

ACHIEVERS JOURNAL OF SCIENTIFIC RESEARCH*Open Access Publications of Achievers University, Owo*Available Online at www.achieversjournalofscience.org**Morphological Differentiation of Wild and Hatchery-Bred *Clarias gariepinus* from Two Different Populations**^{*1}Ekundare, O. V., ²Oyekanmi, F. B., ¹Sanni, M. and ¹Fagbemi, V. O.¹Department of Biology, Faculty of Sciences, University of Ilesa, Ilesa, Osun State, Nigeria.²Department of Agric Science Education, Faculty of Education, University of Ilesa, Ilesa, Osun State, Nigeria.**Corresponding author:** olugbemi_ekundare@unilesa.edu.ng; aquatres2010@gmail.com**Submitted:** April 22, 2025; **Revised:** May 17, 2025; **Accepted:** June 2, 2025; **Published:** June 20, 2025

Abstract

Worldwide, the consumption of aquatic food has increased tremendously at a rate almost double that of annual world population growth rate, pushing the annual per capita consumption to a very high record in 2019. *Clarias gariepinus* is a fish species that has gained wide acceptance in regions of the world mostly for aquaculture usage. Generally, in aquaculture, stock identification is paramount to the success of aquaculture activities and fisheries science employs various techniques for stock identification among which conventional techniques (morphometric) still play a significant role. In view of the aforementioned, this study evaluated homogeneity and heterogeneity between wild *C. gariepinus* from Igun Abandoned Gold Mine Reservoir and hatchery-bred strain from Leventis Foundation Farm from Osun State, Nigeria. Twenty-one morphometric traits examined were subjected to t-test, Principal Component and Cluster analysis using Paleontological Statistical (PAST) software. The t-test results revealed that weight, pelvic fin length, snout length, diameter of eye, anal fin length and dorsal fin length differed significantly ($P < 0.05$) between the two populations while the remaining characters' differences were not significant. The study further revealed a highest Eigen value of 64.725%, with length of spine as the character most responsible for variation, wild and hatchery-bred populations clustered almost intersected completely (95% ellipse) and Bray-Curtis's clustering analysis showed similarity of 91%. The result elucidated the extent of homogeneity and heterogeneity based on morphometric analysis, the morphometric differences serve as a guide to selecting stocks for breeding programs which is considered a potential for commercial fish farming, however genetic marker studies (RAPD) can still be used to either complement or confirm the phenotypic diversities between the populations.

Keywords: *Clarias gariepinus*; Morphological Differentiation; PCA; Wild and Hatchery-Bred

1.0 Introduction

More than ever before, the aquaculture and fisheries sectors have been identified for their role in global food security and nutrition over the last century, even as present global production in fisheries and aquaculture sectors is at a record high sufficient in providing future food and nutrition (FAO, 2022). *Clarias gariepinus* is a member of the family Clariidae indigenous to the inland waters of Africa and Western Asia countries. It is cultured in commercial quantities in Nigeria, Ghana, South Africa and Zambia (Beveridge and Haylor, 1998). World production of clariid catfishes is next to ictalurid catfishes, *C. gariepinus*' production record has reached 235,000 tonnes out of 1.5million tonnes of clariid catfish produced worldwide (FAO, 2021). It attained such a record due to its qualities such as aggressiveness, invasiveness, tolerance to extreme water conditions and high fecundity, however, it has a flexible phenotype. One significant tool for the evaluation of population structure and stock identification is morphological variation among stocks of a species (Rawat *et al.*, 2017). Its study is one of the most often employed and cost-effective ways of stock identification and population structure assessment (Sajina *et al.*, 2011). Despite the fact that genetic variation in a population is very important, phenotypic differences still play a unique function in stock identification among populations of fish (Costa *et al.*, 2003). Initially, univariate comparisons were used for morphometric variable analysis, but these were soon followed by bivariate analysis of geographical variation among fish stocks and detection of ontogenetic changes from fish relative growth (Cadrin, 2000).

