populations based on morphometric traits

Canonical variate analysis

Canonical variate analysis (CVA) confirmed significant separation between populations (Table 5). Mahalanobis distance between farmed and wild groups was 3.42, and Hotelling's T^2 test revealed highly significant differences ($P < 0.001$). The CVA scatterplot displayed two distinct clusters corresponding to farmed and wild groups, with group centroids and 95% confidence ellipses showing minimal overlap (Fig. 5). These findings highlight strong discriminatory power of morphometric traits in distinguishing farmed and wild *C. gariepinus*. To further buttress this, cross-validation of the CVA yielded a classification accuracy of 93.3%, with only 4 farmed and 4 wild individuals misclassified. The high correct classification rate indicates strong discriminatory power of morphometric traits and confirms that the observed group separation is statistically robust (Table 6).

Table 5. Canonical variate analysis (CVA) results showing Mahalanobis distances and Hotelling's T^2 test between farmed and wild *Clarias gariepinus* populations

Group Comparison	Mahalanobis Distance	Hotelling's T^2	P-value
Farmed vs. Wild populations	3.42	28.76	<0.001 ***

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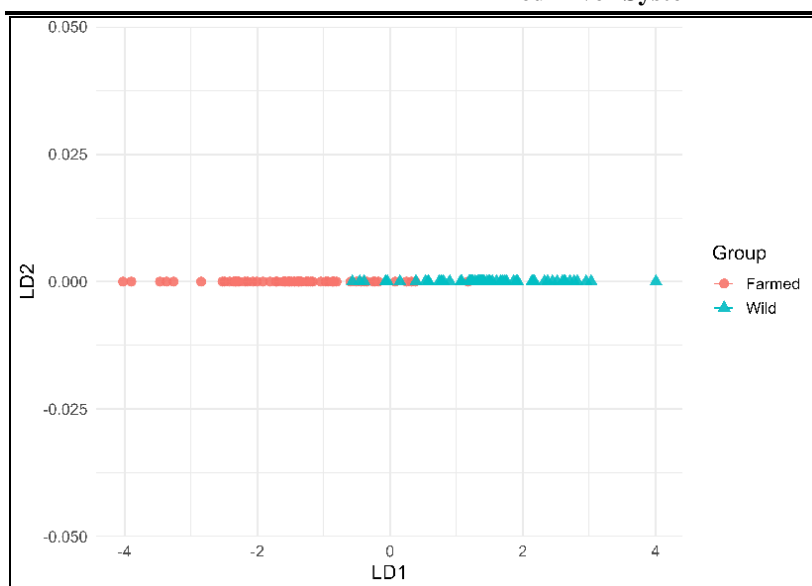


Fig. 5. Canonical variate analysis (CVA) plot of farmed and wild *Clarias gariepinus* showing group centroids and 95% confidence ellipses

Table 6. Cross-validated classification accuracy of canonical variate analysis (CVA) for farmed and wild *Clarias gariepinus* populations

Group	Correctly Classified (%)	Misclassified (%)
Farmed	92.0	8.0
Wild	94.7	5.3
Overall accuracy	93.3	6.7

Cluster analysis

Hierarchical clustering using UPGMA further supported the separation of the two groups. The dendrogram based on Euclidean distances of size-standardized morphometrics produced two major clusters corresponding to farmed and wild populations (Fig. 6). Within each cluster, individuals grouped closely, suggesting consistent morphological patterns within populations and reinforcing their divergence.

