PHENOTYPIC AND GENOTYPIC CHARACTERISATION OF WILD AND CULTURE CICHLID POPULATIONS (*Sarotherodon melanotheron)* IN LAGOS STATE, NIGERIA.

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Abstract

This study was carried out to characterize and identify Sarotherodon melanotheron using morphometric and molecular approach. A total of forty (40) samples were collected; 10 samples each of farm-raised (Akinsateru and NIOMR farms, Lagos) and wild (Lagos and Badagry Lagoon, Lagos) were collected in Lagos State for 3 months. The standard lengths and weights of the fish used for the study ranged from 8.40 cm to 17.20 cm; 26.10g to 133.00g for farm-raised and wild populations respectively .Seventeen morphometric and meristic characters were measured with divider, thread, measuring board and ruler. Data collected were analyzed using t-Test. The results showed there were significant differences ($p \leq 0.05$) among the characters measured in wild and farm-raised S. melanotheron. Random amplified polymerase DNA (RAPD-PCR) analysis was carried out using Operon primers (OPC 04, 05, 10, OPR 02 and OPI 05).Of the 5 primers, only 4 primers showed both stable amplification and polymorphism except on some samples (both wild and culture) having low reproducibility. The bands generated from the molecular results showed that the inter-specific similarity coefficient between the wild was 78%; culture was 80%; and 100% for both wild and culture samples.

Keywords: tilapia, morphometrics, meristics, DNA, RAPD

Introduction

The fisheries resources of Nigeria contribute immensely to the nutritional needs, economic growth and thus development of the nation. For example, fish provides essential amino acids like lysine and methionine which are limiting in livestock. It is also rich in vitamins A and D as well as lipids which help to reduce thickness of blood thereby allowing it to flow easily in the body (Akande, 1990). Species identification and population are important in the conservation of biodiversity, natural resources, and fisheries management. It is also often necessary to identify individual specimen associated with a particular population when investigating biological traits such as growth, mortality, fecundity, trophic relationships, and parasite relationships, historical and paleontological studies. Different methods are used for identification but phenotypic method based on morphometric and meristic characters are considered as earliest and authentic methods for the identification of fish species in fish biology. This method measures discreetness and relationships among various taxonomic categories, and provide useful results used to differentiate fish populations (Ihssen *et al*., 1981; Zafar *et al*., 2002; Costa *et al.,* 2003; Barriga-Sosa *et al*., 2004; Doherty and McCarthy, 2004; Naesje *et al*., 2004).

Morphological studies have been successful in defining species and in organizing them into genera. These groupings have usually been confirmed when examined with molecular approaches. Molecular characters have revealed some cryptic species (Avise, 1994) and identified some incorrectly split groups (Stepien and Rosenblah, 1991). Although morphological studies have been successful in defining genera, it is rare to find studies which present a hypothesis of relationship above the level of species comprising a genus, primarily due to a lack of congruence of characters (Stepien and Kocher, 1997). However, this is one of the strengths of molecular data, and inter- and intrageneric relationships are now being rapidly tested and elucidated. Molecular data are also used to assess the phylogenetic relationships among populations.

Genetic diversity or variation and its measurement have vital importance in interpretation, understanding and management of populations and individuals. Development of allozyme electrophoresis and chromosomal techniques has significantly increased ability to observe the genetic variation and the former has for many years been the standard tool in genetic studies of wild and cultured fish stocks, but in recent years, it has been increasingly replaced by DNA markers. These molecular markers combined with new statistical developments enable the determination of differences and similarities between stocks and individuals, population and origin of single fish, resulting in numerous new research possibilities and applications in practical fisheries and aquaculture stock management. Various molecular markers, proteins or DNA (mitochondrial DNA or nuclear DNA such as mini satellites, microsatellites, transcribed sequences, anonymous c DNA or RAPDs) are now being used in genetic characterization of fish and improvement of genetically modified fish for aquaculture purposes.

