ASSESSMENT OF GENETIC STRUCTURE OF *CLARIAS GARIEPINUS*, BURCHELL, 1822 POPULATION IN ASEJIRE LAKE

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Abstract

Wild brood-stock is a major genetic reservoir for sustainable culture of *Clarias gariepinus.* This has been observed to be declining in major freshwater dams in Nigeria. There is inadequate information on factors responsible for this decline and their effects on genetic structuring of the fish resources in these dams. This study therefore investigated genetic structure of *C. gariepinus* in relation to environmental condition of Asejire Dam.

The Dam was spatially divided into Oyo State (O_YS) and Osun State (O_SS) strata. Thirty-eight sites were randomly selected, nineteen sites from each stratum. Water Quality Parameters (WQP) were sampled bimonthly in wet and dry seasons for 24months. The WQP selected were temperature, Dissolved Oxygen (DO), Total Hardness (TH) and Total Alkalinity (TA). Catchment area was assessed for indices of threat to environmental condition; Watershed Forest Degradation (WFD), frequencies of Partial Dam Gate Opening (PDGO) and Complete Dam Gate Opening (CDGO). *Clarias gariepinus* catches from fishermen's landings were used to study genetic structure by examining variability in phenotypes and genotypes. Phenotypic data obtained were regrouped to subgroups of sex, size, and grades of Possession of Anteriorly Serrated Pectoral Spine (PASPS). Regrouped cases that had significantly different subgroups' phenotypes were further screened for presence of Private Allele (PA), polymorphism of protein, DNA bands and genetic distance using standard procedures. Data were analysed using descriptive statistics, student's *t-test* and cluster analysis.

Seasonal variations in WQP for wet and dry seasons were 27.4±3.2 and 30.0±2.5^{o}C (temperature); 6.1±1.8 and 5.0±2.1 mg/l (DO); 51.7±27.1 and 52.0±38.0 mg/l (TH); 55.3±43.7 and 134.00±89.5 mg/l (TA) respectively. The WQP values of 28.6±2.7 and 28.7±4.0^{o}C (temperature), 6.1±1.2 and 6.5±1.5 mg/l (DO), 52.7±6.2 and 51.7±38.3 mg/l (TH), 146.7±58.3 and 91.0±43.4 mg/l (TA) were recorded at O_YS and O_SS respectively. There was 8.5% reduction in catchment area while 66.0% wetland areas were under human activities. The PDGO for wet and dry seasons were 30 and 8 times respectively. Wet and dry seasons' CDGO occurred 2 times. Thirty-seven *Clarias gariepinus* were identified from 1,392 fish catches. Dorsal ray counts ranged from 63 to 71. Dorsal ray counts were significantly different (F=3.51, p=0.008) between size subgroups. Anal fin lengths in PASPS subgroups were between 39.0 and 44.0% of standard lengths. These values were significantly different (F=4.25, p=0.001) among the subgroups. Polymorphism and PA of protein markers occurred in PASPS at 14.7kDa. The DNA analysis revealed 82.5% polymorphic sites from 746 bands. The PASPS subgroups genotypes formed two different clusters and had within cluster variability at 62.0% CV.

Watershed forest degradation indices: catchment areas' reduction and increase in wetland areas under human activities in addition to frequency of opening of the dams' gate were the main threats to *Clarias gariepinus* population in Asejire Dam. Genetic structure indicated presence of strains with high variability in *Clarias gariepinus*.

Key words: *Clarias gariepinus,* Fish phylo-genetics, Asejire Lake

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Dedication

This project is dedicated to the Almighty God the Father, Son and the Holy Spirit who gave knowledge and exposed hidden things for discovery in life.

Certification

This is to certify that this project was carried out by Oyediran Olusegun OYEBOLA under my supervision, in the Department of Aquaculture and Fisheries Management, Faculty of Agriculture and Forestry, University of Ibadan, Oyo state, Nigeria.

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CHAPTER ONE

INTRODUCTION

1.1 Background

Fisheries and aquaculture play an essential role in the livelihood of millions of people around the world (FAO, 2008). Fish production from capture fisheries no longer meets the current demand (Gabriel *et al*., 2007). Aquaculture has been known to become the important source of protein for the world's growing population, having major roles in rural development as food security, source of foreign exchange earnings, manpower development, income and employment generation in several developing countries.

Capture fisheries is believed to have reached its peak and it is likely to continue to decline as stocks from the wild are diminishing. Faturoti (1999) asserts that the decline in capture fisheries is a trend all over the world. Omitoyin (2007) opines that maximizing exploitation of capture fisheries resources is no longer necessary. However, capture fishery resources would have to be properly managed for socio-economic reasons and most importantly for sustenance of benefits for aquaculture. Capture fisheries provide a genetic bank where hatchery stocks could be improved and sustained. It also provides socio-economic roles for populace in localities of fresh water environments.

Management of declines in capture fisheries would involve both ecological and genetic approaches. Challenges to capture fisheries are mainly from anthropogenic sources, as these influence both fish distribution and genetic structure of fish populations. The most important anthropogenic influences that have caused the extinction or have endangered species are: excessive exploitation, effects of introduced predators, competition, diseases, habitat destruction and conversion (Freeman, 1995). Anthropogenic factors can result in small and fragmented populations, which are subject to the deleterious effects of inbreeding and demographic instability.

The effect of anthropogenic factors is more felt in freshwater environment. A total of 84% of globally threatened fish species are from the fresh water (IUCN, 1996). According to McAllister *et al.* (1994), water-based threat to freshwater bio-diversity include: dam construction, introduction of exotic species, over-harvesting and aquaculture. FAO (1995) attributes declines in freshwater fish population to channelization and flood control, hydro-dams and pollution. Construction of hydro-dams has direct relationship with all the other highlighted factors. Damming has been the mostly implicated factor. It changes a running ecosystem to a stillwater ecosystems,

depriving species of their preferred habitats; blocks migrations; and changes seasonality of flow, water temperatures and many other qualities. Dam and water diversion projects cause declines of many native aquatic resources, affect breeding habitat and egg survival in fish (Lind *et al.*, 1996). They also result in loss of fisheries and degradation of habitat owing to detrimental off-season and fluctuating water releases (Petts, 1984, Burt and Mundie, 1986).

Fresh water dams are gradually losing significant portions of their catchment and this is having negative impact on catch and livelihood of rural communities; the effect on aquaculture will however, be more dangerous. Lake Chad has lost 90% of its catchment (Murray, 2007) and this is likely to be the trend in many other lakes on the continent. Gideon (2012) observes that lack of good data and indicators on the environment hide the extent to which most developing regions have suffered extensive environmental degradation over the past decade and are not on track to achieving environmental sustainability. Deleterious effects of dam construction could include catchment area loss, habitat fragmentation and degradation. Catchment area loss reduces available area for fishery activities, thus creating conditions of survival of the fittest organism. The consequence of such condition is extinction of local populations Habitat fragmentation may prevent exchange of genetic materials between populations, thereby reducing vigour. This will cause loss of genetic diversity. Overall sustainability of a fishery could be reduced by removing its genetic diversity. Genetic losses/degradation may come from actual loss of species and or loss of geographic populations or spawning stocks (Abramovitz, 1996).

According to Abramovitz (1996), information on genetic variability could be used for identification and management of fish stocks as well as for distinguishing and classifying species. Existence of genetically distinct stocks gives rise to special concerns for genetic exploration in populations. Information on genetic variability of populations has potential for management, improvement and conservation of declining fisheries.

Furthermore, genetic variation pattern could reveal sources of environmental stress to which plastic organisms are adapting and this could be used to trace reasons for extirpation, loss of species diversity and endangerment. Genetic and environmental factors would have influence on population structure. Management and conservation of declining wild fisheries would require assessment of genetic structure of fish species alongside environmental conditions. This is especially essential in hydrodynamic systems of fresh water environments. However, studies on fresh water lake fisheries in Africa

have concentrated on catch composition and measurement of ecological parameters while genetic components were mostly not documented.

Clarias gariepinus is one of the economically important catfish species in Africa. It belongs to the family *Clariidae*. The large African species of catfish which are of interest to aquaculture belong to the subgenus *Clarias* (FAO, 1996). Four genera, which comprise 97 species of the family are distributed in Africa and South-East Asia (Teugels, 1986). *Clarias gariepinus* has increasing commercial importance in fisheries and aquaculture (Turan *et al.,* 2005). It has Pan African distribution, being preponderant from Nile to West Africa, from Algeria to South Africa and Asia (Teugels, 1986). *Clarias gariepinus* is widely considered as the most important tropical catfish species for aquaculture in West Africa (Clay, 1979).

The versatile adaptive nature of the species (Pienaar, 1968; Bruton, 1979; De Moor and Bruton, 1988) underlines the need for periodic characterization of its phenotypic and genotypic structure for better management. This is especially essential in the face of reported catch decline and great environmental challenges from anthropogenic factors in fresh water dam systems.

Omoike (2004) reported declining stock of Asejire reservoir fisheries of which *C. gariepinus* was estimated to have 0.6% of total catch of 620 fish specimens from fish catch made between 2001 and 2003. Changes in physico-chemical parameters compared to previous findings was also reported, while catchment size was deduced as one of the responsible factors. Assessment of catchment-based threat to sustenance along with genetic structure is relevant for its better management and could be used to propose management strategies as *C. gariepinus* is a highly flexible specie. The information will be a clue to an understanding on the basis of declining stock pattern and provide baseline information for future management.

Morphometric and meristic data are the oldest and most economic methods employed in fish stock identification, population structure, adaptation and evolution studies. Morphological attributes are ready tools in taxa discrimination and useful in sexual differentiation (Skelton, 1993; Orlov and Cotton, 2011) and ecological adaptation studies (Santos *et al.,* 2011). Studies on morphology have been the historical basis for the sciences of taxonomy and evolution (Mayr 1969; Schreck and Moyle 1990; Rohlf, 1990). However, some of the measured values could be influenced by within-population variation and environmental factors.

Phenotypic variability is considered to be greatest in fish which has relatively higher within population coefficient of phenotypic variation. Carvalho (1993) and Herler *et al.*, (2010) noted that mean shapes differ significantly between sexes, population and species even though within-sex variation exceed the divergence among population in genus *Tropheus.* Morphometric and meristic characterization can be used to achieve diverse objectives. Choice of attribute for such phenotypic variability study depends on the objectives to achieve. Selected characters for phenotypic studies are sometimes skewed to some attributes that are not of relatively high importance to aquaculture. In some other cases, within-population phenotypic variations were not captured.

Reservoir fisheries are constantly facing various anthropogenic factors. the extent of which may reflect on phenotypes. Habitat conditions exert influence on genetic structure and genetic variation of species, which will make a difference to their adaptability (Saunders *et al.*, 1991). The less flexible species will migrate or extirpate, while plastic species will show heterogeneous phenotypic structure. The pattern of such structure could be predictive to the challenges of the environment. For instance, Cunico and Agostinho (2006) over that fish species inhabiting reservoirs are those possessing morphologies that allow behavioural plasticity, or those adapted to cope with new standing water conditions. When phenotypic attributes were captured in some studies on reservoir fisheries, the physical environments and anthropogenic factors of importance were inadequately or not reported despite the role of environments in shaping phenotypes.

It is important to undertake phenotypic and genotypic structure analyses alongside assessment of environmental challenges, especially in fresh water dam system. This important in developing management strategies for both the biotic and abiotic components in the fresh water dam environment. It would also generate relevant information for management, improvement, conservation and brood stock management of economically and culturally important species like *C. gariepinus* in lake or culture environments.

1.2 Justification for the study

Clarias gariepinus is the most cultured fish in Nigeria; and the second in Africa. It is a hardy fish. In spite of the strong adaptive traits possessed by this species, its population in Asejire Lake was reported to be declining (Omoike, 2004). The Lake is one of the major sources of wild brood stocks for aquaculture development in Nigeria. Reports have shown that lake/reservoir fisheries are constantly facing anthropogenic

challenges. The choice of the species and the water body for the current study was based on the aforementioned issues.

The habitat condition exerts influence on the genetic structure and genetic variation of species which will make a difference to their adaptability (Saunders *et al.*, 1991). In cases of environmental stress, less flexible species would migrate or extirpate, while plastic species would show heterogeneous phenotypic structure. Phenotype data are traditional tools for studies on fish adaptation, evolution, stock identification and population structure. Hence, assessment of phenotypic structure was carried out in order to trace trends in adaptation and structure of the studied fish population.

Phenotypic variability studies generate information for development of strategies for stock management, conservation and breed improvement (Turan *et al.*, 2005). It could reveal the functional attribute(s) of importance for adaptation to environmental conditions in specific ecosystems (Cunico and Agostinho, 2006). Phenotypic variability studies utilize morphometric and meristic data and generate information for predicting threats to species in habitats. Hence, assessment of phenotypic structure of the declining *C. gariepinus* population in Aseijre Lake was carried out using morphometric and meristic data.

Phenotypic heterogeneity is a likely structural form for versatile species in a dynamic environment, such as fresh water lake catchment. The heterogeneous phenotypic structure sometimes reflects taxonomic implications. This necessitates an assessment of discriminate factors that may have been responsible for cases of heterogeneous phenotypes. Therefore, analysis of discriminate factors for delineating heterogeneous phenotypic structure of *C. gariepinus* in Asejire lake was carried out in this study.

It would be important to delineate environment and genotype sources of morphological variability in cases of heterogeneous phenotypic structure. Consistent structural adaptation to environmental conditions may result in differential expression of some traits to which the population can be regrouped. In advanced situations of such phenotypic flexibility, morphotypes of biochemical and or genotypic implications could emerge. The morphological groups may however be potential varieties or subspecies of importance for genetic improvement of such species. Therefore, phenotypic structure and phylo-genetic implications of sub-populations of *C. gariepinus* was assessed.

Molecular tools are capable of delineating between genetic and environmental influence on phenotypes (Mayr, 1969) and it can establish pattern and spectrum of genetic variability in populations (Reisch *et. al.*, 2005). Electrophoresis of protein and DNA

fragments are ready tools for molecular studies. It is necessary to employ molecular tools using protein and DNA markers to highlight genetic implications of phenotypic variability in cases of morphological divergence in the studied population.

Inbreeding is a phenomenon in small populations. Inbreeding depression is an indicator of eroding genetic vigour in stocks. Tendencies of inbreeding depression could be proposed for the surviving small populations of *C. gariepinus* in Asejire Lake. Owing to impairment to gene flow across downstream as necessitated by dam embankment, the small population may have undertaken consistent mating within themselves. Bilateral asymmetry has been attached to inbreeding depression in fishes (Dunham, 2004). Therefore, possibility of using bilateral asymmetries of paired (median) phenotypes to evaluate inbreeding tendencies in the *C. gariepinus* population was assessed.

Management of fish genetic resources depends in part on availability of baseline information on key players in the environment of the studied population. This has to be carried out alongside genetic studies for reference purpose. With respect to Asejire Lake, there is inadequate information on combined data on the two parameters. Therefore, environmental condition of the studied *C. gariepinus* population was also assessed alongside genetic structure of the species.

Catchment structure as well as area and physico-chemical parameters are important factors that could influence the genetic structure (phenotypic and genotypic) of inhabiting fish population in environment. Potential threats from these parameters include: catchment fragmentation; losses in catchment area and effective area for fisheries activities and variations (high and low) in water quality parameters. Organisms would adapt to these threats and this would reflect in the phenotype. The parameters could change over time due to different anthropogenic factors. These potential threats were investigated alongside assessment of genetic structure of *C. gariepinus* for better management of the resource.

Determination of catchment structure and area measurements in large lakes require remote sensing techniques. Application of remote sensing and geographic information system has attracted scientific attention in fisheries and aquaculture. The technique has capacity to be used to update information on existing maps, determination of current area and activities at watershed of water bodies. With respect to the studied catchment, this has not received enough scientific attention. The technique is capable of removing ambiguity in assessing catchment loss and structural challenges which could

affect genetic structure, diversity and fish abundance. The technique was utilized in the current study.