Different technologies and procedures have been utilized in the study of fish diversity such as molecular markers, isozymes, cytology and morphometrics (Ferguson and Dangaman, 1998), despite the aforementioned development, conventional methods such as morphometrics still remain important in contributing its role in stock identification (Swain and Foote, 1999). Series of studies has been conducted on morphometrics of *C. gariepinus* by authors such as Fagbuaro *et al.*, 2015 and Ekundare *et al.*, 2015 on growth and heterosis of wild and hatch-bred *C. gariepinus*. However, no study has been published on the comparison of *C. gariepinus* between wild population of *C. gariepinus* from Igun Abandoned Gold Mine Reservoir, Atakunmosa Local Government Area and the hatchery-bred population from Leventis Foundation Farm, Ilesa East Local Government Area, Osun State using multivariate analysis. The study of the two populations morphological traits can be used to evaluate the genetic integrity of wild the *C. gariepinus* population in the era of increasing domestication and a decreasing genetic diversity and reduced fitness over generations among cultured population (Sanda *et al.*, 2024). Virtually little is known about the morphological characteristics of the wild *C. gariepinus* from Igun Abandoned Gold Mine Reservoir, Atakunmosa Local Government Area, Osun State Nigeria whose population may have genetic potentials to improve reduced fitness among would be cultured populations.

This study therefore aims at assessing the significant morphological differences (heterogeneity) or similarities (homogeneity) between the two populations of *C. gariepinus*, the result of which will inform or equip farmers and breeders on stocks to be used for breeding activities.

2.0 Materials and Methods

2.1 Fish Sample Collection

Fifty (50) samples (Batubara *et al.*, 2018) of wild *C. gariepinus* were collected from fishermen at Igun Abandoned Gold Mine Reservoir, Atakunmosa Local Government Area, Osun State, Nigeria. Fifth (50) samples of hatchery-bred *C. gariepinus* were obtained from Leventis Foundation Farm, Ilesa West local Government, Osun State, Nigeria. Both strains were transported to the laboratory of the Department of Biology, Osun State College of Education, Ilesa, Nigeria. The fish were identified according to Teugels, 1986 and Teugel *et al.*, 2007.

2.2 Fish Sample Measurement

Fish sampled, both wild and hatchery-bred were subjected to morphometric measurements. Twenty-one morphometric characters were measured for each of the fish examined. Weights of the fish were measured using digital weighing scale to the nearest 0.1g. Length measurements were taken using transparent meter rule on measuring board. Length measurements such as total length, standard length, predorsal length, prepectoral length, prepelvic length, preanal length, pelvic fin length, pectoral fin length, c. pend. depth, snout length, length of spine, body depth, diameter of eye orbit, interorbital length, upper jaw length, lower jaw length, head width, head length, anal fin length and dorsal fin length were recorded.

2.3 Data Analysis

The data obtained from the measurements were subjected to T-test analysis to test for significant differences in morphology between the wild and hatchery-bred *C. gariepinus* populations.

The morphometric parameters measured were expressed as percentage of standard length following the protocol of Reist (1985), $Mn = (Mo/SL) \%$ where Mn is the standardized size, Mo is the original measurement (morphometric length) and SL is the standard length. All values obtained from standardization were transformed \log_{10} prior to statistical analysis thereby replacing each data point with its logarithm. The results were subsequently subjected to Principal Component Analysis via multivariate data analysis using PAST 3 software (Hammer *et al.*, 2001). With the aid of the PAST software, the most significant component contributing to the variance was identified. All data were also subjected to Bray-Curtis clustering analysis. All analyses were done at 5% significance level.

3.0 Results

The result on table 1 shows that most of the means of morphometric characteristics of the two populations show no significant difference. The mean values of weight, pelvic fin length, snout length, diameter of eye, anal fin length and dorsal fin length differ significantly between the two populations ($P < 0.05$). The greater the Eigen value, the larger the variance in the dependent variable as described by the principal component (PC). From table 2, PC 1 has the highest percentage (64.725%) followed by PC 2 (8.2985%), this principal component PC 1 based on the morphometric parameters has the highest variability showing that PCA was very successful (Hammer *et al.*, 2001). The clusters representing each of wild and hatchery-bred population intersected almost completely in the PCA scatter diagram (fig 2). In Fig 1, PCA loadings of morphometrics of the wild and hatchery-bred *C. gariepinus* population showed length of spine (loading 0.700) as the character most accountable for the variation between the two populations. At the second component, the scree plot (fig 3) curve commenced to flattened, showing that component 1 and 2 were significant while other components were not significant. According to Hammer *et al.*, 2001, all other components with eigen values under the broken stroke are not significant hence analysis was based on the first two component 1 and 2. The Bray-Curtis's clustering similarity coefficient of the morphometrics of the wild and hatchery-bred populations of the *C. gariepinus* is 91% (Fig 4).