Sarotherodon melanotheron (Ruppell, 1852) is a typical estuarine species which can be found in abundance in most of the lagoons and estuaries of West Africa which has been a major supporting to lagoon fishery. It can live and reproduce in a wide range of salinities. They have adapted to diverse habitats: permanent and temporary rivers, large equatorial lakes, tropical and subtropical rivers, open and closed estuaries, lagoons, swampy lakes, deep lakes and coastal brackish lakes (Trewavas, 1983). For instance, the brackish *Saratherodon melanotheron*are the last species recorded during droughts in the very saline waters of the Casamance River (Leveque, 1997). They are however not found at high elevations and generally require water warmer than 20ºC (Fitzsimmons, 2000).

This fish has a great economic importance, ranking among the major species caught within the lagoon fisheries and there is an increasing interest in this fish for aquaculture purposes, particularly in areas of high or variable salinities, characteristic of the estuaries and extensive lagoon systems which constitute its natural range. In this habitat, other species more traditionally used in ‘tilapia’ culture are either not locally available (*Oreochromis mosambicus*) or do not tolerate the prevailing saline conditions (*O. niloticus*). *Sarotherodon melanotheron,* species is not well known for aquaculture purposes. Therefore, this study is carried out to establish the morphometric and genetic characterization for the delineation of this Cichlidspecie (*Sarotherodon melanotheron* as an important specie not only for aquaculture and hatchery operations, but also for capture fisheries management.

Materials and Methods.

Study areas.

The study was carried out in Lagos State and study sites selected were Akin-Sateru Farms at Ajah lies between longitudes 3° 53′ and 3° 28′ E and between latitudes 6° 46′ and 6° 48′ N and Nigerian Institute for Oceanography and Marine Research Fish Farm at Badore lies between longitudes 3° 59′ and 3° 68′ E and between latitudes 6° 51′ and 6° 65′ N at Lagos State respectively for the cultured species while Lagos Lagoon at Oworo end and Badagry Lagoon, Lagos State both along the west coast of Nigeria were used for wild samples.

The Badagry Lagoon lies between longitudes 3° 94′ and 3°80′ E and between latitudes 6° 41′ and 6° 46′ N. It is part of a continuous system of lagoons and creeks along the coast of Nigeria from the border with the Republic of Benin to the Niger Delta. Most of the year it is characterized by fresh and slightly brackish water. The lagoon is approximately equidistant from the entrances of Lagos and Cotonou harbours. As a result, it is influenced by tides and floods from the Lagos Lagoon and Cotonou harbour through Lake Nokue and Lake Porto-Novo (Anyanwu and Ezenwa, 1988).

Lagos Lagoon, on the other hand, lies between longitude 3º 39´ and 3º 53´ E and between latitude 6º 49´ and 6º 61´ N. It also forms part of an intricate system of waterways made up of lagoons and creeks that are found along the western coast of Nigeria from the Republic of Benin border to the Niger Delta.