Catchment structure could reflect threats such as fragmentation and degradation of the hydrologic area as well as its adjoining watershed. Fragmentation and degradation of habitat are the main causes of biodiversity loss and can endanger the genetic identity of a species (Wu *et al.*, 2003), and interrupting gene flow and consequently modifying population structure and diversity (Horreo *et al*., 2011). Frequency of opening of dams' gate could have negative impact on stability of physic-chemical parameters and physical condition to which species may adapt. Water level is maintained in Asejire Lake through opening of the dam's gate-valve. Dam's gate opening, catchments' degradation and fragmentation were also investigated as threats.

1.3 Research objectives

The general objective of this work was to investigate the genetic structure of *Clarias gariepinus* in relation to environmental condition of Asejire Lake for sustainable production.

The following were the specific objectives:

1. To update information on Asejire Lake's catchment condition with reference to structure, dimensions and potential threat to fish abundance and diversity.
2. To document morphometric, meristic and phenotypic variation of *C. gariepinus* population in Asejire Lake.
3. To evaluate discriminant factors in sub-grouping *C. gariepinus* population in the study area.
4. To establish genetic and biochemical structure of *C. gariepinus* population in the study area.
5. To investigate genetic variability of *C. gariepinus* population in the study area using deoxyribonucleic acid (DNA)-based markers.
6. To assess inbreeding tendencies in the *C. gariepinus* population.

CHAPTER TWO

LITERATURE REVIEW

2.1 Relevance, biology and distribution of *Clarias gariepinus*

Clarias gariepinus is also referred to as African catfish. According to FAO (2012a), Nigeria is, by far, the largest producer of farmed African catfish but the Netherlands, Hungary, Kenya, the Syrian Arab Republic, Brazil, and Cameroon, Mali and South Africa also produce significant quantities. *Clarias gariepinus* is widely considered as the most important tropical catfish species for aquaculture in West Africa (Clay, 1979). It is well known in both culture and artisanal environments in Nigeria being known by different names among different ethnic groups: *Tarwada* (Hausa), *Imiunu* (Ijaw), *Ejengi* (Nupe), *Aaro* (Yoruba) and *Arira* (Igbo) (Okonkwo and Obiakor, 2010). It equally supports socio-cultural and research purposes in most regions of the country. Research interest has been on its mass propagation techniques, development of recirculation system, along with quality feed development and genetic improvement of broodstock (FAO, 2012a).

FAO (2012a) gives the distribution, habitat and biology of *C. gariepinus* thus; African catfish has pan-African distribution but are naturally absent from the Maghreb (Upper and Lower Guinea and Cape provinces). It is equally present in Jordan, Lebanon, Israel and Turkey. It has been introduced into most other countries in Africa, as well as several in Europe, Asia and South America. China has adopted it within its rice-fields and is currently among the main producing countries. *C. gariepinus* is omnivorous; feeds on adults and larvae of gastropods, crustaceans, small fish, birds, aquatic plants and debris, as well as terrestrial seeds and berries.

2.1.1 Ecology of *Clarias gariepinus*

The most common habitats of *Clarias gariepinus* are floodplain swamps and pools where they can survive during the dry seasons. They can undertake lateral migrations from larger water bodies to temporarily flooded marginal areas in order to feed, breed and mature at about the age of 12 months *Clarias gariepinus* is a poor swimmer that spends most of the time on the bottom of lakes and rivers (Pienaar, 1968).

Ecologically, *C. gariepinus* is known for flexibility in feeding; ranging from grasping, zooplankton grazing, individual foraging and shoveling. It is slow foraging predators with very small eyes, using its four pairs of barbells to feel its way around in the

dark. It is omnivorous fish with high tendency of predation (Micha, 1973). It is an omnivorous slow moving predatory fish which feeds on a wide variety of food items from zooplankton to fishes of half of its length (Janssen, 1987). It also possesses versatile locomotory behaviour being capable of migrating overland to another water source by sculling with its tail as it elbows along on its spines (Gunder, 2004). *C. gariepinus* is easily adapted to environment where the temperature is higher than 20^0C (FAO, 2012). It has versatile adaptive features and can adapt to interspecific competition and predation pressures through body size, shape, head protection, pectoral spines and piscivorous habits; this enables it to survive almost all conditions (Bruton, 1979; De Moor and Bruton, 1988).

Clarias gariepinus has been described as threat to native catfish species owing to its ecological role in some situations. Na-Nakorn *et al.* (2004) note that the native catfish in Thailand (*Clarias batrachus*) was nearing extinction as a result of population expansion of farmed *C. gariepinus* in marshes and swamps and backcross of the species with hybrid of the two species, which resulted in reduced genetic variation of the native catfish. It is also implicated as threat to native fish species in rivers with the fear of local variety being wiped out. This has led to its ban as a variety of fish for culture in India (Daily News Agency, 2010). The hybrid and exotic catfish poses a threat to native species through competition, predation, hybridization and introgression (Philipp, 1991; Avise *et al.*, 1997)

2.1.2 Systematic position of *Clarias gariepinus*

More than 100 species of the *genus Clarias* have been described all over the world. *C. gariepinus* is also known as *Clarias lazera* and *Clarias mossambicus* (synonyms) (FAO, 2012). It has an anguiliform shape, having an elongated cylindrical body. It has scale-less, slimy skin which is darkly pigmented in the dorsal and lateral parts of the body. The pigment turns lighter when exposed to light but mosaic-like pattern of dark and light spots during stress. However, morphometric traits in *Clarias gariepinus* could be influenced by sex and or size. Skelton (1993) claims that males grow larger than females of the specie, while Gunder and Fink (2004) view metamorphosis as part of its attributes.

2.1.3 Morphometric and meristic attributes of *Clarias gariepinus*

Morphology in *Clarias gariepinus* has been described by Teugels (1986). The head is flattened, highly ossified with the skull bones forming a casque. The head length is 30-35% of body length, mouth circumference about 25% of total length. It has dorsal, caudal and anal fins as unpaired, while pectoral and ventral fins (pelvic) are paired. These set the pace for assessment of local population structure and adaptation. It has been observed that it is vitally important to obtain detailed knowledge on the population structure in commercially exploited *C. gariepinus* and to apply such knowledge on the management of the fisheries (Teugels 1986, Carvalho and Hauser, 1992). Turan *et al.* (2005) observed dearth of information on morphological population structure of *C. gariepinus* in river systems of Turkey and found that its samples were highly divergent with respect to morphological traits.

2.2 Location and relevance of Asejire Lake

Asejire Lake is a major man-made dam constructed on River Osun, which links the Ogun River and drains ultimately to the Lagos Lagoon in south western Nigeria. It is located between latitude 04^0 07' E and $07^0$21' N at an altitude of 137m above sea level (Omoike, 2004). The Asejire dam project was completed in 1972 and has a capacity of about 80 milliom litres per day, of which 80% is used for domestic purposes (Central Bank of Nigeria, 1999). Agricultural Development Programme (2010) views Asejire reservoir as a reservoir with plentiful water supply that remains full throughout the year; farming is totally banned in the catchment area and trees have been planted on the banks to prevent erosion. The reservoir provides raw water to the Asejire and Osegere water treatment plants in Ibadan (ADF, 2010).

Asejire Lake has accommodated villages and industrial activities along its catchment (Omoike, 2004; Obadara, 2006) and it maintains water level through a gate-valve control system. Omoike (2004), citing Oyo State Water Corporation, Ibadan (2003), avars that the dam authorities usually maintain water level around 156.2 above Mean Sea Level during the flood (rain season) by passing water under the gates and the water level of the reservoir has always been kept between 512 and 513 metres above sea level.

2.2.1 Catchment condition and fisheries of Asejire Lake

Asejire Lake is a man-made fresh water dam system. Dams are constructed impoundment that are either 7.62m or more in height and greater than 18,502.2 m^3 in capacity or 1.83m or more in height and greater than 61,674.0 m^3 in capacity (EPA, Environmental Protection Agency, 1993). Dam habitats are created and maintained by hydro-modification processes, such as channelization, channel modification, dams and stream bank and shore erosion. Fish community and other organisms are suffering rearrangements, with successive colonization of the environment for certain species and the decrease or even loss of others as a result of the change in watershed landscape emanating from damming (Agostinho *et al.*, 1999).

Catchment environment include the biotic and abiotic components. The aquatic flora and fauna constitute the biotic component, while the abiotic factors can be grouped under the basin shape, its area dimensions and water quality. The shape and physico-chemical characteristics of Asejire catchment has been reported in Egorge (1970), Aransiola (1990) and Omoike (2004). Fish communities in the catchment could be following the above-mentioned trend of theory proposed by Agostinho *et al.* (1999). Thirteen families and 23 species of fish were encountered by Elliot (1986), 41 species and 14 families in Akinyemi (1987), while 18 species and 12 families were reported in Omoike (2004). These show a trend of fish catch decline. Omoike (2004) notes that loss of species diversity and changed physicochemical values occurred in the catchment. Loss in species diversity in the catchment has been proposed to be linked with basins area value (Omoike, 2004).

Welcomme (1985) observes that considerable difference in number of species inhabiting the various river systems in Zaire, Nigeria and Ghana are due to a difference in basin area or some correlation of it. This opinion is supported by Payne (1986) and Akinyemi (1987). Basin difference could be measured in length of the main channel or stream order and, the larger the basin area, the greater is the potential for habitat diversity and increasing number of species in African lakes and rivers. Decrease situation could occur as a result of dam age, usage pressure and management. Rivers tend to decrease in number of fish species as they increase in age, (Welcomme, 1085). Omoike (2004) attributes less number of encountered fish in Asejire to ageing of the reservoir. These trends could be due to reduction or loss in the area of the catchment as a result of consistent dam usage and management over years. However, catchment loss or shrinkage and structure have not been captured in recent times.

2.2.2 Anthropogenic factors in fresh-water lake ecosystems

Freeman (1995) noted that habitat loss is one of the most important anthropogenic influences that have caused the extinction or endangerment of species. However, Boyd and Tucker (1998) argued that growth and survival of fish, which together determine the ultimate yield, are influenced by a number of ecological parameters and management practices. Omoike, (2004) found changing physico-chemical values in Asejire dam. Santos *et al*. (2011) noted that eventual consequence of impoundment may trigger some morphological divergence between closely related species. Habitat destruction and fragmentation of wildlife populations in dam systems are the primary factors reducing biological diversity (ICN, International Conservation News, 1988). Habitat loss and habitat isolation caused by landscape fragmentation not only affects ecological processes but also exert an influence on genetic structure and genetic variation of species, which will make a difference to their adaptability to changing environments (Saunders *et al.*, 1991). Opening and closing of dam gates result in high variation in flow, which is associated with more frequent floods where organisms could be physically harmed or swept away (USGS, United State Geological Survey, 2012).

Pattern of physico-chemical parameters could be central to fish health. Environments with unfavourable physico-chemical value could set natural selection pressure and thus select organisms, species, individuals and or phenotype of interest in the catchment. Ecological factors, such as catchment fragmentation, shrinkage, hydrologic area losses are potential threats to the fisheries of a catchment. Spatial pattern of some routine physico-chemical parameters and management practices such as, frequency of dams' gate-valve opening could be taken as potential threats to fish abundance and diversity. All these factors could also be assumed to be contributory to genetic/phenotypic structure of organisms.

2.2.2.1 Catchment structure and degradation

Certain portions of habitats are lost to development of land and water for agriculture, grazing by livestock and unsustainable use, such as draining of wetlands (IBCR, International Biodiversity Conservation Research, 2001). These activities have resulted in water catchment loss and alteration of valuable aquatic habitats. According to NWF, National Wildlife Foundation (2012), habitat loss could be in the form of physical change of wetland by filling, and dredging waters; habitat fragmentation, which includes much of cutting into fragments by dams and water diversions; habitat degradation through

pollution, presence of invasive species and disruption of ecosystem processes. Habitat may be so degraded that they no longer support native wildlife.

The need for assessment of lake dimensions could be best explained from the report by Murray (2007) that Lake Chad, once Africa's largest freshwater body supporting the livelihoods of about thirty million people in Cameroon, Chad, Nigeria and Niger has shrunk by 90% and this is having negative impact on catch and livelihood of rural communities around it. Lack of good data and indicators on the environment hide the extent to which most developing regions have suffered extensive environmental degradation over the past decade and were not on track to achieving environmental sustainability (Gideon, 2012).

Degradation undermines rural incomes and contributes to poor health and rural-urban migration, and settlement in environmentally fragile peri-urban areas. The application of Geographic Information System (GIS) and remote sensing (RS) has attracted scientific attention in fisheries and aquaculture. Kapetsky *et al.* (1988) view GIS as useful in catfish farming development. Salem (1998) utilized RS in detecting temporal environmental changes and El-Bayomi (2010) applied it in analyzing basin morphometrics. Extensive information on RS functions in aquaculture and inland fisheries is presented in www.fao.org/DOCREP/003/t0446E09.htm.

Guillera-Arroita *et al.* (2010) utilized geographic information technology (GPS) to determine coordinate and habitat suitability from satellite imagery. However, there appears limited information on digital mapping of most dam catchments in Nigeria. This introduces ambiguity in assessing catchment loss and the effect of its structure on genetic structure, diversity and abundance of fish community in the catchments.

2.2.2.2 Physico-chemical parameters

Changes in values of physico-chemical parameters would influence fish growth and survival (Ajani *et al.,* 2011) as fish performs all its metabolic activities in water. Deviation in values of some physico-chemical parameters and their spatial pattern would reveal them as potential threats to fish abundance and diversity in the catchment. Some of the routine physico-chemical parameters are discussed below.

Temperature is a measure of degree of hotness or coldness of a substance. Temperature of tropical river is between 26.5^{0}C and 32^{0}C (Gross *et al.,* 2000). This value agrees with values reported in Boyd (1979), Ugwumba and Ugwumba (1993) and King (1998). It also agrees with Onada (2010), who reported 27.95-30.21^{0}C in fresh water fish

culture medium. Omoike (2004), reporting on Asejire dam catchment, observes that temperature is a major determinant of distribution pattern of species. Temperature could vary at different portions of dam and this can be attributed to decomposition of organic effluents (Adeyeye and Abuludi, 2004). A temperature increase of 10^0 C often doubles the rate of decomposition and oxygen consumption in aquatic environment. Temperature could also vary with depth owing to the amount of solar energy that decreases with depth (Boyd, 1995). Transfer of heat from upper to lower layers of water depends largely on mixing of water by wind (Boyd, 1979).

Dissolved oxygen is a measure of amount of dissolved oxygen in aqueous solution and it plays vital roles in the biology of organisms (Thunjai *et al.*, 2001). Boyd (1979) and Boyd and Lichtkoppler (1979) give 5.68-5.7 mg/l as optimum range for fresh water organisms. Saloom and Duncam (2005) opine that minimum dissolved oxygen should be 5mg/l for tropical fish. Omitoyin (2011) claims that 4-9 mg/l would be better for fish health management. However, Fafioye *et al.* (2005) recorded values as low as 1.4-4.8 mg/l range in a water body in south-western Nigeria. Dissolved oxygen concentrations are greatest at 0^0C and decrease with increases of temperature (Boyd, 1979). Natural waters are never completely quiescent and oxygen transfer is regulated by the amount of turbulence (Welch, 1968). Diffusion of oxygen into natural waters is slow, except under conditions of strong turbulence (Boyd, 1979). Temperature is an important physical controller of dissolved oxygen (Ajani *et al.*, 2011).

Acidity (pH) is a conservative parameter; its range of values in an environment can be used to detect the effect of pollution. Hodson *et al* (1978) assert that a decrease in pH of one unit from any reference (6-10) results in an increase of lead by a factor of 2.1 units in blood of exposed rainbow trout. Boyd (1979) notes that if a sample of mud which contains sulphide is treated with hydrogen peroxide, the sulfide will be oxidized to sulfuric acid. Singh and Singh (2000) proposed pH range of 6-9 as suitable for most animals. The range proposed by Boyd (2005) for fresh water pond system (6.5-8.5) also falls within that of Singh and Singh.