Table 1: the probabilities and means of morphometric traits of wild and hatchery-bred *C. gariepinus* from two different populations.

S/N	Characters	P	Mean of wild	Mean of hatchery-bred
1	Total length	.007	36.700±2.0792 ^a	29.504±1.547 ^a
2	Standard length	.005	32.224±1.829 ^a	25.658±1.344 ^a
3	Predorsal Length	.012	10.596±0.582 ^a	8.698±0.458 ^a
4	Prepectoral Length	.009	7.118±0.40917 ^a	5.752±0.309 ^a
5	Prepelvic Length	.010	14.266±0.802 ^a	11.590±0.616 ^a
6	Preal Length	.019	17.464±0.976 ^a	14.516±0.752 ^a
7	Pectoral fin length	.039	3.928±0.247 ^a	3.274±0.192 ^a
8	C. pend. depth	.011	2.502±0.139 ^a	2.044±0.109 ^a
9	Length of spine	.218	2.290±0.160 ^a	2.030±0.135 ^a
10	Body Depth	.018	4.4140±0.270 ^a	3.584±0.211 ^a
11	Interorbital length	.016	3.896±0.219 ^a	3.218±0.169 ^a
12	Upper jaw length	.012	15.040±0.902 ^a	12.168±0.676 ^a
13	lower jaw length	.013	13.772±0.811 ^a	11.202±0.612 ^a
14	Head width	.005	5.558±0.294 ^a	4.4980±0.217 ^a
15	Head length	.007	8.9440±.49491 ^a	7.240±0.373 ^a
16	Weight	.001	544.304±63.896 ^a	294.6732±34.217 ^b
17	Pelvic fin length	.004	3.098±0.1887 ^a	2.410±0.133 ^b
18	Snout length	.004	2.262±0.133 ^a	1.784±0.096 ^b
19	Diameter of eye orbit	.001	0.576±0.026 ^a	0.462±0.021 ^b
20	Anal fin length	.001	14.348±0.859 ^a	10.888±0.609 ^b
21	Dorsal fin length	.001	21.192±1.220 ^a	16.612±0.919 ^b

Mean on the same row with different superscript (a and b) differ significantly (P<0.05)

Table 2: Eigenvalues and percentage variation for different component of the PCA

PC	Eigenvalue	% variance
1	0.023517	64.725
2	0.003015	8.298
3	0.002275	6.260
4	0.001707	4.697
5	0.001281	3.525
6	0.000977	2.689
7	0.000912	2.509
8	0.00061	1.678
9	0.000415	1.142
10	0.00039	1.072
11	0.00029	0.797
12	0.000222	0.611
13	0.000206	0.567
14	0.000156	0.429
15	0.000116	0.320
16	9.55E-05	0.262
17	7.81E-05	0.214