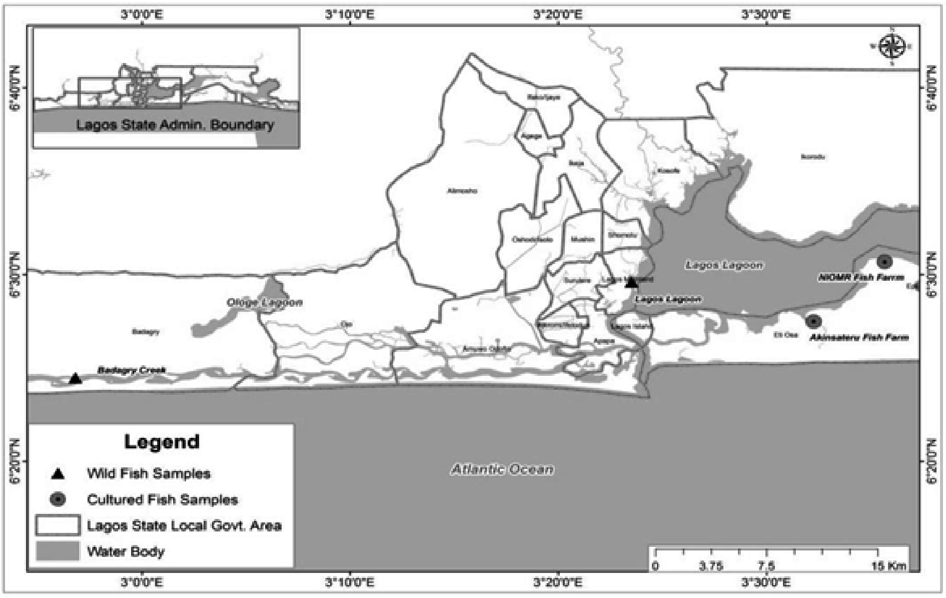

Figure 1: Map of Lagos State showing the Sample Locations.

Collection of specimen

A total number forty (40) samples of *Sarotherodon melanotheron* (plate 1)ranging between 8.40 cm and 17.20 cm standard length (which range between 26.10 to 133.00g by weight) were collected from the both wild and culture (NIOMR and Akinsateru fish farm, Lagos State; Lagos and Badagry Lagoon, Lagos State) environments. Fish samples were collected at the intervals of 4 weeks for three months (April - June), to ensure that samples were obtained as close to same period of the year as possible. The samples were transported in ice chest to the laboratory at -2ºC, where extraction started immediately to avoid DNA denaturation and followed by morphometric analysis.

Identification of these species of cichlid was done using taxonomic classification by Daget (1991); the confirmation of the identified species was carried out based on their colour and meristic characters.

Plate 1: ***Sarotherodonmelanotheron***

Morphometric and meristic measurements.

The morphometric features (traditional and truss measurement) measured were total length (TL), standard length (SL), Pre-dorsal length (PDL), Pre- anal length (PAL), Pre-pelvic length (PPL), Pre-pectoral length (PPEL), dorsal fin length (DFL), caudal fin length (CFL), anal fin length (AFL), head length (HL) and interorbital width (IOW). All measurements were taken with the aid of steel divider, thread, wooden measuring board and a ruler to the nearest cm. The meristic counts measured were dorsal fin rays (DF), pectoral fin rays (PEC), anal fin rays (AF), caudal fin rays (CAU), pelvic fin rays (PEL) and weight (WEI). Measurements of body parts were made with the head of fish pointing to the left side.

Deoxyribonucleicacid (DNA) isolation.

DNA isolation was done using salting-out method from caudal fin according to Lopera-Barrero*et al*., (2008). Portions of caudal fins (approximately 3.5-4.5 g) of the sample fish from different water bodies were cut into eppendorf tubes and DNA extracted immediately to avoid denaturation .after extraction, isolates were dissolved in TE buffer and samples were stored at – 20 ^{0}C until they were ready to be used for Polymerase Chain Reaction (PCR).

DNA purity and quantification.

Purity and concentration of the DNA samples were carried out with the use of nano-spectrophotometer by measuring absorbance at 260and 280 nm using TE buffer as blank. This was achieved by dropping 1µl of the DNA samples on nano- spectrophotometer after blanking with TE buffer that was used for the elution of the DNA. For each samples analysis, results were printed out displaying DNA concentration purity in ng/µl

Polymerase Chain Reaction (PCR) conditions.

The PCR amplification was performed in a Biorad I- cycler programmed for initial denaturation step at 95 ^{0}C for 5 min followed by 30 cycles of denaturation at 95 ^{0}C for 30 sec, annealing at 55ºc for 60 sec and extension at 72ºc for 2min; a final extension at 72ºC for 10 min was carried out. After PCR amplicons were cooled at 4ºC.

Agarose Gel Electrophoresis.