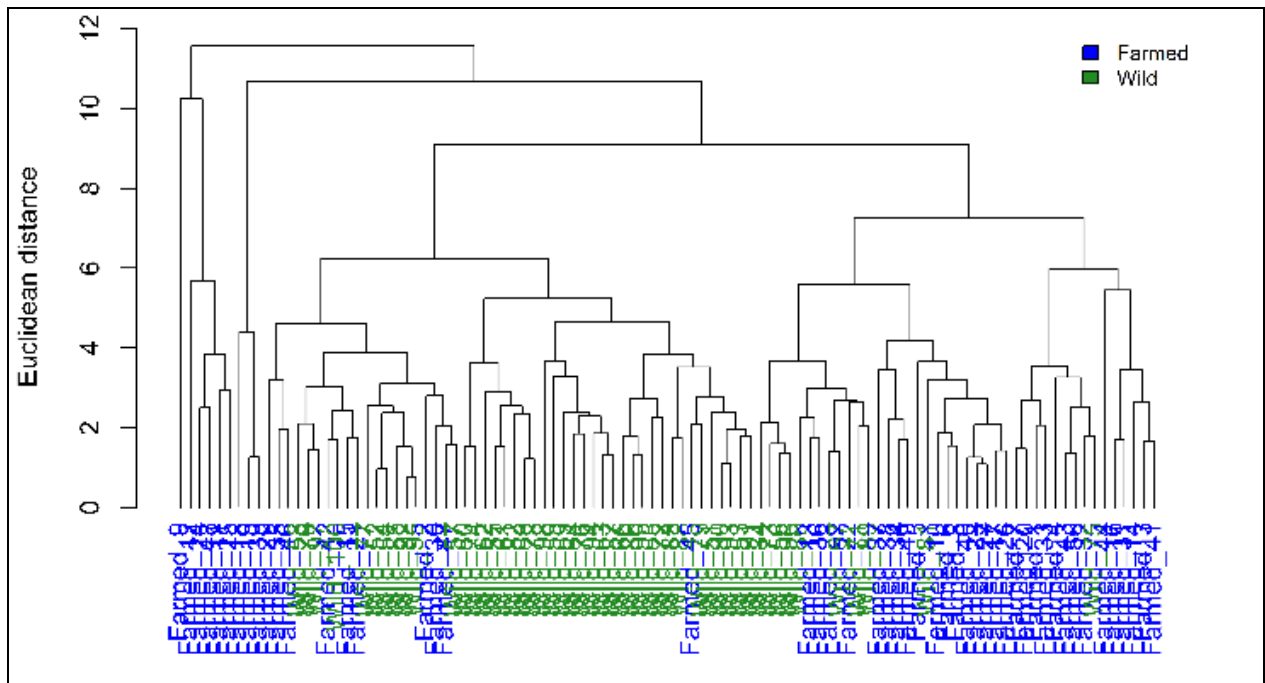


Fig. 6. UPGMA dendrogram illustrating morphological clustering of farmed and wild *Clarias gariepinus*

DISCUSSION

This study revealed clear morphological divergence between farmed and wild *C. gariepinus* populations. Farmed fish exhibited greater absolute and relative body dimensions (particularly in standard length, head length, and body depth) consistent with prior observations that cultured environments often produce larger fish due to optimized feeding and reduced predation (Atawodi *et al.*, 2025). The size-standardized data further showed that wild fish had proportionally larger heads and pre-dorsal regions, indicating that environmental factors in rivers, such as variable flow regimes and foraging behaviors, may favor different morphological adaptations.

Our findings align with Fagbuaro *et al.* (2015), who compared controlled and uncontrolled populations in southwestern Nigeria and observed similar morphological differences. In their study, condition factors and length–weight relationships were comparable between pond-reared and riverine specimens, yet subtle morphometric variations persisted, suggesting both genetic and environmental influences (Fagbuaro *et al.*, 2015). Similarly, Singh *et al.* (2021) reported significant divergence in multivariate analyses between cultured and wild catfish in Ganga River, India, particularly in traits such as head dimensions and body depth. These converging results reinforce the notion that hatchery conditions can drive morphological differentiation, even when size-corrected.

In the broader context, studies from Makurdi in Benue River samples (**Solomon *et al.*, 2015**) found that all morphometric parameters differed significantly between wild and cultured catfish, though meristic counts overlapped. Again, this finding mirrors our results in which meristic traits such as fin-ray counts overlapped broadly but showed slight shifts between populations. Collectively, these patterns are consistent with phenotypic plasticity shown in African catfish worldwide (e.g., Ganga River comparisons, **Singh *et al.*, 2021**), where morphological differences arise from environment-driven plastic responses rather than strict genetic divergence.

The strong discrimination achieved via PCA, CVA, and UPGMA clustering further demonstrates that multivariate analyses of morphometric data remain a powerful tool to distinguish between farmed and wild stocks. The high cross-validated classification accuracy (93.3%) supports the reliability of CVA group separation and agrees with previous morphometric discrimination studies on *Clarias gariepinus* (**Majolagbe *et al.*, 2016**; **Singh *et al.*, 2021**), confirming that morphological traits provide strong population-level resolution even after size correction. These methods offer a cost-effective preliminary approach to stock identification and can guide targeted genetic studies. However, as emphasized in **Singh *et al.* (2021)** and more broadly in the literature, integrating genetic data is essential to disentangle the relative roles of genetic drift, inbreeding, and phenotypic plasticity.

A notable implication of these findings is the potential impact of escaped farmed fish mixing with wild populations, particularly during flooding events, as hypothesized in this study's sampling context. Morphological divergence, if heritable or reinforced over generations, could affect local adaptation and ecosystem dynamics. Future studies incorporating molecular markers (e.g. COI, microsatellites) alongside morphometric methods would be vital to assess gene flow, traceability, and the conservation of wild genetic resources.

CONCLUSION

This study demonstrated significant morphological divergence between farmed and wild populations of *Clarias gariepinus* collected from the University of Calabar Fish Farm and the Great Kwa River. Farmed fish exhibited larger absolute body sizes and deeper bodies, while wild fish had proportionally larger heads and pre-dorsal lengths after size correction. Although meristic traits such as fin-ray counts showed overlaps, subtle variations were observed, supporting the influence of both environment and culture practices. The PCA, CVA, and UPGMA analyses successfully distinguished between populations, confirming the effectiveness of morphometric approaches in assessing stock structure. These results highlight the potential ecological consequences of farmed fish escape into wild populations during seasonal flooding, with implications for genetic

integrity and local adaptation. Therefore, integrating morphometric and molecular approaches is strongly recommended to provide a comprehensive understanding of population structure, support sustainable aquaculture practices, and safeguard natural stocks of *C. gariepinus*.

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