18	6.00E-05	0.165
19	1.22E-05	0.033

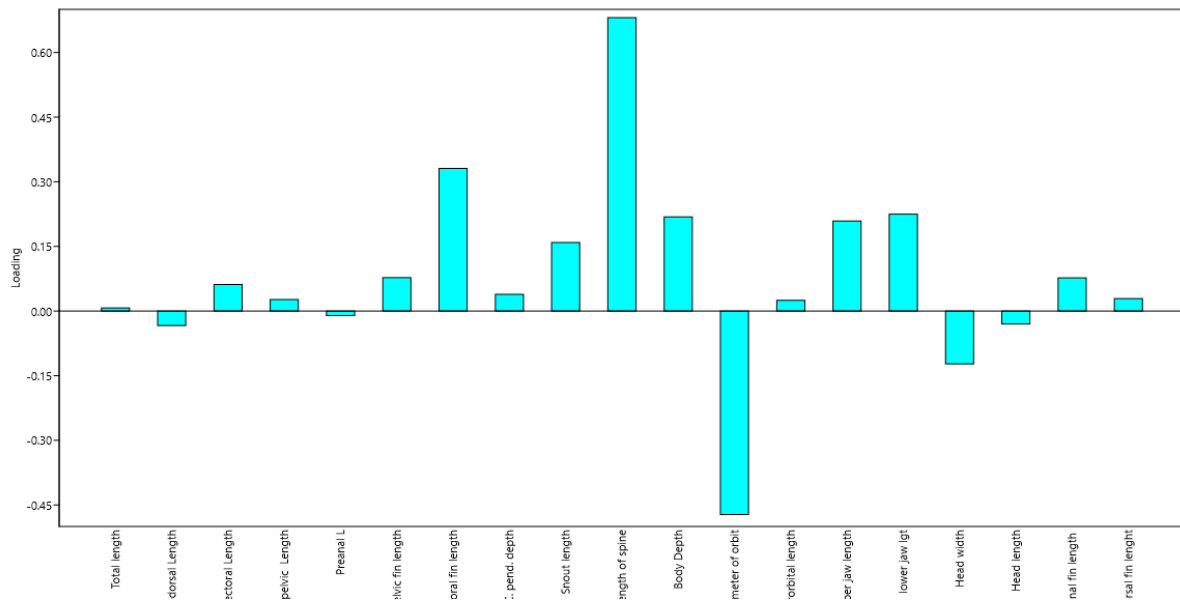


Figure 1: Morphometric traits of *C. gariepinus* (wild and hatchery-bred) and their loading on PC1 of the principal components analysis showing length of spine as the trait most responsible for variation among the two populations studied.

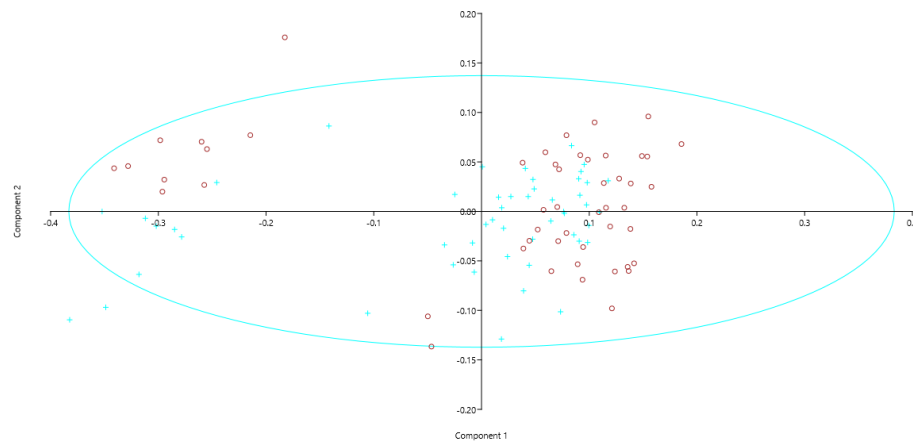


Figure 2: PCA scatter diagram (95% ellipse) *C. gariepinus* showing overlapping of characters between the two population.

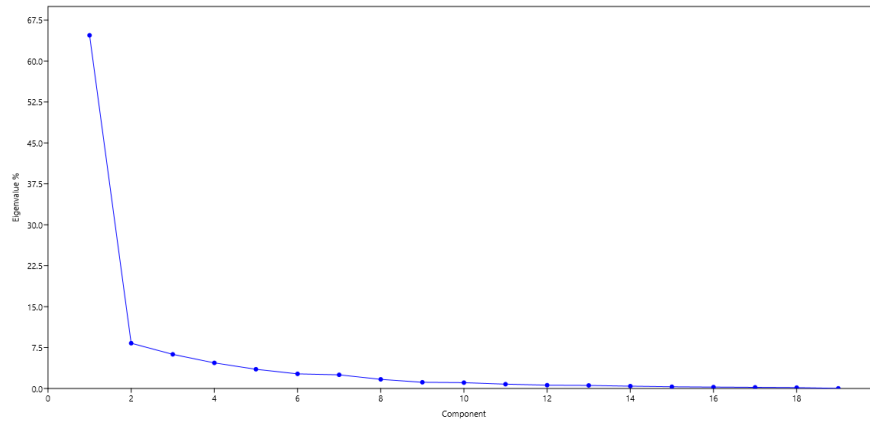


Figure 3: Scree plot of the Eigen values of the various principal components.