Agarose gel electrophoresis was used for quantification and separation of the amplified DNA. The gels were then viewed with UV transilluminator and the pictures of the gels were taken for scoring.

Statistical procedure.

The morphometric features, meristic counts and gel results were analyzed using Statistical Package for Social Sciences (SPSS version 2.0); descriptive, t-Test and NTSYS software respectively.

Results

Morphometric measurements.

Table 1 shows the morphometric measurements between *Sarotherodon melanotheron* from the wild samples, indicating the ranges and standards deviation of the samples from both Lagos and Badagry Lagoon. It indicates that no significant differences ($P \geq 0.05$) were observed between *S. melanotheron* from the wild in all the morphometric measurements except the Head Length.

Table 2 shows morphometric measurement between the *Sarotherodon melanotheron* from cultured samples. There were significant differences at Total Length (TL), Standard Length (SL), Pre-Dorsal Fin length (PDL), Pre- Anal Fin Length (PAL) and Pre-Pectoral Length (PPEL) while there were no significant difference at Dorsal Fin length (DFL), Caudal Fin Length (CFL), Anal Fin length (AFL), Head length (HL), Pre-Pelvic Length (PPL) and Interorbital Width (IOW).

Meristic counts.

Tables 3 show the meristic counts of wild samples. There were no significant differences (P≥ 0.05) in all the meristic counts. Also, Table 4show the meristic counts of cultured samples. There were no significant differences (P≥0.05) in all other meristic measurements except in Dorsal Fin, Dorsal Fin rays (DF), Pectoral fin rays (PEC) and weight for cultured.

DNA purity and quantification results.

The modified protocol using salt- out (NaCl) method according to Lopera-Barrero*et al*., (2008) enabled total genomic DNA extraction from fin without DNA degradation or fragmentation. Concentration and purity values are shown in Table1, with mean Purity values range of 1.63 to2.10 using nano-Spectrophotometer.

RAPD amplification results.

RAPD analysis was performed on 40 genomic DNA samples of fishes using five 10 bp-oligo-nucleotide random primers (Table 6). Out the five primers, only four showed stable amplification and polymorphism except on some samples having low reproducibility. RAPD OPC 02 had 66 loci and produced 229 bands. RAPD OPI O5 (50 loci; 110 bands), RAPD OPC 05 (71 loci; 261 bands), RAPD OPC 04 (67 loci; 224 bands) while OPC 10 was not amplified.

Dendrogram results.

Figure 1 showed five major clusters which consists of minor clusters at degree of co-efficient phylogenetics analysis. SW6, SW7, SW13 and SW14 which are wild samples from both sites form a cluster at co-efficient 1(100%) indicating a very high level of genetic similarity. 1st cluster(SC19, SC13, SC15, SC14 and SC20), 2nd cluster (SC12, SC16, SC8 SC7 SW10 and SW8), 3rd cluster (SC2,SC5, SC4, SC3, SW19, SC11 and SW18) 4th cluster (SW14, SW16, SW15,SW12, SW11, SW14, SW13, SW9,SW7,SW16 and SW15) and 5th (SC16, SC17, SC18, and SW1) respectively.