Total hardness is a measure of concentration of calcium and magnesium ions expressed as equivalent of calcium carbonate. Hence, presence of inorganic salts, such as magnesium chloride, calcium chloride, magnesium carbonates and calcium carbonates, in water can cause water to be hard. Total alkalinity is the total concentration of bases in water expressed as mg/litre equivalent of calcium carbonate ($CaCO_3$); it normally results primarily from bicarbonate (HCO_3) and carbonate (CO_3) ions (Boyd, 1979). High

alkalinity may be due to carbonate contents of rocks and soils of watersheds and bottom mud (Boyd, 1979). Hardness and alkalinity are closely related. Combination of values of these parameters would therefore be indicative of ionic / nutrient availability in an aquatic environment (Mairs, 1966).

Omoike (2004) has suspected insufficient nutrient availability in Asejire Lake catchment. Increase in major ions such as carbonate, bicarbonate and hydroxide ions in water will cause significant increase in pH level (Stone and Thomforde, 2003). High values of these parameters are normally encountered in wet seasons due to runoff. When the total alkalinity of a water sample exceeds its total hardness, some of its bicarbonates and carbonates are associated with potassium and sodium ions rather than calcium and magnesium ions. Likewise, if the total hardness is greater than the total alkalinity, some of the calcium and magnesium ions are associated with Sulphide, Chloride, Silicate, or NItrate rather than with bicarbonates and carbonates (Boyd, 1979).

Limitation or abundance of mineral elements can be traced via measures of alkalinity and hardness. Moyle (1945) and Mairs (1966) claim that alkalinity value of <40 mg/l is indicative of soft water. Information on the recommended range of values for hardness in fresh water environment is scarce. However, Parker (1995) opines that fish does best at alkalinity between 20-30 mg/l but hardness value was not reported. However, Omitoyin (2011) recommended water hardness value of 50-300 ppm and alkalinity of 50-200 ppm for warm water fish culture.

Ayoade *et al*. (2006), while assessing limnological features of Oyan and Asejire lakes, reported that mean surface water temperature, transparency, dissolved oxygen content and pH were 29.9±2.34°C, 1.5±0.19 m, 7.1±0.96 mg/l and 7.4±0.43, respectively, in Oyan lake; and, for Asejire lake, the values were 28.5±1.91°C, 1.3±0.35 m, 6.9±1.33 mg/l and 7.4±0.54, respectively. The physic-chemical properties of the two lakes varied with seasonal changes in the rainfall of the drainage area. Oyan and Asejire lakes exhibited features typical of tropical environment. The high dissolved oxygen content values indicate that these water bodies can successfully support aquatic life including fish.

2.2.2.3 Reservoir management

Dam construction hinders flow regimes, hinders migration and gene flow between upper and lower courses of dammed rivers. Opening and closing of dam gates results in high variation in flow, which is associated with more frequent floods in which organisms

can be physically harmed or swept away (USGS, 2012). In frequently very low flow situations, volume of water is limited and species are likely to be subjected to large and rapid changes in pH, dissolved oxygen and water temperature. Omoike (2004), citing Oyo State Water Corporation, Ibadan (2003), claims that Asejire dam management maintains water level through a gate-valve control system. This indicates a flushing method of managing the water level which could have influence on the dam's topography, hydrography, fish distribution and phenotypic structure.

2.2.3 Anthropogenic factors and genetic resources diversity in fresh water lake

Santos *et al.* (2011) aver that eventual consequence of impoundment may trigger some morphological divergence between closely related species. Habitat destruction and fragmentation of wildlife populations in dam systems are the primary factors reducing biological diversity. Habitat loss and isolation have been greatly implicated in homogenization of populations of fish (ICN, 1989). Habitat loss and habitat isolation caused by landscape fragmentation not only affect ecological processes but also exert an influence on genetic structure and genetic variation of species, which will affect their adaptability. (Saunders *et al*., 1991)

Fragmentation and degradation of habitat are the main causes of biodiversity loss and can endanger the genetic identity of a species (Wu *et al.*, 2003), interrupting gene flow and consequently modifying population structure and diversity (Horreo *et al.*, 2011). Many fish species transform in body shape during growth and hydrodynamic condition. Body shape and fins from fish, ranging in size from larvae to mature adults, reflect disproportionately increased span of fins and body changed shape from elongated to streamline owing to hydrodynamic changes. (McHenry and Lauder, 2006).

Relatively larger head, longer caudal peduncle and mouth were linked with large prey and swimming capacity, thus implicating morphological diversification in order to explore different habitat and feeding resources (Santos *et al.*, 2011). Also, genetic introgression in *C. gariepinus* and native stock in the wild have been reported (Na-Nakorn *et al.*, 2004). Phenotypic and genetic Identity of dam fisheries would be influenced by several factors which could be location-specific and highly dynamic based on prevailing situation.

Characters may be influenced by local environmental condition which increased differentiation at small geographic scales (Turan, 2004). Development of broodstock for breeding programme cushions inbreeding in aquaculture but this relies on availability

and quality of wild stock (Dunham, 2004), hence the need for frequent update on phenotypic and genetic structure of important aquaculture candidates in wild environment such as Asejire Dam. This will be better carried out alongside catchment environmental characterization for better management. However, the literature revealed dearth of such information with respect to *C. gariepinus* in Asejire Dam.

2.3 Morphometric and meristic identity in fish population

Phena identification plays vital role in fisheries management, aquaculture and evolution studies. Effective fishery management and implementation of worthwhile stock rebuilding programmes utilizes knowledge of stock structure, distribution of fishing efforts and mortality among the various components (Begg *et al.*, 1999). Poor understanding of fish and fisheries can lead to traumatic changes in the biological attributes and productivity of a species (Ricker, 1981; Smith *et al.*, 1991). Morphological measurements have been widely used to differentiate various fish populations (Lowe McConnell 1972; Teugels, 1986; Elliot *et al.*, 1995; Uiblein, 1995; Hurlbut and Clay, 1998). Morphometric (linear measurements) and meristic counts are used to delineate stocks (Heincke, 1898; Mayr, 1969; Teugels, 1982; Aluko and Popoola, 2002; Turan, 2004, Turan *et al.*, 2005; Cunico and Agostinho, 2006; Gunawickrama, 2007 and Santos *et al.*, 2011).

Morphometric characters are continuous characters describing aspects of body shape, while meristic characters are the number of discrete, serially repeated, countable structures that are fixed in embryos or larvae (Turan, 2004). Holden and Reed (1978) assert that meristic counts of the dorsal and anal fins are more important in fish identification. Meristic characters, like number of spines and fin rays, permit greater accuracy than do linear measurements and are favoured in echinoderms, fishes and reptiles systematics of populations (Mayr, 1969).

Morphological traits can be used to predict species or community patterns of food and habitat use (Wainwright and Richard, 1995). Species morphology is somehow linked to habitat use and its performed niche, alteration in the environment, such as those resulting from dam construction, may restrict the permanence of certain previously existing species (Santos *et al.*, 2011).

Morphological features are adaptive; that is, they evolve and diversify owing to competition, predation, or other biotic interactions. This would lead to changing structure

as a result of complex interactions with other species or new environmental constraints (Bock, 1990). However, traits selection for population study depends on objective of study (Mayr, 1969). Some morphological characters of fish are useful in generating heterogeneity in morphology (Gunawickrama, 2007).

2.3.1 Phenotypic (morphometric and meristic) variation in fish population

One of the most ignored areas in aquatic genetics and biotechnology research is the effect of the environment and experimental procedure on genetic expression, the phenotype and phenotypic variation (Dunham, 2004). However, breeders or geneticists accomplish genetic gain by utilizing the variation of phenotypes of individuals in a population or by introducing new genotypes to genetically improve the performance of individuals and populations (Dunham, 2004).

Schreck and Moyle (1990) described two components to the development of variation within a species: first, the variation that arises from the different phenotypic responses to environmental factors, depending on the genotype; second, the existence of random, stochastic within-population variations for a species environmental condition, as well as the relationship between environmental conditions and the genotype. These may have a strong influence on phenotype expression (Schlichting, 1986). Traditionally, homogeneity in fish samples could be taken below 10% coefficient of phenotypic variation (Mayr, 1969).

Among the vertebrates, phenotypic variability is considered to be greatest in fish which have relatively higher within-population coefficients of variation of phenotypes (Carvalho, 1993). The variability is likely to have arisen from the great phenotypic plasticity of fishes in response to changes in environmental factors, (Wimberger, 1991; 1992). Phenotypic variation is affected by a combination of genetic and environmental factors, following the formula: $V_P=V_G+V_E+V_{GE}$ where V_P= phenotypic variation, V_G= genetic variation, V_E = environmental variation and V_{GE} = variation from genotype-environment interactions.

Measurement of genetic effects may not be accurate and may even be incorrect if the subtle differences emanating from effect of environment on genetic factors are not understood. Evaluation of genetic diversity is significant for understanding species adaptability, distribution of genetic resources and the origin of species (Sui *et al.,* 2009). Genetic diversity is the sum of genetic information carried by an organism (Barrett and Kidwell, 1998; Yan, 2005; Sui *et al.*, 2009). It includes distribution pattern of variation

(genetic structure of population), level of variation and the direct forms of expression of the genotypes (Hamrick and Loveless, 1989).

Elistrand and Elam (1993) assert that genomic flexibility can be used as a raw material for adaptation because low genetic variability often reduces the capacity to adapt to changing environmental conditions. This results in inability to cope with abiotic and biotic stresses (Valen, 1965). Eyo and Inyang (2004) presented the coefficient of difference and taxonomy of *Clarias* in Anambra, Nigeria in which *C. gariepinus* was included. Specific difference in meristic counts in the anal fin rays and vertebral counts was found to have close numerical relationship in the *Clariid* species. Teugels *et al.* (1998) compared morphometric in wild and cultured *C. gariepinus* specimens in Vietnam and found that the F1 can be considered intermediate of the parents as meristic traits (dorsal fin rays and anal fin rays) had intermediate values. Turan *et al.* (2005) studied pattern of morphometric differentiation among six populations of *C. gariepinus* in Turkey. Univariate analysis of variance revealed that the samples were highly heterogeneous when 30-32 individuals were analyzed per location. Turan *et al.* (2005) suspected presence of morphologic sub-species in *Clarias gariepinus* population which could be differentiated using molecular genetics tools.

Ferrito *et al.* (2003) studied morphological and genetic variation in four Italian populations of *Lebias fasciata* to understand their congruence in the population. Isozyme variation among four catfish genus *Clarias,* including *C. gariepinus,* is presented in Na-Nakorn *et al,* (2002). However, a combined morphometric, meristic and molecular genetics report on Asejire reservoir's *C. gariepinus* population seems unavailable.

The study and comparison of intra-specific population variation has become major objective of population systematic (Mayr, 1996), management of aquaculture candidates (Na-Nakorn *et al.*, 2004; Dunham, 2004) and conservation genetic studies (ICN, 1988). Measurement of phenotypic variation in meristic and morphometric traits could be compared using percentages, coefficient of variation, ratio and multivariate. The coefficient of variation (CV) of most meristic characters is smaller than those of linear characters and is not permissible to compare the CV of the two kinds of variants (Mayr, 1969). The coefficient of variation for linear dimensions in mammals is usually between 4 and 10, occasionally between 3 and 4 in homogeneous samples; however, zones of secondary intergradations between sub-species are often characterized by a greatly increased coefficient of variation (Mayr, 1969). Periodic assessment of fish population for

changed phenotype is important because Intra-specific morphological divergence has been associated with habitat use (Langerhans *et al.*, 2003).

Morphometric measures are performed in order to reflect traits associated to habitat use (Watson and Balon 1984, Balon *et al.*, 1986 and Santos *et al.*, 2011). Omnivorous fishes have broad morphological variations probably related to lack of specialization for feed (Horn, 1998).

Morphology would reflect fish adaptation to reservoir condition (Santos *et al.*, 2011). However, there is dearth of information on *C. gariepinus* population's morphological identity and diversity in Asejire Dam system despite its current ecological and economic status in the catchment.

2.4 Independent / discriminant factors in heterogeneous phenotypes

In order to permit reliable conclusions in population differentiation, a sample should be homogenous, and unbiased (Cochran, 1959). A heterogeneous sample can often be segregated into smaller homogenous samples by separating the specimens according to age, sex, locality, or other factors that have introduced heterogeneity (Mayr, 1969). Significant linear correlation between all morphometric characters and standard length of fish has been reported (Elliott *et al.*, 1995; Gunawickrama, 2007).

Kutano *et al.* (2012) observe that males tend to have deeper bodies than females in both forms but the magnitude of sexual dimorphism is reduced in stream-resident forms of *Gasterosteus aculeatus.* Closely associated set of traits that showed sexually dimorphic growth was positively allometric (changes in body shape as organism develop) in males when size range 31-91mm were analyzed in *Oreochromis niloticus* (Oliveira and Almada, 2005). Sexual dimorphism of buccal cavity of multiple mouth brooding species was reported by Barnett and Bellwood (2005). Growth was found to be positively allometric in *Pterogogus auriganus* with males possessing larger first and second spinal rays in dorsal fin than females (Park *et al.*, 2005). Kassam *et al.* (2004) observed statistically significant body shape differences among species but not between sexes when interspecific variation of body shape and sexual dimorphism was considered in three co-existing species of tilapia. Eastman and Eakin (2001) found no significant difference between sexes in morphometric and meristic features in *Dolloidraco longedorsalis* from the Ross Sea.

Posti *et al.* (2008) utilized geometric method and found that only dentary characters showed significant differences among head measurements of populations. Allometry growth and sexual dimorphism was reported in *Clarias gariepinus*. Skelton (1993) found that males grow larger than females of the species, while Gunder (2004) observed metamorphosis (changes in body shape during developmental stages) as part of its attributes. Turan *et al.* (2005) reported high morphologic differentiation among *C. gariepinus* populations with high phenotypic differences between samples from the studied rivers.

Homogeneity is particularly important in comparative studies because samples which differ in their components owing to heterogeneity cannot be legitimately compared. This leads to regrouping into definite classes, determined by the presence of certain conspicuous characters frequently controlled by a single gene resulting in polymorphism which has great biological importance because it proves the existence of selective differences between apparently neutral characters (Mayr, 1969).

High phenotypic variation leads to suspicion and detection of morphotypes in fish populations. Turan *et al.* (2005), while discussing high phenotypic differences observed in *C. gariepinus* population, suspected the presence of other taxa and the need for application of molecular genetics techniques to confirm the detected phenotypic differentiation.

2.4.1 Morphologic typology and genotypic structure in morphotypes

Morphologic divergence analysis has resulted in deciphering morphotypes in fish populations. Detection of within-population morphotypes has taken genetic approach in concluding phenotypic variation patterns (Mayr, 1969; Carvalho and Hauser 1992; Turan *et al.*, 1998; Shaw *et al.*, 1999). Resource polymorphism was reported in *Salvelinus alpines* from Lake Hazen by combining morphometric variation in head, body and fin shape with population structure assessment using molecular tool. However, lack of genetic differentiation was observed in the morphologically different sub-groups (Arbour *et al.*, 2011)

Prelimnary morphometric data for four traits in *Pimelodella chagressi* revealed significant differences between two lineages for two of those traits, namely caudal peduncle depth and proportion of pectoral spine covered with posterior projection of teeth (Martin and Birmingham, 2000; Beland 2004). Benthic-limnetic morphs in postglacial Arctic and boreal lakes with few fishes have been reported by Skulason and Smith

(1995). Strong morphometric and meristic differentiation was linked with self-recruiting population or sub-species of horse Mackerel in Marmara Sea (Turan, 2004). Four morphs of Arctic char reported in Sandlund *et al.*, (1996) differed in morphology, habitat use, trophic ecology and life history.

Differences in body shape and head morphology have been linked with differing trophic ecology in sympatric morphs as well as other polymorphic fish populations (Skulason *et al.*, 1989; Schluter, 1993; Adams *et al.*, 2006). Genetic analysis revealed that the lake was colonized once by Arctic char and that morphs subsequently diverged rather than being colonized by benthic and pelagic morphs independently (Volpe and Ferguson 1996; Gislason *et al.*, 1999). Arbour *et al.* (2011) distinguished between two morphs by using morphometrics of head, body shape and fin shapes; longer, deeper head, longer abdomen and shorter caudal peduncle differentiated their body shapes; fin lengths (anal and pelvic fins) were different between the morphs.