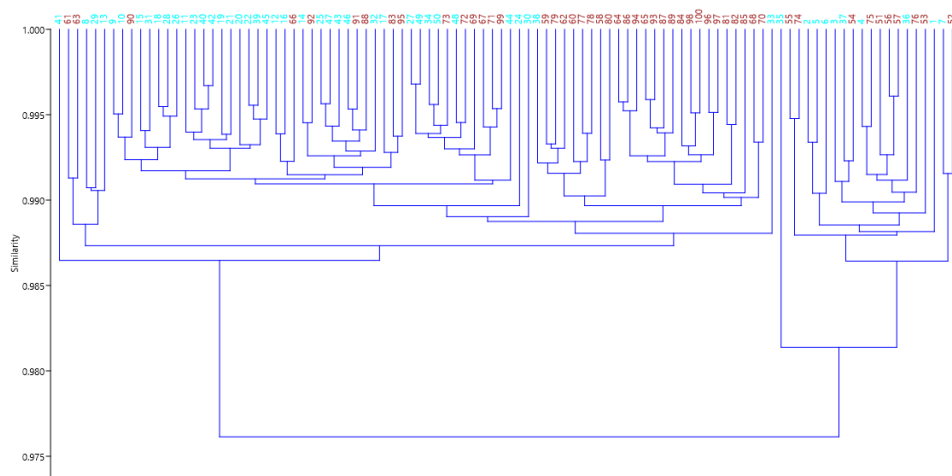


Figure 4: Dendrogram showing similarity coefficient (91%) of the morphometric of wild and hatchery-bred population of *C. gariepinus* using Bray-curtis's clustering algorithm,

4. Discussions

Mean values of morphometric characters obtained in this study share both similarities and differences with the work of Fagbuaro *et al.*, 2015 and Ola-Oladimeji *et al.* (2016). Fagbuaro *et al.* (2015) reported similarities in the mean values of morphometric traits of two populations of *C. gariepinus* from a fish pond in Emure-Ekiti and Ogbese River. Their report is similar to the outcome of this study as most of the means of morphometric traits in this study do not differ significantly between wild and hatchery-bred populations. Similarities in morphometric characters between cultured/hatchery-bred populations could have resulted from the introgression of genes of cultured escapees into the wild gene pool after introgressive hybridization that can cause a loss of genetic distinctiveness in the wild population. This could occur due to repeated backcrossing of hybrids with either of the cultured or wild parents (Allendorf *et al.*, 2001).

On the other hand, Ola-Oladimeji *et al.* (2016) reported significant difference in the mean values of their morphometric characters between wild and cultured populations. The varied morphometric relationship among populations can be a result of the interplay of forces of genotypes and environment factors operating in different geographical areas and the genetic improvement or degradation *C. gariepinus* has been exposed to in the

culturing environment (Parish and Sharman, 1958). The variation in morphometric traits was mentioned by Klug *et al.*, 2011 as a likely product of spontaneous mutation, chemicals and induced forces by external factors. They reported that fish often show greater variation in morphometric traits within species, within population and among population than any other members of the vertebrates. The result of this study is in line with the conclusion of Duong, *et al.* (2017). They reported that phenotypic plasticity occurs in catfish species in response to natural and captive environments

Statistical PCA is employed to derive a small number of variables from many variables with a view to summarizing information for further analysis (Mwanja *et al.*, 2016). The cluster from the two populations of wild and hatchery-bred *C. gariepinus* almost intersected completely; this indicated a minimal difference between the wild and the hatchery-bred populations. The reason for the closeness might be due to interaction between the wild population and the hatchery-bred escapees which has resulted in inbreeding in the wild *C. gariepinus* population (Mwanja and Mwanja, 2009). The incompletely intersected cluster in the scatter diagram is an indication of incomplete homogeneity of character between the two populations. Solomon *et al.* (2015) reported that morphometric characteristics vary across different populations. The Bray-Curtis dendrogram shows 91% similarity which is an indication of populations that are not totally morphologically differentiated (Mwanja *et al.* 2016). This study revealed length of the spine as the character that most accounts for variation between the wild and hatchery-bred *C. gariepinus*. This is different from the result of Ola-Oladimeji *et al.*, 2016 where they emphasized anal fin length as the character most contributing most to differences between the wild and cultured populations. The reason for the differences might be drawn from the report of Parish and Sharman (1958) where they stated that differences in morphological characteristics of a species may result from differences in geographical location, genotype and environmental forces acting on either or both of the factors.

5. Conclusion

This study revealed similarities in the morphometric characteristics of wild and hatchery-bred populations of *C. gariepinus* which may be due to loss of genetic distinctiveness caused by introgression from hatchery-bred escapee. Some morphometric characteristics varied between the populations as PCA loadings of morphometrics described length of spine as the character accounting for most variation between the two populations. Hence this study also affirms the phenotypic plasticity found in catfish in response to natural and captive environments. However, the combined assessment of the populations using molecular analysis is encouraged.

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