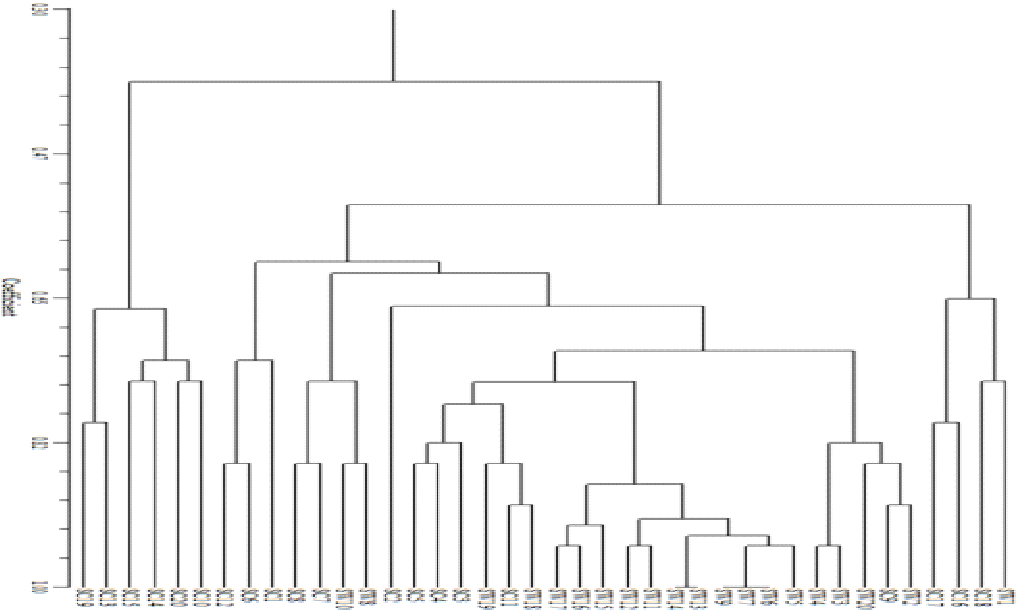

Figure 1: Dendrogram depicting the degree of relationship among *Sarotherodon melanotheron* from wild and cultured samples.

SW1 - SW10 =*S. melanotheron*from the Lagos Lagoon.

SW11 -SW20 = *S. melanotheron*from the Badagry Lagoon.

SC1 - SC10 =*S. melanotheron*from the Akinsateru farm.

SC11 - SC20 = *S. melanotheron*from the NIOMR farm.

Table 1: Morphometric measurements between the *Sarotherodon melanotheron* from

Morphometric measurements	Lagos Lagoon Range(cm)	Mean ±SD	Badagry Lagoon Range(cm)	Mean ±SD	T-Value
TL	13.50-16.30	15.00±0.98	12.70-16.30	15.10±0.99	-0.32
SL	10.70-12.50	11.70±0.62	10.50-13.10	11.60±0.82	0.22
PDL	4.20-5.10	4.70±0.30	4.10-4.90	4.60±0.25	0.17
PAL	7.60-9.10	8.50±0.44	8.00-9.50	8.70±0.53	-1.06
PPL	4.10-5.40	4.90±0.38	4.20-6.00	5.00±0.58	-0.59
PPEL	3.60-4.60	4.20±0.34	3.80-4.90	4.30±0.44	-0.36
DFL	5.70-7.00	6.30±0.42	5.70-7.10	6.20±0.42	0.04
CFL	2.30-3.30	2.90±0.35	2.60-3.80	3.00±0.33	-0.59
AFL	1.60-2.20	1.90±0.21	1.20- 2.70	1.90±0.37	-0.08
HL	3.30-4.60	3.90±0.48	3.20-4.30	3.50±0.30	2.87*
IOW	1.20-1.90	1.50±0.23	1.50-2.00	1.70±0.17	-2.68

Wild samples.

Standard error indicated with mean values.

Significant at 5% level of significance while tabulated value is 1.96 in t-Test

TL = Total Length, SL = Standard length,
PAL =Pre-Anal length PPL =Pre- Pelvic length,
PDL = Pre-Dorsal Length PPEL =Pre-Pectoral fin length
DFL = Dorsal Fin Length CFL = Caudal Fin Length
AFL = Anal Fin Length HL = Head Length
IOW = Interorbital Width

Table 2: Morphometric measurements between the *Sarotherodon melatheron* from cultured samples. *Standard error indicated with mean values*