Bimodality in phenotypic traits has been observed between morphs (Eastman and Devries 1997; Guiger *et al.*, 2002). Eastman and Devries (1997) identified morphs by measuring dorsal and ventral views of head shape and found that, although intermediate morphs were not apparent, caudal peduncle depth was nearly significantly different. However, gape width and upper jaw length did not scale iso-metrically with head length and were useful measures of trophic morphology. The attributes separated the morphs in nearly bimodal fashion, thus sibling or cryptic species was concluded.

Precise measurements sometimes display bimodal characteristics and the two modes can be correlated with additional characters with differences in the number or structure of the chromosomes which has led to recognition of sibling species which may differ in their pathogenicity, susceptibility, suitability and are better confirmed through biochemical analysis (Mayr, 1969). Arbour *et al*. (2011) observe that, without an examination of genetic relationships of morphs, the role of factors such as phenotypic plasticity and genotypic composition in determining morphological differences cannot be fully resolved. Smith and Skulason (1996) opine that study of divergence among sympatric morphs provides opportunity to examine the influence of functional morphology, heritable variation and phenotypic plasticity during early stages of reproductive isolation and speciation.

The genetic structure of a population is important in understanding species biological characteristics and exploration of evolutionary processes and mechanisms. Genetic differentiation within and between populations reflects genetic structure and

coefficient of genetic differentiation is the most commonly used index (Sui *et al.,* 2009). Genetic variation is subject to combined effects of mutation, gene-flow, natural selection and genetic drift (Liu and Zhao, 1999). Understanding of genetic variation in a specific population is advantageous to monitoring gene-flow, while genetic rescue of genetically eroded populations could be achieved by gene-flow (Richards, 2000 and Ingvarsson, 2001); gene flow is the most important factor to counteract the effects of selection (Grant, 1991); it could resist genetic drift and reduce inbreeding depression in order to maintain the diversity of genetic variation (Leigh *et al.,* 1993; Liu and Zhao, 1999).

2.5 Assessment of genotypic structure in fish population

Assessment of genotypic structure in fish population utilizes molecular tools. The encountered studies on this are reviewed below**.**

2.5.1 Assessment of biochemical and genotypic variability in fish population

Studies on genetic structure in population have employed biochemical molecular genetic analyses (Mayr, 1969; Sui *et al.,* 2009; Labonne *et. al.,* 2008; Wu *et al.,* 2009; and Zhang *et al.,* 2009). Madan *et al.* (2002) and Reisch *et al*. (2005) note that pattern and spectrum of genetic variations within or between populations can be compared and analyzed using molecular tools. The most frequently used tool is the protein electrophoresis. Gottileb (1971) claims that electrophoresis has an advantage, in that it can directly equate variation in protein banding patterns to genes encoding these proteins. Protein electrophoresis has been found useful as genetic marker (Gottileb 1971; Cherry and Ory, 1972; Oladejo *et al.,* 2009). However, molecular markers based on relative difference in DNA sequence between individuals generally detect more polymorphisms than morphological and protein-based markers and constitutes a new generation of genetic markers (Sakai *et al.,* 2008).

2.5.2 Electrophoresis of DNA fragments in fish populations

Microsatellite and randomly amplified polymorphic markers seem to be the most popular markers encountered on fish genetic characterization and diversity studies. Microsatellite markers have been employed in molecular characterization (Galbusera *et al.,* 1996; Durmic-Pasic 2005; Johnson and Banks 2008; Bucklin *et al.,* 2011).

Randomly Amplified Polymorphic Deoxy-ribonucleic Acid (RAPD) has been one of the most commonly used molecular/DNA markers. It has been used in constructing

trees in animals, such as buffalo, cattle, goat, and sheep (Appa- Rao *et al.*, 1996), fish (Bardakci and Skibinski, 1994), bacteria (El Hanafy *et al.*, 2007) and Date palm (Soliman *et al.*, 2003). RAPD has found wide application in gene mapping, population genetics, molecular evolutionary genetics, plant and animal breeding (Bardakci, 2001). Application of the technique in several fish characterization and genetic variation studies has been reported in Bardakci (2001). It is fast, cost effective, utilizes small DNA fragment, does not require knowledge of DNA sequence for the targeted gene, able to generate large numbers of markers in a short period compared with other methods (Bardakci, 2001; Sabir *et al.*, 2012). Protocols in randomly amplified polymorphic DNA markers in comparative genome studies have been presented (Chang *et al.*, 1991).

Genetic disparity between *Clarias gariepinus* and some other catfishes using molecular tools has been reported (Galbusera *et al.*, 1996; Agnese and Teugels, 2001: Na-Nakorn, 2004). Yapi-Gnaore (2001) claims that genetic analysis using microsatellite and restricted fragment length polymorphism markers have been carried out on potential culture candidates in Cote d'Ivoire (*Sarotherodon melanotheron, Oreochromis niloticus, Oreochromis aureus* and *Siluriformes-C. gariepinus, C anguillarus, Heterobranchus longifilis, H. bidorsalis* and *Chrysichthys nigrodigitatus*). However, similar report in Nigeria context was not encountered. Dearth of information on molecular genetic structure of culturable fish species alongside morphological characterization in wild fisheries was also observed despite the principal role of the wild stock as genetic reservoir for improvement and sustainability of aquaculture industry in developing African countries.

2.6 Assessment of in-breeding depression tendencies in fish population

Inbreeding affects reproductive success (Slate *et al.*, 2000) and survival (Keller *et al.*, 2001). However, it could be utilized in aquaculture via selective breeding (Tave, 1995). Inbreeding results in lack of genetic variation or too much homozygosity, which can be detrimental to individual's or a population's survival traits and fitness; highly homozygous species has severe reproductive problems and this is linked to bilateral asymmetry - unbalanced meristic counts on the right and left halves of the body in fishes (Dunham, 2004). Inbreeding in small, natural populations increases extinction rate (Doyle, 2003). Levels of homozygosity and inbreeding can be important in domestic or aquaculture as well as wild fish populations. However, its deleterious effects can be prevented in natural population via migration (Dunham, 2004). Monitoring phenotypic

values from both sides of individual fish (especially the paired fins) in population would reveal inbreeding status and or depression.

2.6.1 Habitat condition and in-breeding depression tendencies in fish population

Among population at risk of imminent extinction, there is diversity in population structure, selective pressures of the environment and modes of adaptation to the environment (ICN, 1988). Small populations that narrowly survive demographic contraction may undergo close inbreeding, genetic drift and loss of overall genomic variation owing to allelic loss or reduction to homozygosity in addition to ecological and demographic perils (O'Brien, 1994).

Wild populations are increasingly subjected to uncontrollable stochastic factors. As a population declines in size, inbreeding becomes likely and genetic variation is lost owing to increasing genetic drift (ICN, 1988). Although habitat destruction and fragmentation of wild population are the primary factors reducing biological diversity, genetic loss in population might be due to a series of severe declines in population (O' Brien, 1985). Schaffer (1987) mentions uncertainty in environment that can influence population size as random events in demographic condition (change in survival and reproduction, like shift in sex ratio at birth or mortality due to accident); environmental (unpredictable weather, food supply and population of competitors, predators, parasites and so on; natural catastrophes (flood, fire, drought and so forth) and genetic (random changes in genetic make-up due to the founders effect, genetic drift or inbreeding). Predicting possibility of maintaining genetic pool against inbreeding will be assisted by knowledge of catchment structure which most of the available studies do not reflect.

CHAPTER THREE

METHODOLOGY

3.1 Location and geography of the studied area

The study area was Asejire Lake. It is a major artificial dam constructed on River Osun which links the Ogun River and drains ultimately to the Lagos Lagoon in south western Nigeria. It lies at borderline between Oyo and Osun States of Nigeria. It is on latitude 04^0 07'E and $07^0$21'N at an altitude of 137 m above sea level. Asejire River is one of the series of West African Rivers that do not drain into Niger system but discharge into coastal lagoons and creeks bordering the Atlantic Ocean (Omoike, 2004). The reservoir has an approximately 7,403 million litres and a flooded area of 6 km^2 (Welcomme, 1985).

The Lake receives supply from Rivers Osun and Oba at the left arm, while Agbora arm feeds the dam from the right, making the reservoir to have a Y shape when viewed from the point of impoundment. Its entire length is 11.2 km, catchment area above the dam is about 7,800 km^2 and the impounded area is 2,342 hectares. According to Elliott (1986), the area is well watered as numerous tributaries of the Osun River cut through the surrounding rolling country area; however, most of the smaller tributaries dry up from November to March and refill during the rains in May. A map of the study area is presented in Figure 1.

3.1.1 Climate, ecologic and economic importance of the studied area

Information on the climate of Asejire Lake was obtained through secondary meteorology data. This was obtained from Nigeria Institute for Meteorology (NIMET), Ibadan. Secondary data was used because there was no meteorological station in the study area. The climatic data for Ibadan was used, being the nearest reported station by NIMET. According to the data, between 2006 and 2008, minimum temperature range was (^{o}C) 21.5 (Aug) - 24.6 (Mar) in 2006, 21.0 (Dec) - 24.4 (Mar) in 2007 and 20.2 (Jan) - 24.3 (Mar) in 2008. Maximum temperature range (^{0}C) was 28.1 (Jul) - 36.9 (Mar) in 2006, 27.7 (Aug.) - 34.9 (Feb) in 2007 and 27.2 (Aug) -36.2 (Feb) in 2008. Relative humidity range (%Sat) taken in the 9th hour was 63 (Feb) – 89 (Aug) in 2006, 70 (Jan & Dec) – 88 (Jul & Aug) in 2007 and 50 (Jan) – 88 (Jul) in 2008. Rainfall (mm)

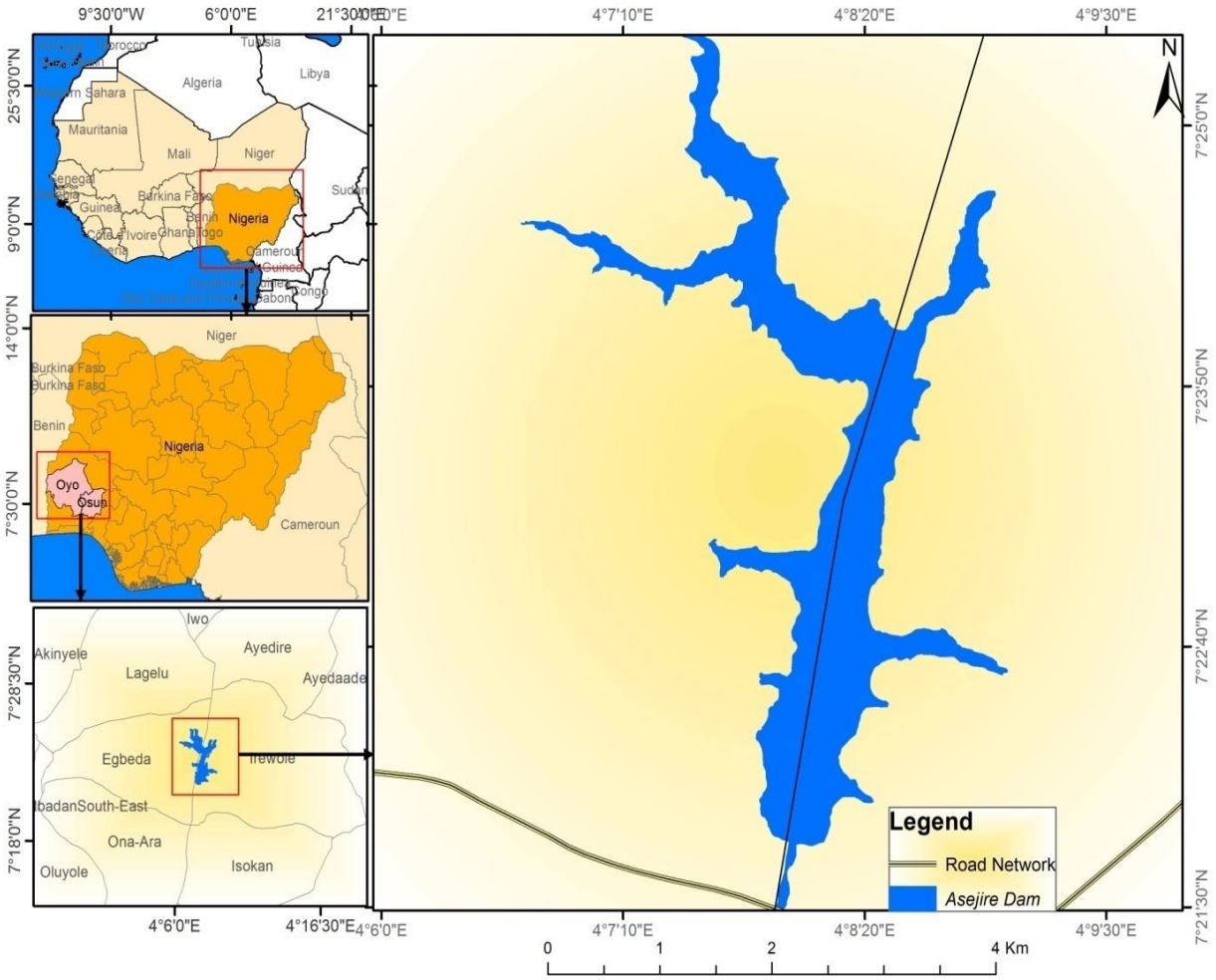


Figure 1: Map showing location of the study area

range was 0 (Dec.) - 312.5 (Sept) in 2006, 0 (Jan) - 303.8 (May) in 2007 and 0 (Feb.) - 200.4 (Mar) in 2008.

Asejire Lake has served socio-economic and research purposes in the south western Nigeria. It supplies raw materials for Oyo and Osun States Water Corporations, the Coca-Cola Industry and the Nigerian Breweries. The adjourning villages depend on its fisheries for sustenance because the majority of their populace are fisher-folks. Villagers utilize its water resource for domestic, small-and medium-scale food processing, agriculture, laundry and for spiritual activities. According to Obadara (2006), Asejire Lake contributes largely to fish supply for research and consumption.

3.2 Assessment of Asejire lakes' environmental condition

Asejire Lake environment was assessed for indices of threat to fisheries. The assessment was carried out between November, 2009 and December, 2012. Environmental condition that indicated threat to fisheries was assessed alongside Water Quality Parameters (WQP). The assessment was preceded by production of digital image and estimation of area dimension of the lake and its fishing zones.

3.2.1 Production of digital image

In order to facilitate production of digital image of the lake, geographical survey of the catchment was conducted. This was carried out on board of dug-out canoes between November and December, 2009. The survey covered water inlet sources, confluences, tributaries (Lake arms) and floodplains beyond the impounded area. Coordinates of the sites were obtained using Geographic Positioning System (GPS) (GARMIN, GPS 76) obtained from Department of Geography, University of Ibadan, Nigeria. Satellite imagery of the catchment was obtained from Google Earth (www.google.com), surveyed sites' coordinates were geo-referenced and digitized on the satellite image using ArcGIS 9.3 software.

Shape/structure of the fishing zones were also delineated using the earlier described method of digital imaging of the entire lake. The lake was spatially divided to two strata. These were the eastern (Osun State strata- O_SS) and the western (Oyo State strata - O_YS) strata of the lake. Fishing zones, such as the main axis of the lake, diverted portions (tributaries) and water inlets of the main axis, were identified and mapped on each stratum. Identity of the zones followed their local nomenclature: Main lake course (area from impounded end to the confluence), Koloko inlet (area covered along Koloko

arm up to the confluence on O_YS), Agora inlet (area covered along Agora village arm up to the confluence on O_SS), Ikoyi arm (tributary located along Ikoyi village on the O_SS), Ikire minor (minor tributary located along Ikire village on the O_SS), Ikire major (major tributary located along Ikire village on the O_SS), Asala major (major tributary located along Asala village on the O_YS) and Papa Asala (minor tributary located along Asala village on the O_YS). Structures of the adjoining watersheds of the strata, swamps and man-made facilities directly located on the lake were also documented. The obtained shapes were compared with earlier description to determine structural deviation.