Morphometric measurements	Akinsateru farm Range(cm)	Mean ± SD	NIOMR Farm Range(cm)	Mean ± SD	T-Value
TL	16.20-19.50	18.10 ± 0.98	14.00- 20.00	16.40 ± 1.58	3.10*
SL	12.30-16.50	14.30 ± 1.23	11.60 - 16.00	13.20 ± 1.21	2.25*
PDL	4.50 - 6.20	5.40 ± 0.49	4.40 - 5.60	5.00 ± 0.36	2.61*
PAL	8.00- 11.70	10.00 ± 1.06	7.80-10.90	9.20 ± 1.02	2.49*
PPL	5.10-6.30	5.70 ± 0.39	4.00-6.00	5.00 ± 0.57	1.274
PPEL	4.00-5.40	4.60 ± 0.46	3.10 - 5.10	4.20 ± 0.64	4.27*
DFL	7.20-9.30	8.20 ± 0.64	6.00-8.70	7.00 ± 0.73	1.71
CFL	2.00-2.60	2.30 ± 0.18	1.80 - 2.60	2.10 ± 0.24	0.91
AFL	2.20-3.00	2.70 ± 0.28	2.10 - 3.10	2.50 ± 0.33	0.91
HL	4.00 - 4.70	4.40 ± 0.25	3.50 - 5.60	4.30 ± 0.61	0.65
IOW	1.40 - 2.10	1.70 ± 0.21	2.00 - 2.90	1.70 ± 0.54	0.10

Standard error indicated with mean values.

Significant at 5% level of significance while tabulated value is 1.96 in t-Test

Table 3: Meristic counts between the *Sarotherodon melanotheron* from wild samples.

Morphometric measurements	Lagos Lagoon Range(cm)	Mode Value(cm)	Mean ±SD	Badagry Lagoon Range(cm)	Mean Value (cm)	Mean ±SD	T-value
DF	27.00-28.00	27.30	27.30±0.48	25.00-27.00	25.90	25.90±0.56	0.00
AF	11.00-13.00	12.00	12.00±0.47	10.00-13.00	12.00	11.40±0.84	1.00
PEC	11.00-13.00	12.00	11.90±0.74	10.00-12.00	12.00	11.30±0.82	-1.07
PEL	10.00-12.00	12.00	11.50±0.71	10.50-12.00	12.00	12.00±0.00	0.00
CAU	14.00-15.00	15.00	14.60±0.52	13.00-16.00	15.00	14.60±0.84	-0.89
WEI	18.70-26.00	72.50	72.50±36.66	53.20-98.30	65.90	65.90±13.51	0.18

Standard error indicated with mean values.
Significant at 5% level of significance while tabulated value is 1.96 in t-Test

Table 4: Meristic count between the *Sarotherodon melanotheron* from cultured Samples.

Morphometric measurement	Akinsateru farm			NIOMR farm			
	Range(cm)	Mode Value(cm)	Mean ±SD	Range(cm)	Mode Value(cm)	Mean ±SD	T-value
DF	28.00-29.00	28.00	28.10±0.32	27.00-28.00	27.70	27.70±0.48	2.52*
AF	12.00-13.00	11.90	11.90±0.52	12.00-14.00	12.00	12.40±0.78	-0.73
PEC	11.00-12.00	12.00	11.90±0.32	10.00-12.00	11.00	11.20±0.63	4.43*
PEL	11.00-12.00	12.00	11.90±0.32	10.70-12.00	12.00	12.00±0.00	-1.00
CAU	16.00	16.00	16.00±0.00	15.00-17.00	16.00	15.90±0.57	1.51
WEI	55.40-133.40	104.50	104.50±25.24	53.30-130.30	75.20	75.20±21.57	4.97*

Standard error indicated with mean values.
Significant at 5% level of significance while tabulated value is 1.96 in t-Test

Table 5: DNA concentration (ng/µl) and ratio of absorbance (260/280nm) of fish population from different source.

Sample source	Species	Species ID	Concentration	Purity	Mean Purity(X^{-1})	Mean ±SD
Lagos Lagoon	*S. melanotheron*	SW1-SW10	538.58-4391.73	1.48-2.10	1.95	1.95±0.17
Badagry	*S. melanotheron*	SW11-SW20	831.37-4279.56	1.74-2.04	2.10	2.10±0.11
Akinsateru Farm	*S. melanotheron*	SC1-SC10	28.60-717.09	1.24-2.00	1.63	1.63±0.25
NIOMR Farm	*S. melanotheron*	SC11-SC20	70.36-2407.24	1.30 - 1.93	1.73	1.73±0.22

SW1- SW10 =*Sarotherodon melanotheron* from Lagos Lagoon.
SW11 - SW20 = *Sarotherodon melanotheron* from Badagry lagoon.
SC1 - SC10 = *Sarotherodon melanotheron* from Akinsateru farm.
SC11 - SC20 =*Sarotherodon melanotheron* from Nigerian Institute for Oceanography and Marine Research Farm.

Table 6: RAPD primers and amplification conditions for *Sarotherodon melanotheron*

Primer number	Sequence (5'-3')	GC Content (%)	Total bands *Sarotherodon melanotheron*
OPC 04	5' CCGCATCTAC 3'	60	123
OPC 10	5' TGTCTGGGTG 3'	60	0
OPC 05	5' GATGACCGCC 3'	70	139
OPI 05	5' TGTTCCACGG 3'	60	58
OPR 02	5' CACAGCTGCC 3'	50	107

The primers have the same annealing temperature of 55^{0}C.

Discussion

It is common to find morphometric measurement and meristic counts being used to determine the amount of variation among widely distributed organisms. Tagging experiments have often been used either separately or together to arrive at any result (Kusemiju, 2010).

Electrophoresis is now being used world-wide in arriving at more convincing result. In this study, however, only meristic counts and morphometric measurements were used to evaluate racial relationship within the cichlid population (*Sarotherodon melanotheron*). The objective of a racial study is to establish, with some degree of confidence and the taxonomic identity of a species in differently located bodies of water. This becomes more important in the utilization of its fishery resources because the quality of the existing strain is very crucial for any successful breeding programme. However, this research used meristic counts, morphometric and molecular approach as they still remain dependable tools to characterize fish species.

A total of forty (40) specimens of *Sarotherodon melenotheron*from wild and culture which made up of 10 samples each from the four study sites were examined and analyzed. There were significant differences between the *S. melanotheron* in head length from the wild; also there were significant differences between *S. melanotheron* from the culture samples (Akinsateru and NIOMR fish farms). There were no significant differences in all the meristic counts from both wild of *S. melanotheron*. These differences were attributed to environmental factors such as temperature and salinity according to Kusemiju (2010). This gives indication that the samples from both water bodies may not be genetically separable. Clayton (1981) reported that the major limitation of morphological characters at the intra-specific level is that phenotypic variation is not directly under genetic control but subjected to environmental modification. There were no significant differences in all other meristic measurements; Dorsal Fin count (DF), Pectoral rays (PEC) and weight (WEI) for *S. melanotheron* from the culture. The natures of substrata, as well as variation in dietary items, have been observed to influence morphometric features of species populations (Marcus, 1986). Hence, the significant differences observed in the morphometric may have occurred as a result of isolation caused by variation in these ecological factors in the two habitats.

The significant variations observed to occur in culture samples may be as a result of environmental fluctuations hence, the significant differences observed in the morphometric measurements; Dorsal fin, pectoral and pelvic rays might have occurred as a result of isolation caused by variation in the ecological factors in the two habitats The fairly constant values of fin rays observed in the two populations from the wild agree with the findings (Holden and Reed, 1990) that fin rays of the tribe *Tilapiini* do not vary much.