3.2.2 Estimation of area values of the catchment and its fishing zones

Area estimation was carried out through computing area function on ArcGIS software. Digital image of the catchment was utilized to estimate area dimensions of the entire catchment (CA) and its fishing zones. The separately digitized fishing zones gave the opportunity for accurate estimation of contribution from each fishing zone to the total catchment area of the lake measured in metre square (m^2). This was taken as:

$$\% \text{ Contribution by Zone} = \frac{\text{Area covered by zone}}{\text{Catchments' Area}} \times 100\% \quad \ldots\ldots\ldots\ldots 1$$

Area covered by swamps and man-made facilities was also estimated and used to derive Fishing Area (FA) for the catchment. For the purpose of the study, fishing area was taken as total area available for fishing and navigation. Total portion of the catchment area that was not covered by swamp and man-made facilities was presumed to be total fishing area. Man-made facilities were physically observed and their area dimensions estimated. Fishing Area was taken as:

FA = CA- (Area covered by swamps + Area covered by Man-made features) ……2

3.2.3 Determination of potential threats to fisheries in Asejire Lake

Potential threats to fishing were assessed through the generated baseline information from geographical survey, maps and the estimated area values of the reservoir and its fishing zones. The assessed potential environmental threats included:

i. Catchment Fragmentation (CF), Catchment Area Loss (CAL)
ii. Reduction in Effective Area for Fishing Activities (EAFA)
iii. Loss of Adjoining Watershed Forest to Degradation by Human Activities (WFD)
iv. Frequency of Complete Dam Gate Opening (CDGO),
v. Frequency of Partial Dam Gate Opening (PDGO)
vi. Water quality of the Lake

3.2.3.1 Catchment fragmentation

Structural evidence of catchment fragmentation was examined from the digitized image of the catchment. Presence of water diversion routes (zones of tributaries) were taken as evidence of fragmentation. Zones of tributaries were taken as fragments when they can be differentiated by their orientation with respect to inlets, distance apart and area dimensions.

3.2.3.2 Catchments' area loss

Loss in total catchment area of the lake as revealed by reduction of catchment area when compared with the earlier reported value of 7,175,000m^2 (Aransiola, 1990) was taken as catchment area loss. This was presented as percentage loss using the formula:

$$\% \text{ CAL} = \frac{\text{Initial catchment area – (minus) current catchment area}}{\text{Initial catchment area}} \times 100\% \quad \ldots\ldots 3$$

3.2.3.3 Loss of effective area for fishing activities (EAFA)

The total area of the catchment that was available for fishing and navigation were considered as potential areas for effective fisheries activities in the catchment. Meanwhile, presence of silt threatened area, man-made features and poor quality swamp composition was considered as threat to effectiveness of fishing in the lake.

Portions of the catchment that reflected presence of siltation as observed from satellite image were referred to as silt threatened area and these were estimated. Swamps were considered as loss when it reflected loss of flora richness and when flora activities disturbed fishing and navigation. Swamp characteristics, flora activities and richness were monitored during a two-year bi-monthly survey of the catchment. Activities and nature of swamps were documented with the aid of digital camera (Sanyo, VPC, S1070, 10.0 Mega Pixel). The EAFA of the catchment was taken as:

$$\text{EAFA} = \frac{\text{FA- Siltation Threatened Area}}{\text{Total Catchment Area (CA)}} \times 100\% \quad \ldots\ldots\ldots 4$$

3.2.3.4 Loss of adjoining watershed forest to degradation

Evidence of deforestation and other human activities such as farming, erection of buildings and industrial activities at the watershed were taken as indices of watershed forest degradation. This was observed from satellite image of the catchment as well as during geographical survey of the catchment. The degraded areas of the adjoining watersheds' forest of the fishing zones at the main course of the lake, inlets and tributaries of the strata were estimated and presented using the formular:

$$\% \text{ WFD} = \frac{\text{Estimated degraded watershed area}}{\text{Estimated watershed area}} \times 100\% \quad \ldots\ldots 5$$

3.2.3.5 Frequency of dams' gate opening

Assessment of frequency of opening of the dams' gate (Dam gate-valve opening-DGO) and its effects on fisheries was used to determine opening of the gate of the dam as potential threat to Asejire Lake fisheries. Formal document on the frequency of opening of the gate valve of the dam was sought from Water Corporation of Oyo State which manages the dam. This was followed by bi-monthly data capture of observations on frequency and type of opening of the dam's gate.

Gate opening was taken as Partial Dam Gate Opening (PDGO) when the dam's gates were opened but not entirely, while Complete Dam Gate Opening was identified as a situation where the gates were entirely opened. Frequency of each type was documented bi-monthly. Interval (number of days) in between a complete opening of the dam's gate and any other gate opening was also documented.

Pictures were obtained to show the effects of the gate opening on shore activities and the lake's fishery. Monitoring of opening of the dam's gate was concurrently carried out with sampling for water quality.

3.2.4 Assessment of water quality parameters of Asejire Lake

Spatial values of water quality parameters of water samples of Asejire Lake was determined and assessed for variability. The studied water quality parameters were temperature, Dissolved Oxygen, Total Alkalinity (TA) and Total Hardness (TH).

3.2.4.1Experimental design

The design for sampling of water quality parameters of the lake was based on available information on water inlet sources and structure of the Lake (Elliott, 1986). Asejire Lake was spatially divided into Oyo State (O_YS) and Osun State (O_SS) strata. A total of thirty-eight sites were randomly selected for sampling, nineteen sites from each stratum. Main reservoir axis of each stratum was sampled at approximately 1000m apart from the embankment towards the inlet axis (the location coincided with the locations of impounded area, pre-tributaries, and post-tributaries). Each of the three divisions has three sites located at equidistant from the shore to the constructed reservoir arms of the embankment. The three sites were 126.00±2.82m apart on the O_YS and 156.00±16.86m apart on O_SS.

Major and minor tributaries along each of the strata (O_YS and O_SS) were also selected for sampling. Four sites were selected on a minor tributary. The sites were located at point of entry and the last accessible point on the leeward and windward sides of each minor tributary. Six sites were selected on each of the major tributary of each of the stratum. The sites were located at point of entry, mid-point and the last accessible point on the leeward and windward sides of each of the stratum. Compensation for relatively larger size in major tributary was the basis for selecting mid-point sites for major tributaries. This made the total sampling sites to be 38. Information on the sampled sites and their identity is presented in Appendix 2. Map of the sampled sites is presented in Plate 1.

3.2.4.2 Sampling procedure

Water quality parameters were sampled bimonthly in wet and dry seasons for 24 months from the 38 selected sites of the catchment. Samples were collected as described in Omoike (2004) with modifications. Samples were obtained on board dug-out canoes between January and December, 2010-2011. Samplings were carried out in January, March, May, July, September and November. Samples obtained during October-November, December-January, and February-March sampling periods were taken as dry season samples while those of April-May, June-July and Aug-September were taken for wet (rainy) season samples. Samplings were completed within one week during each sampling period. Water samples for analysis of physico-chemical parameters were taken at about 30cm depth from each of the 38 sites between 7.00a.m. to 9.00 a.m. during each sampling period.

3.2.4.3 Determination of values of water quality parameters of Asejire Lake

The spatio-temporal values of each of the studied water quality parameters were determined. Values were determined for strata across wet and dry seasons. All the parameters were measured per site at every sampling period. Examination of water quality followed Omoike (2004). Temperature was determined on-site and measured using mercury-in-glass thermometer. Water samples for determination of Dissolved Oxygen Content (DO), Total Alkalinity (TA) and Total Hardness (TH) were obtained in water sampling bottles and were immediately taken to the Central Chemical Laboratory of the Water Corporation of Oyo State upon landing. Determination of values of the parameters followed Boyd (1982).

Dissolved oxygen was determined by the Winkler's method. Water samples were fixed with 2ml of Winkler's solutions A and B shaken properly then 2ml H_2SO_4 was added and vigorously shaken. The treated samples were then titrated with 0.025N Sodium thiosulphate using fresh starch solution as indicator until the colour changed from yellow to colourless. Titrations were repeated and the average value recorded. Volume of the titrant is assumed to be equal to the amount of the iodine liberated and this is equivalent to the original dissolved oxygen content of the sample (Boyd, 1982).

Total Alkalinity and Total Hardness were also determined by titrating sampled water against standard indicators. For determination of Total Alkalinity, sampled water were titrated with 0.02N H_2SO_4 after 2 drops each of Sodium thiosulphate mixed with methyl orange had been added. Total hardness was determined as the portion of Calcium and Magnesium ion in the samples. 2ml of ammonia buffer solution and a pinch of erichrome Black T was added to 50ml of samples and titrated with EDTA solution until the colour changed to blue. Values of each physico-chemical parameter obtained throughout the sampling period was used to compute mean values per site and strata across seasons.

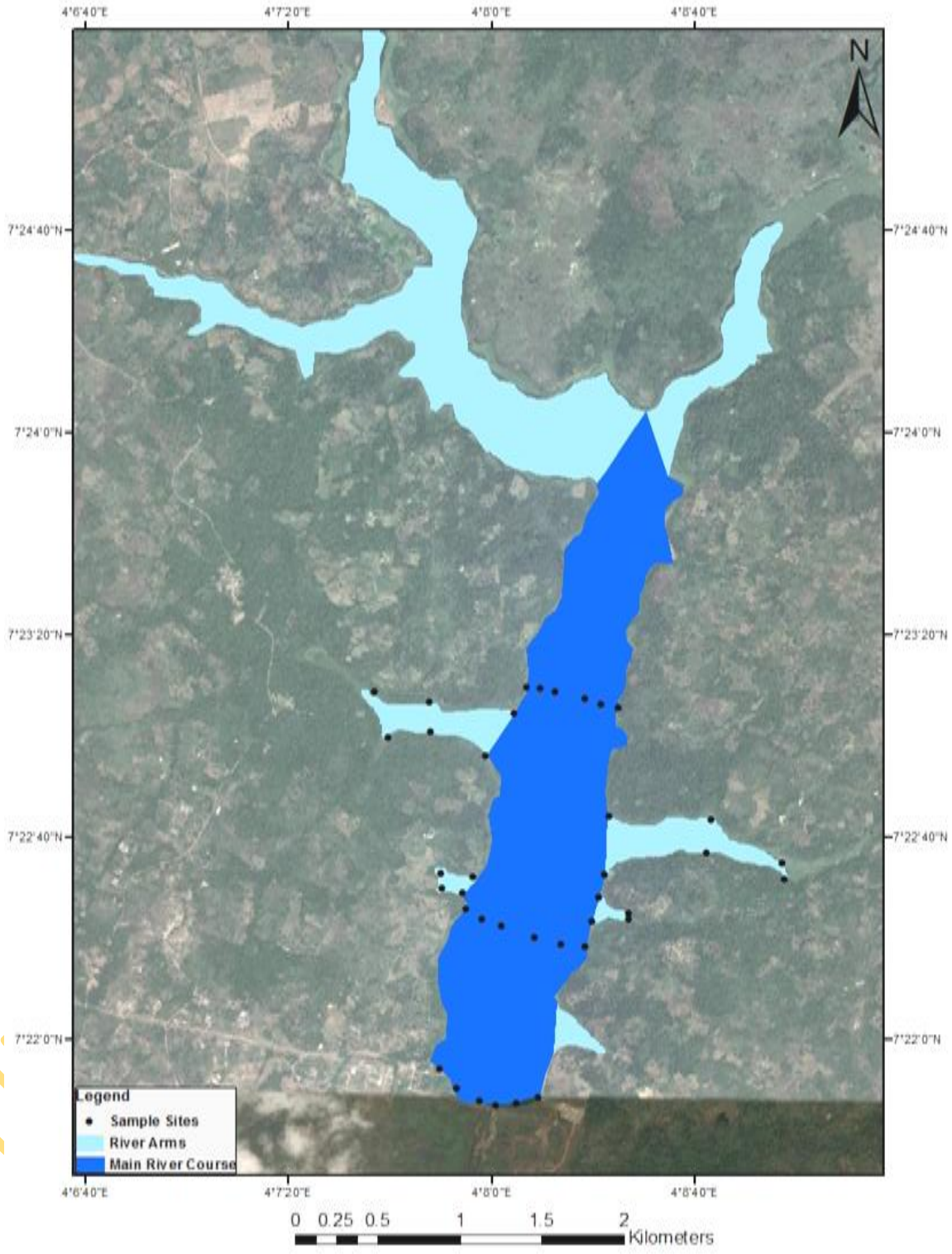


Plate 1: Map showing the 38 sampled sites at Asejire Lake

3.2.4.4 Assessment of variability in water quality parameters of Asejire Lake

Variability of the obtained mean value of the water quality parameters of the lake was studied. The assessed indices of variability were Heterogeneity of Spatial Values (HSV), Limiting Spatial Value (LSV) and Extremely High Spatial Values (EHSV). The presence of significantly heterogeneous Coefficient of Variability (CV) in any of the studied parameters was taken to indicate HSV. This was determined from the obtained mean values of the parameters across the strata and seasons. The minimum and maximum columns of the descriptive statistics of each of the parameters were assessed for sites that reflected LSV and EHSV. The presence of spatial values below and above the minimum and maximum ranges of recommended values of water quality parameters for healthy fish production presented in Omitoyin (2011) were taken as benchmark for determining LSV and EHSV.

Values below and above the recommended range were taken to indicate LSV and EHSV, respectively. The percentage number of sites that ever showed deviation (LSV and EHSV) during sampling was also obtained across seasons. This was calculated using the formula:

$$\% \text{ Deviant sites} = \frac{\text{Number of sites which reflected deviation}}{\text{Total number of sampled sites (38)}} \times 100\% \quad \ldots\ldots\ldots\ldots 6$$

3.2.4.5 Determination of factors responsible for variability in WQP

Determination of number of the principal factors that were contributory to variability of water quality parameters utilized statistical methods. The expected number of principal factors (components) responsible for variability was electronically generated along with the matrix of the studied parameters on the extracted component. The matrixes were assessed for deviations from their normal relationships presented in Boyd (1982).

Significant variations in seasonal data as well as catchment fragments (strata) data were hypothesized as major possible sources of variability and were therefore analyzed for significant differences. Relationship of parameters on the seasons and strata were compared with that extracted by statistical factor analysis to get their alliance.

3.3 Assessment of morphometric, meristic and phenotypic variability of *Clarias gariepinus* population of Asejire Lake

Assessment of morphometric, meristic and phenotypic variation of *Clarias gariepinus* population at Asejire Lake was preceded by spatial fish sampling of the Lake. Spatial fish sampling of the catchment was carried out to collect representative sample of the species for the study as well as to document the current fish abundance and distribution pattern at the lake.

3.3.1 Assessment of fish catch structure, abundance and spatial distribution

Apart from collection of *C. gariepinus* samples for genetic studies, catch data from spatial sampling of the catchment was used to determine spatio-temporal distribution of fish species at the lake. Data were collected on fish catch composition, relative spatial distribution of fish at strata, dominant fish species and their sites of dominance in the study area.

3.3.1.1 Sampling design

Sampling for fish followed that of water quality. The sampling design described under assessment of water quality parameters was utilized for collection of fish samples for this study (same sites were sampled at same frequency). However, sampling for water quality preceded fish sampling during each sampling period. Procedure for fish sample collection was also different.

3.3.1.2 Sampling procedure

Before commencement of sampling, sites were initially marked for subsequent sampling by suspending plastic floaters on stone-weighted synthetic ropes at the selected sites. Two years' bi-monthly catches were made from the marked 38 selected sites using weighted and baited Malian Gura trap. The map of the sampled sites is presented (Plate 1). Selection of the gear was supported by its efficiency in lake fishing, as noted by Ipinjoju *et al.* (2007). Twenty (20) traps of the same dimensions and the same materials were constructed, dyed and used for the sampling.

3.3.1.3 Trap description / specification

The Gura trap used for this experiment was made from lianas and nylon netting materials with the following specifications: Mesh-size - 1.0 cm, Total height - 60.0 cm, Base Diameter - 50.0 cm, Non-return Valve Diameter - 9.0 cm, Top opening diameter -

10.0 cm. Two non-return entrance valves made of strong netting materials which permit a variety of fish to be caught was utilized. The top of the trap has loose hanging net that could be opened for catch retrieval and bait placement. Similar description was reported by Ogunfowora *et al.* (2011). Samples of Gura trap used in this study are presented in Plate 2.

3.3.1.4 Trap setting and catch retrieval

Traps were set at the 38 selected sites on board a dug-out canoe and retrieved after 48 hours during each sampling. Duration of setting was based on giving allowance for maximum fish aggregation inside the traps following the advice obtained from Gura trap users.

3.3.1.5 Processing, transportation and identification of sampled fish specimens

Total samples obtained from each site was collected in well-labelled separate containers and transported via a dug-out canoe to landing site where they were sorted to species, counted and transported thereafter to the Department of Wildlife and Fisheries Management, University of Ibadan for further analysis. Caught fish samples from each site were identified at landing site using taxonomic keys (Lowe McConnell 1972; Holden and Reed, 1978) and thereafter sorted by species.

3.3.1.6 Determination of fish distribution, species richness and dominance at spatial sites at Asejire Lake

Fish distribution was determined for the catchment. During each sampling, catches were sorted to species and counted. At the end of 24 months' sampling period, the obtained data for each of the sampling period were pooled and used to generate information on total catch for the catchment across seasons, sites and strata. Dominant species were mapped against their sites of dominance on a digital map of the catchment. The most abundant species were taken as the predominant species. These were determined for each site and for the catchment across seasons. Percentage number of sites at which each species was dominant was determined as:

$$\% \text{ Site of domination} = \frac{\text{Number of sites of dominance of a species}}{\text{Total number of sites (38)}} \times 100\% \quad \ldots\ldots\ldots 7$$

Plate 2: Constructed gura traps used for fish sampling at the selected sites

Percentage composition of the target fishery (*C. gariepinus*) in the catch was determined from the obtained data. This was derived as:

$$\% \textit{ C. gariepinus} \text{ in catch} = \frac{\text{Total number of } \textit{C. gariepinus} \text{ in catch}}{\text{Total catch}} \times 100\% \quad \ldots\ldots\ldots\ldots 8$$

The number of species in total catch was taken as species richness and this were derived per site and season. Total catch for wet season was compared with dry seasons' catch. Also, total catch at O_YS was compared with catch at O_SS. Relative abundance and specific locations of catch of *C. gariepinus* were identified

3.3.2 Assessment of phenotypic structure of *Clarias gariepinus* in Asejire Lake

Phenotypic values and variations of *Clarias gariepinus* in Asejire Lake were assessed to infer the phenotypic structure of the population. Phenotypic values and their coefficient of variation were generated for selected morphometric and meristic attributes of *C. gariepinus* catches from the lake and heterogeneity established, following Mayr (1969) and Gunawickrama (2007). Determination of the most functional attribute as well as presence of underlying factors responsible for the phenotypic structure was also carried out.

3.3.2.1 Experimental design

This experiment was designed and conducted based on the following assumptions:

(1) Phenotypes would have begun to take new shape in response to environmental condition before declining stock could be observed.

(2) The most functional phenotype with respect to environmental condition would reflect the greatest intra-specific variation value.

(3) Effect of environmental factor on individuals may vary as a result of difference in location within a large water catchment area such as the study site. Hence, analysis of phenotypes of spatial catch would be more relevant in intra-specific phenotypic structuring.

(4) In a declining population, sampling may not generate enough individual for analysis, which may be partly due to gear selectivity and, partly, the smallness of the population.

(5) It would be useful to augment catch from sampling with fish collection from fishermen at the catchment who could rely on their experience to use diverse gears as well as sample some important sites that random sampling may skip.

Based on these assumptions, morphometric and meristic measurements of some attributes in intra-specific population of *C. gariepinus* - a known plastic species (Pienaar, 1968) whose population is declining in Asejire Lake (Omoike, 2004), was undertaken with the aim of generating baseline information on the current phenotypic values for the species identification, to assess its current most functional phenotypic traits in the face of the current environmental condition of the lake and to determine its current phenotypic structure useful for future prediction of structural adaptations.

3.3.2.2 Sample collection

Collection of samples for this study followed the earlier described design for water samples and catch collections. However, apart from sample collection based on the design, collections of *Clarias gariepinus* samples were also made from fishermen's catches at the catchment. This fish sample collection method followed Gunawickrama, (2007), with modifications. Live specimens of *C. gariepinus* were collected from Gura traps set at various experimental locations (38 randomly selected sites) in Asejire Lake. Samples were also collected from fishermen at landing sites during the two-year bimonthly sampling of the lake's catchment covering wet and dry seasons. Collection from fishermen was carried out with caution in order to safeguard mix-up of catches from sources outside the catchment. The obtained samples were further screened and utilized for the study.

3.3.2.3 Specimens identification and screening

Collected fish samples were preliminarily identified at the landing site using taxonomic keys (Lowe McConnell 1972; Holden and Reed, 1978) and transported to the University of Ibadan for further screening. The dorsal and anal fin ray counts (61-80 and 45-65 respectively) were used for further screening of the *Clarias gariepinus* population following Teugels (1986). Individuals within the species with values below or above the reported value in either one or both counts were screened out. The entire remaining specimens were utilized for the study.

3.3.2.4 Data collection for determination of phenotypic values

Phenotypes of all collected individuals were measured according to the method of Teugels (1982), with some modifications. Owing to the need to establish bilateral asymmetry by using values from left and right sides for detecting inbreeding tendencies

in the population (Dunham, 2004), measurements were taken for the paired fins, from the left and right sides of each fish.

(i) Procedure for data collection

Thirteen (13) morphometric and nine (9) meristic attributes were characterized. Data were collected from 37 live individuals, being the entire population size after samples were screened. Morphometric measurements were taken in all the collected individuals and measured to the nearest 0.01cm, using Vernier calipers. All length measurements (morphometric) were taken between identical points along the anterior to the posterior axes of the fish, whereas body depths were taken perpendicularly between the identified points taken at the base of the 1st dorsal ray and at caudal peduncle (BD MAX and BDMIN, respectively). However, caudal fin width (CFW) was taken as the point of greatest perpendicular length from dorsal position of caudal fin to its ventral position.

The 13 measured morphometric attributes and their acronyms were Standard length (SL), Head length (HL), Maximum body depth (BD-MAX),Minimum body depth (BD-MIN), Pectoral fin length of left side fin (PECFL-L),Pectoral fin length of right side fin(PECFL-R), Pectoral spine length of left side fin (PECSL-L),Pectoral spine length of right side fin (PECSL-R), Dorsal fin length (DFL), Pelvic fin length of left side fin (PELFL-L), Pelvic fin length of right side fin (PELFL-R),Anal fin length (AFL) and Caudal fin width (CFW). The measured 9 meristic attributes were Pectoral fin rays count on left side (PECFR-L), Pectoral fin ray count on the right side (PECFR-R), Possession of anteriorly serrated spine on the left side (PESES-L), Possession of anteriorly serrated spine on the right side (PESES-R), Pelvic fin rays counts on left side (PELFR-L), Pelvic fin rays counts on right side (PELFR-R), Dorsal fin rays counts (DFR), Anal fin rays counts (AFR) and Caudal fin rays counts (CFR). Each meristic attribute were counted and the number obtained was taken as their phenotypic value. However, PESES was observed in the binary form, in which presence of serration at anterior position of pectoral spine was taken as 1, while absence was taken as zero (0). Measurements were taken from each sample when the fish was observed to be calm, after its restriction. Measurements were taken by the same person to maximize consistency. Meristic counts were repeated on the same specimens using hand-held magnifying lens to ensure accuracy. Coefficient of variation of morphometric and meristic attributes were presented in percentages.

(ii) Determination of phenotypic values

Determination of phenotypic value of each attribute followed the technique of Gunawickrama (2007). Morphometric value of each individual was used to generate phenotypic value (body shape factors). Phenotypic value was determined as:

$$\text{Phenotypic value} = \frac{\text{Morphometric /linear Value}}{\text{Standard Length}} \times 100\% \quad \ldots\ldots\ldots\ldots\ldots 9$$

Standard Length was preferred because its values were consistent compared to total length (Turan *et al*., 2005; Gunawickrama, 2007). Total length of some specimens could be affected by mutilation of caudal fins. Absolute values of meristic counts were taken as phenotypic values.

(iii) Determination of phenotypic variability

Coefficient of phenotypic Variation (CV) and multiple modal attributes are tools in assessing within-population variation (Mayr, 1969). These indices were utilized in establishing variability in attributes and the phenotypic structure of the population. Multiple modes in phenotypic attributes were statistically derived, while CV was calculated using the formula:

$$CV = \frac{\text{Standard Deviation of Phenotypic Value}}{\text{Phenotypic Value}} \times 100\% \quad \ldots\ldots\ldots\ldots 10$$

Attributes with CV of greater than ten percent (>10%) and or that possessed multiple modal values were considered to be heterogeneous (Mayr, 1969).

(iv) Determination of phenotypic structure and most functional attribute of the population

Phenotypic structures were determined based on the number of attributes (phenotypes) that reflected heterogeneity. That is, percentage number of studied phenotypes that reflected heterogeneity. This was determined as:

$$\%\ \text{heterogeneity of population} = \frac{\text{Number of heterogeneous sites of population}}{\text{Total number of assessed phenotypes}} \times 100\% \quad \ldots\ldots\ldots 11$$

This was calculated separately for the morphometric and meristic characters. Presence of heterogeneous sites and multiple modes were taken as indicative of heterogeneity of sample. Sites with the widest difference between values from left and right sides of paired

fins were also recorded. The most varied attribute with respect to CV, mode, and differences in left and right phenotypes was suggested to be the most functional.

(v) Determination of presence of underlying factors for phenotypic structure

Extraction of information on whether there existed any important but latent factor that is responsible for the phenotypic structure was carried out through a computer-based statistical tool - Factor Analysis. It is a method of data reduction that seeks underlying but unobserved characters that are reflected in the manifested character (Oyediran, 2009). From the phenotypic data, latent factors were extracted along with phenotypes iteration on the extracted factors.

3.4 Evaluation of discriminant factors in sub-grouping of C. *gariepinus* population

Morphometric and meristic characterization of subgroups of three regrouped cases of the population was utilized to assess the discriminant factors for sub-grouping the studied population. This was preceded by evaluation of the phenotypic structure: morphometric, meristic and phenotypic variation, determination of the most functional attributes and analysis of presence of underlying factors responsible for the phenotypic structure of the sub-groups.

3.4.1 Assessment of phenotypic structure of sub-groups of *C. gariepinus*

Assessment of phenotypic structure of the sub-groups of the studied population followed the earlier described methods under section 3.4

3.4.1.1 Procedure

Phenotypes of the studied sample were re-grouped to three cases: sex, size and PESES/PASPS (pectoral spine variants). The cases were considered as potential factors for discriminating delineating the phenotypes of the population as they could be contributory to the populations' phenotypic structure.

3.4.1.2 Identification of sub-groups

Sub-groups of sex and PESES/PASPS were identified via visual examination, while linear measurements were the basis for sub-grouping the size re-grouped case. The studied sample was separated into sex sub-groups of male and female by observing external genital organs, following FAO (1996). Individuals with the same sex were

grouped together and each group named by its sex (male/female). Size range of the population was utilized to sub-group the sample to four sub-groups of sizes based on standard length measurements. Individuals having values 10.1 - 20.0 cm, 20.1 - 30.0 cm, 30.1 - 40.0 cm, and 40.1 - 50.0 cm were allocated to groups 1-4, respectively. Sub-division of the population based on pectoral spine variation (PESES/PASPS) utilized presence and absence of toothed spines at anterior portions of pectoral spine in individuals of *C. gariepinus*. This was based on the observed trend during sample collection period. Samples that did not possess toothed pectoral spine at the anterior portion of their pectoral spine were referred to as smooth, denoted as S and grouped as S-PESES/PASPS subgroup. Those with only one of the two spines serrated were referred to as partial, denoted as P and grouped as P-PESES/PASPS subgroup. Those with the two spines serrated were referred to as complete, denoted as C and were grouped as C-PESES/PASPS sub-group.

3.4.1.3 Determination of phenotypic structure in sub-groups of *C. gariepinus*

Determination of phenotypic values and structure of sub-groups of each of the regroup cases of the population and analysis of presence of latent factors for the phenotypic structure was investigated following the described method for the entire population. These were carried out separately for the sub-groups of the three regrouped cases. Morphometric attributes, their respective coefficient of variation and mode values for meristic attributes were determined. Percentage number of heterogeneous phenotype in the sub-groups and the most varied phenotypes were also determined. Latent factors responsible for heterogeneity were extracted along with phenotype iteration using factor analysis. A summary of the subgroups phenotypic values was finally produced.

3.4.2 Assessment of canonical discriminate factors in phenotypic structure of *C. gariepinus*

Assessment of canonical (fundamental) discriminate factors responsible for the phenotypic structure of the studied population of *C. gariepinus* was carried out. This assessment utilized the data on phenotypic values of the sub-groups of the regrouped cases. Each of the utilized factors for regrouping the population was hypothesized as potential canonical discriminate factors. Sex, size and PESES/PASPS (pectoral spine variants) were respectively selected as potential discriminate factors based on tendencies of sexual dimorphism, allometric growth pattern and a field observation of variations at pectoral spine of C. *gariepinus* at the lake. Analysis was carried out to test the strength of

each regroup cases as factors for delineating the populations' phenotype; This was used to establish that the subgroups in it were statistically significant morphologically types.

3.4.2.1 Procedure

The three regroup cases were hypothesized as potential canonical classification units and were thus subjected to assessment of canonical classification steps presented by Gunawickrama (2007). Phenotypic values were compared at all the morphometric and meristic sites among the sex, size, and pectoral spine variant sub-groups. When significant difference occurred in at least one of the phenotypic sites between the subgroups in each regroup case, such grouping was considered for stepwise Discriminant Function Analysis (DFA) using statistical tools (presented under the section on statistical analysis). Patterns of the differences were also established. The DFA re-classified individuals to canonical groups and then compared the grouping with the initial group of that individual to get the percentage of classification success. The classification success was noted and territorial map describing the phenotypic relationship of the subgroups values were drawn. However, data on sex and pectoral spine variant regroup cases were corrected of size effect before being subjected to DFA. Sub-groups having significant DFA were considered as morphological classification units.

3.5 Assessment of biochemical (allozyme) variability of *C. gariepinus* sub-groups

Biochemical analysis of universal protein markers reveals better diagnostic genetic potentials and is usually free from genotype X environment interactions (Lombard *et. al.*, 2001; Torkpo *et. al.,* 2006). Biochemical and genetic studies were carried out on sub-groups that showed significant or greatest classification success after DFA. The Sodium Dodecyl Sulphate Polyacrylamide Gel Electrophoresis (SDS-PAGE) method was used.

3.5.1 Sample collection

Eighteen live samples of *C. gariepinus* were randomly selected from the collection of the specimen used for phenotypic structure studies. The group that had most significant canonical discrimination success was utilized for this study. The number of individuals selected per sub-group was determined based on the relative proportion of the subgroup in the obtained population. Subgroup's identity followed the one utilized under phenotypic studies. Blood was obtained from individuals after morphometric characterization and heparinized. About 2ml of blood was drawn per individual; blood

was drawn from the caudal vein beneath the vertebral column via hypodermal needle into anticoagulant - treated (heparinized) vials. Blood collection was carried out at the Department of Aquaculture and Fisheries Management, University of Ibadan, Ibadan and transported in iced container to the Biotechnology Laboratory, Federal University of Agriculture, Abeokuta, where protein extraction and gel electrophoresis was carried out.

3.5.2 Protein extraction and electrophoresis

Serum was extracted from the blood sample of each individual using extraction buffer (800µl of 0.1M tris-HCl at pH 7.6), vortexed for 1min and centrifuged at 10,000rpm/5mins/4^0C. The supernatants were transferred to new Eppendorf tubes and kept in a freezer until usage. Electrophoresis profiling of the soluble proteins were conducted using gel electrophoresis apparatus (Consort EV 231). Electrophoresis preparation, electrophoresis conditions, staining and destaining procedures followed Laemmli, (1970). The serum extracts for all samples was applied to 12.5% polyacrylamide gel. Dye stocks were stored at 4^0 C and later boiled for 3 mins before gel was loaded. Six µl protein sample was added to 3µl of 3x Leammli dye stock. The polyacrylamide resolving and stacking gels composition for the SDS-PAGE is presented in Table 1, while the composition of loading and running gels is presented in Table 2.