The qualitative characteristics (i.e., strong, faint, and sharp) of the Random Amplified Polymorphic DNA (RAPD) bands in this study were always stable across all the primers except primer OPC 10 that had no amplification. The various qualitative characteristic could be because one or more copies of DNA may exist per genome r may be attributed to the variation of the annealing process between the primer and the DNA. In other words, the five random primers in RAPD-PCR analysis generated strong amplification profile with distinct bands albeit with some less distinct bands (mixed bands). As in the study of Bardkci and Skibinski (1994; 1999) the patterns of similarities and differences between populations obtained in this study showed broad agreement across primers and the overall similarity level varied between primers. A polymorphic SCAR-RAPD marker between species of Tilapia. Thus, choice of primer is very important for this technique. Figures 1 shows the similarity coefficients of some of the individuals (SW6, SW7, SW13 and SW12) samples from wild to be 100 %. The similarity of *S. melanotheron* from wild and culture were up to 82% and 88% respectively. Such genetic similarity in populations of a species from both wild and cultured has previously been observed for some tilapia species (Kusemiju, 2010). Macaranas *et al*., (1995) reported low level of genetic variability for both wild and cultured selected tilapiine fishes; Sodsuk *et al*., (1995) intermediate levels of genetic variability of wild *Oreochromis* species (Rognon and Guyomard, 2003) high levels of genetic variability for both wild and culture *O. niloticus*.

The pattern of the dendrogram showed that the cultured samples of the two species are genetically close to that of the wild samples. The description of these similarity coefficients is however, not simple, especially when more than one character is involved in the same cluster. El-Zaeem, *et al.,* (2012) showed that each of the different wild populations of *O. niloticus* sampled showed different percentage similarity coefficient to the cultured populations. The genetic similarity of the cultured and wild populations of the species assessed in this study suggests that the same sustainable utilization techniques can be adopted to manage the populations. However, the study can be extended to other populations of these species and more versatile molecular marker could be used. Further, the findings in this study suggest possibility of hybridization between the species. Inter-generic hybrids among tilapia species, from *Oreochromis aureus* to *O. niloticus* in West Africa has also been reported by Rognon and Guyomard (2003). The study also shows that high quality and quantity of DNA can be obtained using the salt-out method of extraction (Aljanabi and Martinez 1997).

Conclusion

This study supports the fact that among the samples examined could have been as a result of environmental and ecological factors. These findings are indication of the distinct character of *S. melanotheron* from both wild and cultured in spite of the close morphology of body shape possess and depending on environmental conditions. The objective of a characterization study is to establish, with some degree of confidence, the taxonomic identity of species in differently located bodies of water. Such information as this helps in the utilization of the existing strain for any successful breeding programmes. In this study, meristic, morphometric and molecular approach were used as they still remain dependable tools to characterize fish species and also the results revealed that Identified wild species are closely similar to cultured species.

This study also revealed the important steps in the management of fish populations in Nigeria. This is because there is little or no information about genetic status of natural or culture populations of fishes. The reason such information is not available is primarily because there is no appreciable governmental effort at managing the fish populations and possible inadequate research on fish genetics, hence no genetic data available. This study therefore provides the needed genetic information for effective decision toward management of these fishes - that is, a mindset that if there is useful information, it may spur other efforts at making the government to plan toward managing the fish populations, for genetic manipulation in aquaculture; policy making, management and conservation. This study is also important because it used a more versatile genetic marker compared to other previous studies of population of fishes in Nigeria

Recommendation

With the potential shown by *Sarotherodon melanotheron* for aquaculture breeding programme, especially its ability to live and reproduce in a wide range of salinity, coupled with abundance in these water bodies, more effort should be made by prospective farmer to exploit the genetic improved species through the extension services. Brood-stock from either of these natural water bodies can serve as source of getting pure strain of these species but further investigation needs to be done probably using single nucleotide polymorphisms (SSP), *amplified fragment length polymorphism (*AFLP) and Single sequence repeat (SSR) which though expensive but have high resolving power and reproducibility.

In terms of DNA extraction method of tilapia species, the salting-out method is recommended with RAPD-PCR condition applied. In addition to the good bands, high DNA concentration and purity, the method is relatively cheap, easy and less time consuming.

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