Table 1: Solution for 6 % Stacking Gel, 12.5 % Resolving Gel for SDS-PAGE

Substance	Resolving gel	Stacking gel
Acrylamide bis-acrylamide	3.1ml	1.0ml
Tris buffer (1.0M Tris-HCl, pH8.8)	3.0ml	0.63ml
20% (w/v) SDS	38µl	25.0µl
dH_2O	1.30ml	3.6ml
10%APS (Ammonium persulphate)	36µl	25.0µl
TEMED (Tetramethylenediamine)	10µl	10.0µl

Table 2: Composition of Solution for Loading and Running Buffers of Gel

Loading buffer (Laemmli Loading dye)(3x stock)		**Running buffer(Laemmli buffer) (10x)**	
1m Tris-HCl pH6.8	(4ml)	Tris base	(30.3g)
20%SDS	(3ml)	Glycine	(144.0g)
100% Glycerol	(3ml)	SDS	(10.0g)
Bromophenol blue	(0.006g)		
Make up to	10ml	dH_2O make to	1liter

3.5.3 Gel preparation and electrophoresis

Gel was polymerized in gel caster. A thin layer of isopropanol was added for smoothening the gel surface and poured into the caster after which comb was placed to create wells. Samples were loaded in individual wells made by the comb and were run for 2 hours at 150V and 0.5 mini-amp inside the electrophoresis machine. Nine samples were loaded per time based on the number of wells made from the comb. Gels were removed from the electrophoresis cells and images were scanned and stored in a computer system.

3.5.4 Protein profile scoring

Data were collected from the gels, viewed and scored based on presence (1) or absence (0) of protein bands. The positions of the proteins, as enumerated by Gatehouse (1979) and Machuka (2001), were determined using standard molecular weight proteo-ladder (medium) supplied by Norgen Biotec Corp. (www.norgenbiotek.com) and measured in kilodalton (KDa). Resolved bands loci were labelled from the base to the top in increasing order of alphabet following increasing order of molecular weight of the bands.

3.6 Assessment of genetic variability and inheritance of Randomly Amplified Polymorphic DNA (RAPD-DNA) markers in sub-groups of *Clarias gariepinus*

Application of molecular markers based on relative difference in Deoxyribonucleic acid (DNA) between individuals would detect more polymorphism than morphological and protein-based markers (Coulo *et al.,* 1994). The potency of the use of DNA-based technique, Randomly Amplified Polymorphic DNA (RAPD) markers in establishing genotypes' diversity (polymorphism) in sub-groups of *Clarias gariepinus* population was investigated in this study. Selection of the RAPD marker is based on its ability to generate large number of loci; it is less expensive and it requires no prior DNA sequence information to perform the assay (Christopher *et al.,* 2004).

3.6.1 Sample collection, DNA extraction and RAPD amplification

Specimen of the fish samples which were earlier used for phenotype analysis and protein electrophoresis studies were utilized for this study. Subsamples of blood samples of the 18 individuals that were analysed for protein electrophoresis were obtained and used for the study. Blood was also obtained from two (2) other individuals to make a total of 20 individuals that were analyzed for RAPD-DNA markers (the 18 individuals that were utilized for universal protein marker electrophoresis and the 2 individuals that were

excluded from electrophoresis test owing to inadequate gel well). Blood collection followed the earlier described technique. Isolation of DNA from the blood specimens was carried out at the Federal University of Agriculture, Abeokuta (FUNAAB), Abeokuta, Nigeria; while RAPD analysis was conducted at the International Institute for Tropical Agriculture (IITA), Ibadan, Nigeria.

3.6.2 Procedure for DNA isolation and dilution

Norgens Blood Genomic DNA Isolation Kit was employed in DNA isolation. Blood genomic DNA was isolated from the studied individuals following manufacturer's instructions (NORGEN, Biotec. Corporation). Quality of DNA was checked by Nanodrop Spectrophotometry taking ratio of optical density value at 260-280nm. 1:100 DNA dilution was obtained for 10 ul of each extracted DNA.

3.6.3 PCR mix preparation and gel run

Extracted DNA was used for preparation of RAPD-PCR product at the International Institute for Tropical Agriculture (I.I.T.A), Ibadan. PCR mixture contained: 10X Buffer (2.0ul), 25mMMgCl_2,(1.6ul), 5%Tween20(2.0ul), 2.5mMdNTPs,(1.0ul), 2.0mMPrimer (1.0ul), 5u/ulTaq(0.2ul), Water (8.2ul), Diluted DNA (4.0ul). The PCR mix for each sample was spin down at 10,000rpm for 30s inside Eppendorf 5415C. Amplification of PCR mix involved denaturation, annealing and extension processes. Thermal cycler (Techne, TC412) was utilized for amplification. The thermal cycle profile comprised 1cycle of 3 Mins. Initial denaturation at 94^{o}C, 45 cycles of 20 sec at 94^{0}C, 20 sec annealing at 37^{o}C, 40 sec at 72^{o}C, and 1cycle of 7 mins. Final extension at 72^{0}C. PCR products were electrophoresed in 2% agarose gel stained with Ethidium bromide done under standard electrophoresis procedure. Six randomly amplified polymorphic DNA Operon primers (Operon Tecnologies Inc. U.S.A.) were utilized. These were OPAD – 09, OPAE – 04, OPAE – 05, OPAE – 09, OPAF – 07, OPAF – 08. Gel products were photographed and subsequently analysed for polymorphism

3.6.4 Determination of polymorphic primers

A set of 20 decamer RAPD primer were initially screened before selecting some of them for this study. Primers screening was carried using 3 randomly selected samples of DNA templates of the studied population. Presence of polymorphism and clarity of resolution was used in selecting the best 6 primers which were subsequently used for RAPD analysis of the 20 selected individuals belonging to the subgroups of the studied *C. gariepinus* population.

3.7 Assessment of inbreeding tendencies and determination of mean phenotypic values of paired fins

Assessment of inbreeding tendencies and phenotypic values of paired fins were carried out based on the method described by Dunham (2004). Standardized values obtained under morphometric and meristic structure analysis was used in establishing inbreeding tendencies using bilateral asymmetry as indices. Sub-populations from discriminate factor analysis were separately characterized and analyzed for bilateral symmetry by comparing mean values of left and right sides phenotypic values of paired attributes. The studied attributes included six morphometric attributes: pectoral fin length for left and right sides (PECFL-L and PECFL-R), Pectoral spine length for left and right sides (PECSL-L and PECSL-R) and pelvic fin length for left and right sides (PELFL-L and PELFL-R); and four meristic attributes: pectoral fin ray count for left and right sides (PECFR-L and PECFR-R); and pelvic fin ray count for left and right sides (PELFR-L and PELFR-R). The mean values of the left and right side values for all individuals in each sub-groups were determined for each attribute. The mean of the total left side values was also compared with the mean of the total right side values. Significant difference between the mean values from the left and right side values for individual attribute in each sub-groups were determined and taken as evidence of inbreeding. Absence of attributes with significant difference was taken as indicative of bilateral symmetry in the sample.

3.8 Statistical analysis

The statistical tools employed for the study are presented below.

3.8.1 Area dimension and potential threats to fish abundance and diversity

Analysis of area values of the lake's environments was carried out using Spatial Analyst of Arcgis 9.3 computer software. Data on area values, threats to fish abundance and diversity and values on draw-down frequency and number of sites that deviated from standards of water quality parameters for healthy fish life were presented using descriptive statistics (percentage, mean, standard deviation and frequency). Patterns of mean values of area and water quality parameters were established using graphs, histogram and box plotting through PAST Computer package (Hammer, 2005). Differences between values at seasons as well as that of strata were established through paired sample t-test.

3.8.2 Catch structure

Descriptive tools (mean and percentage) were used in presenting data on catch composition. Fish catch abundance was compared across seasons and across strata using paired sample t-test.

3.8.3 Phenotypic structure

Statistical analysis of phenotypic values, coefficient of variation and within-population heterogeneity utilized methods of Turan (2004) and Gunawickrama, (2007). Univariate and multivariate statistical tools were employed for analysis of morphometric and meristic attributes. The univariate tool was employed for generating descriptive values (range, mean, median, mode and standard deviation) of morphometric and meristic attributes. Multiple mode attributes were subjected to multi-variate statistical analysis (Principal Component analysis-PCA) to extract latent components, attributes matrix and attributes preference on the extracted components. The components were further rotated to show attributes iteration using varimax-rotation. PCA followed the Jolliffe rule, which is to retain principal components with eigen-values of at least 0.7 (Oyediran, 2009). All statistical analysis was conducted using the 2006 version of SPSS 15.0 computer software.

3.8.4 Discriminant factors and phenotypic structure in sub-groups of *Clarias gariepinus*

Univariate and multivariate tools were also employed for discriminant factor analysis. Statistical analysis of sub-groups' phenotypes were done for differences at phenotypes' sites followed by factor analysis. Phenotypic values of attributes among sub-groups of sex were compared for significant difference via student *t-test*, while one-way analysis of variance (ANOVA), followed by Tukey multiple comparison test for unequal sample sizes (Zar, 1984), was used to establish significant difference in size and pectoral spine subgroups. Significant difference was taken at $p<0.05$. The SPSS 15.0 Windows Evaluation statistical software was used for correction of size variation effect in data, Discriminant Function Analysis (DFA) for canonical differences in sub-groups and generation of territorial map for sub-groups with significant different phenotypes. Patterns of mean values for the significantly different phenotypic subgroups were established using Paleontological Statistics (PAST) Computer programme (Hammer, 2005).

3.8.5 Biochemical and genotypic variability of *C. gariepinus* sub-groups

Similarities and divergence of individual's band scores were carried out via cluster analysis utilizing Unweighted Pair Group Method using Arithmetic averages (UPGMA) for phenogram grouping (Sneath and Sokal, 1973). Dendogram showing relationship between individuals in the groups was also drawn. Analysis was done with the aid of Computer software (Numerical Taxonomic System-NTSYS). Allelic scores for the groups were used for genotypic classification through Canonical Discriminant package of SPSS 15.0 (Windows Evaluation Version).

3.8.6 Assessment of genetic variability and inheritance of Randomly Amplified

Polymorphic DNA (RAPD-DNA) markers in sub-groups of *Clarias gariepinus*

RAPD gel profile of each primer was scored across electrophoresis lanes as variables. Data were recorded as present (1) and absent (0) of band products from the gel electropherographs. The polymorphic data analysis followed Lathar *et al.* (2010). The generated binary data were used to estimate polymorphism level by dividing the polymorphic bands by the total number of scored bands. Polymorphic Information Content (PIC) was calculated following Zhang, (2009) using the formula:

PIC = 2 Pi (1-Pi), ……12

Pi = frequency of occurrence of polymorphic bands in different primers

Frequencies of alleles as well as presence of private allele per marker and per individual in the groups were observed and documented. Establishment of genetic differences from the generated data and dendrogram drawing followed the methods of Ali *et al.* (2009). Degree of genetic similarity, interrelationship among the studied individuals and calculation of similarity values were carried out using the 2006 version of SPSS 15.0-Windows Evaluation Computer Package. The data were analyzed according to binary values 0 and 1 to show hierarchical pair-wise distance using UPGMA (Unweighted Paired Group Method of algorithms) and constructed dendrogram. The zero (0) and one (1) of the binary values indicated band absence and band present respectively. The pattern of similarity was observed between all primers and between individuals genotypes with dendrogram constructed in both cases. The genotype data in groups were classified using the DFA of SPSS, version 15.0 computer software.

3.8.7 Assessment of inbreeding tendencies and mean phenotypic values of paired fins

Differences between left and right phenotypic values were tested using student *t-test.* Significant difference was taken at $p<0.05$.

CHAPTER FOUR

RESULTS

4.1 Location and climate of the studied area

The description of the study area as well as its climate condition has been earlier presented (sections 3.1 and 3.1.1)

4.2 Environmental condition of Asejire Lake

4.2.1 Digital map, catchment structure and area dimension of Asejire Lake

The produced digital map showed that, structurally, the lake had a letter Y appearance formed by two major water inlets that joined at a confluence to form one main course (Plate 3). Tributaries were located on both water inlet strata (O_YS) and O_SS). The tributaries on the strata were separated by the breadth of the main course of the lake. The main course was formed by water contribution from both strata. Three (3) tributaries were located on O_SS while 2 were on O_YS.

The lake had two (2) inlet zones and five (5) tributaries. The analogue and digital maps of the catchment is presented in plates 4a and 4b, respectively. The digital map (Plate 4b) showed that the lake's structure has some deviation from the analogue map. Certain areas of the O_SS water inlet have been lost to swamps, nomenclature of Osun inlet area have changed from Agboro to Agora. Along O_YS strata, two tributaries were observed instead of one that was indicated on the analogue map.

The current structural condition of the fishing zones of the catchment is presented in plates 5-9. The map showed evidence of human activities at all adjoining watersheds of the fishing zones, while their structures had changed owing to swamp invasion. The changes occurred at the inlets (Plates 5&6), confluence (Plate 7) and tributaries located along the strata (Plates 8&9).

Satellite image of the section of the catchment that shows the locations of all the encountered man-made facilities directly located on the fishing zones of the catchment is presented in Plate 10a.

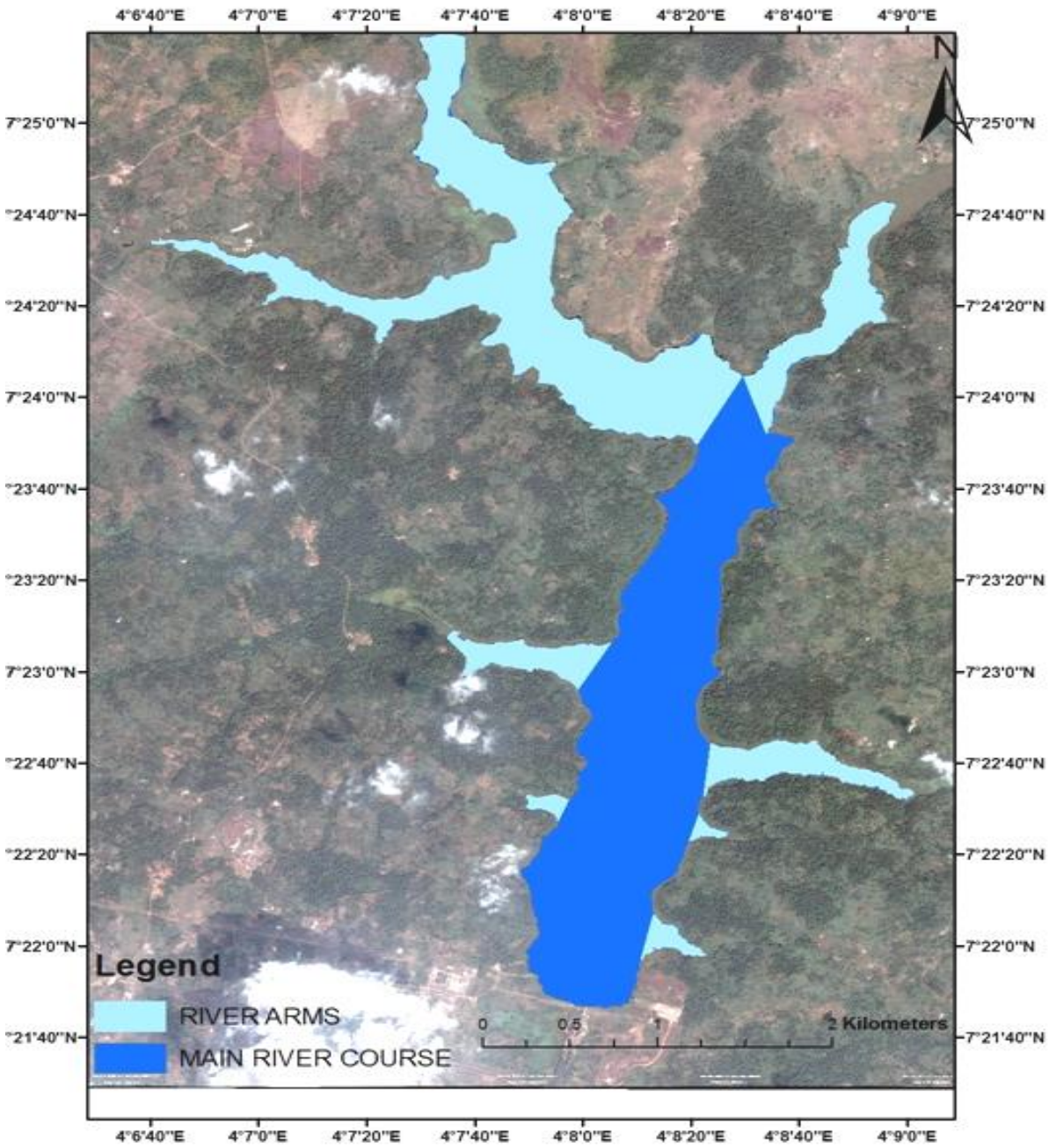


Plate 3: Map showing catchment structure and watershed condition of Asejire Lake during December, 2009 catchment survey

- Dark green= Forest areas; Lines=footpath; white= micro-climatic areas
- Light green after blue colour indicate areas of swamp invasion.

Adapted from www.google.com

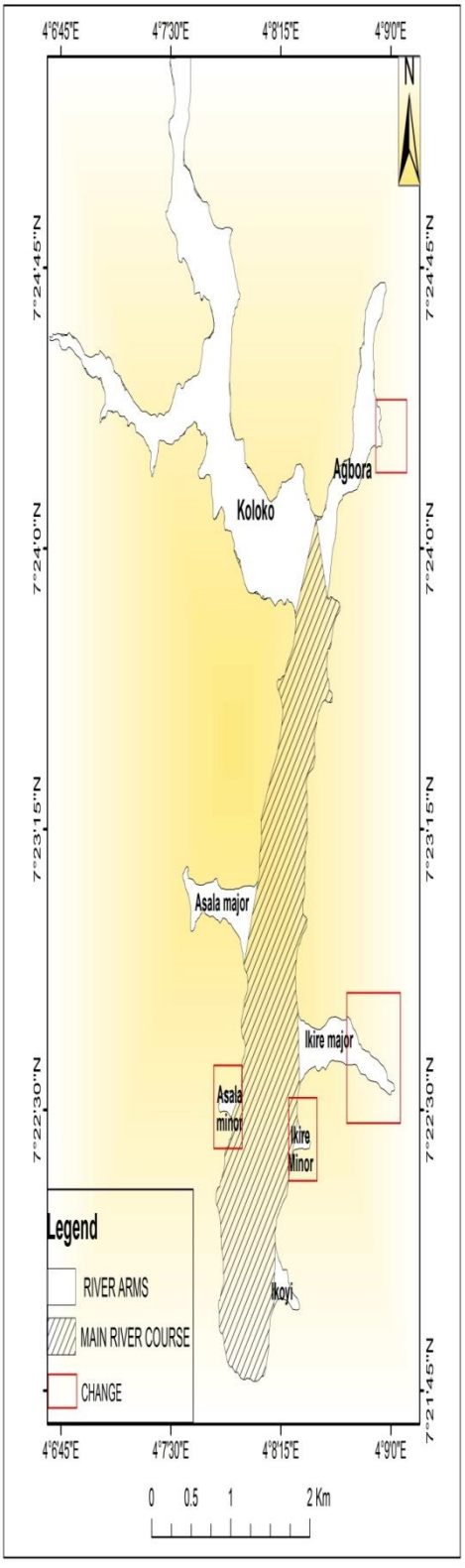


Plate 4a: Map of Asejire Lake (Omoike, 2004) **Plate 4b: Current map of Asejire Lake**

- Boxes in 4b indicates changed structure compared with the 4a

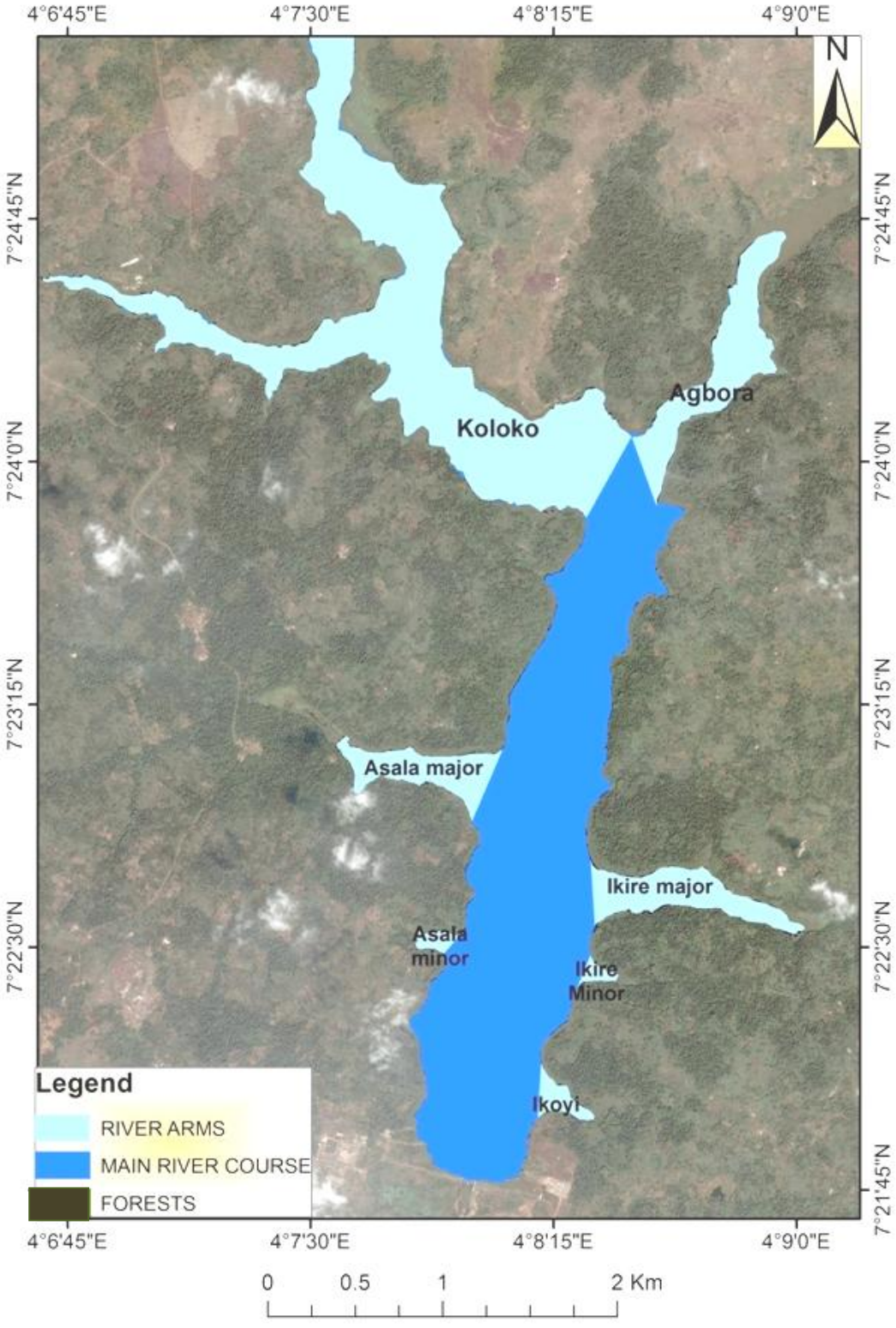
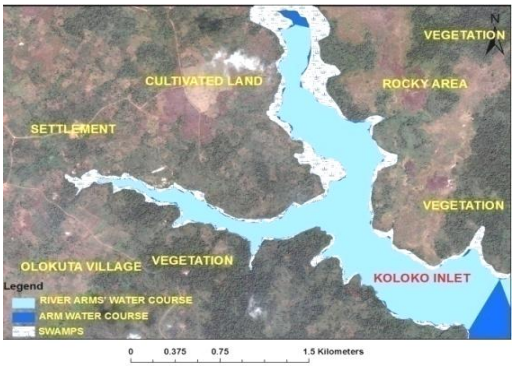


Plate 4c: Digital map showing the natural structures of Asejire Lake (December, 2009)

Adapted from www.google.com



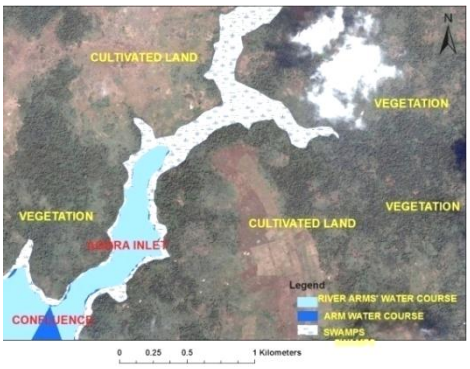


Plate 5: Map of Koloko water inlet on O_YS **Plate 6: Map of Agora water inlet on O_SS**

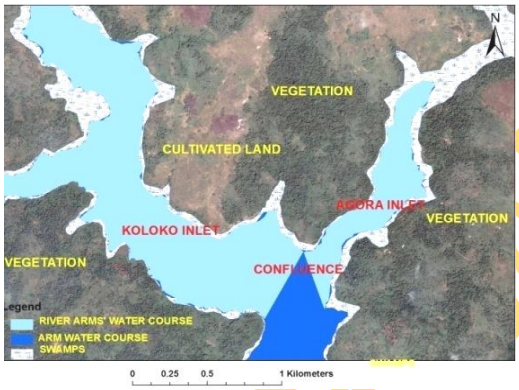


Plate7: Map of Koloko and Agora inlets (O_YS and O_SS) from confluence

Plate 8: Map of tributaries on O_SS **Plate 9: Map of tributaries on O_YS**

***Grey colour indicate areas of swamp invasion; white patches indicate micro-climatic areas**

Adapted from www.google.com

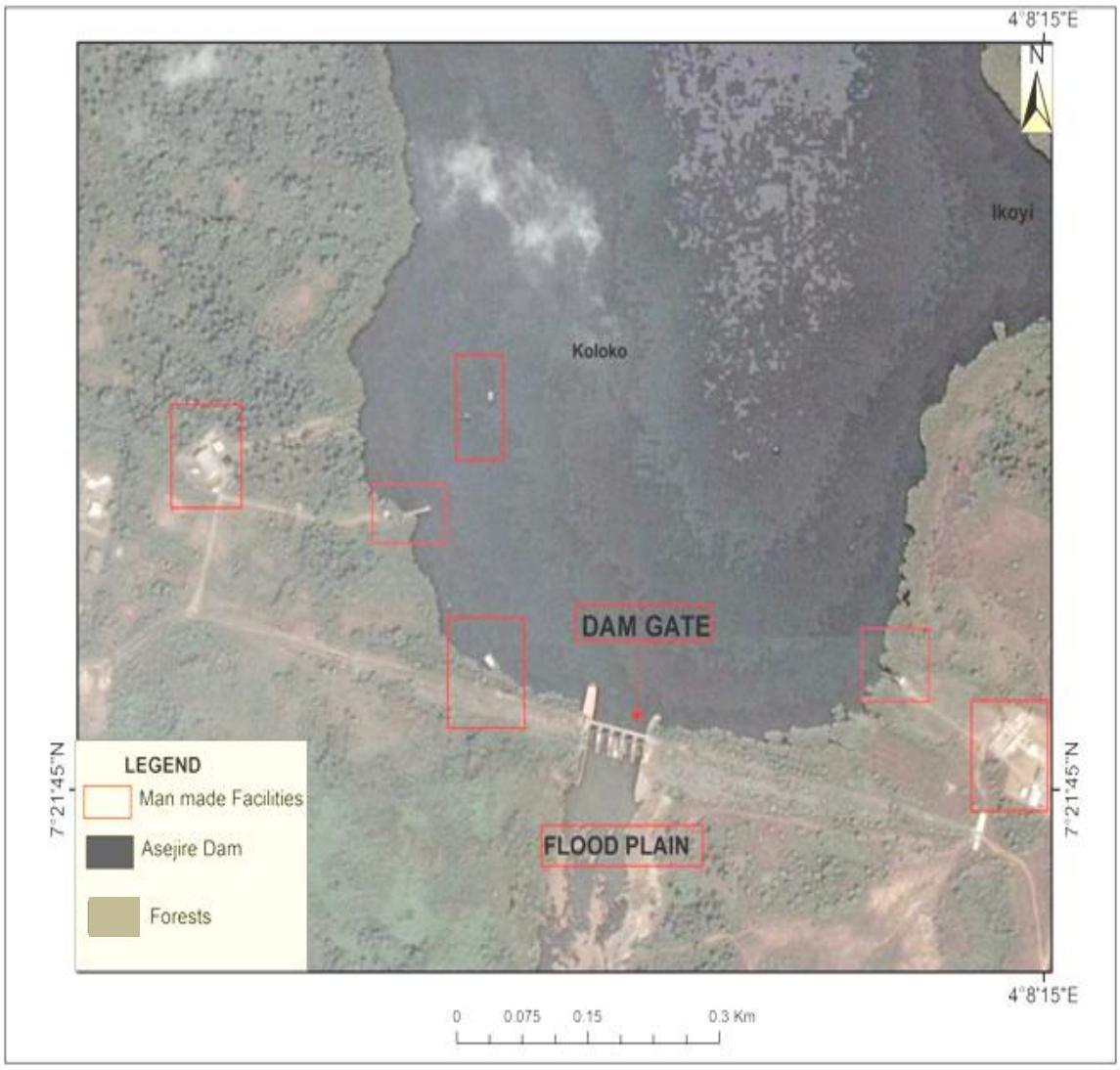


Plate 10a: Satellite image showing location of man-made facilities on Asejire Lake during December, 2009 survey

Adapted from www.google.com

Plate 10b: Rusting underground pipe of water pumping station on O_SS strata of Asejire Lake (Exposed when water level was drawn down- October, 2010)

Water pumping stations were the observed man-made facilities that were located on the lake's water course. The water pumping facilities were four in number; three were on the O_YS, while only one was on O_SS. Evidence of rust was observed on the pumping facility on O_SS (Plate 10b)

The obtained area estimates from the digital image of the catchment is presented in Tables 3and 4. The result on assessment of the currently available catchment area and the area dimensions of the different strata of the catchment is presented in Table 3a. Dimension of fishing area and contribution of different fishing zones is presented in Table 3b. Catchment Area (CA) was 6,564,477 m^2. The main reservoir course contributed 51.6% CA, while O_SS inlet and tributaries had 12.2% CA compared to 36.2% CA contribution of inlet and tributaries on O_YS. The O_SS inlet had comparatively small area contribution to the catchment when compared with O_YS (6.5 and 33.5% CA). Tributaries on O_SS had greater area contribution when compared with those of O_YS (5.7 and 2.7% CA). The total fishing area (FA) was 4,912,791 m^2 (Table 3b).

Man-made facilities that were directly located on the lake covered a total of 368.27m^2, which was equal to 0.0056 % CA (Table 4). Area covered by individual facilities ranged between 0.0006 and 0.002% CA. All these facilities were on O_YS. Rusting underground pipe of a water pumping station entered the water body from the adjoining watershed of O_SS (Plate 10b).

Table 3a: Catchment Area (CA) dimensions and percentage contributions of strata

Fishing Zones	Area (m^2)	Contribution (%CA)
Dam Main Course	**3,387,270.13**	**51.60**
OsS Strata		
Inlet	426,691.01	6.50
Tributaries	374,175.19	5.70
Total	**800,866.20**	**12.20**
OyS Strata		
Inlets	2,199,099.80	33.49
Tributaries	177,560.00	2.71
Total	**2,376,659.80**	**36.20**
Total Catchment Area	**6,564,477.00**	**100.00**

Table 3b: Fishing Area (FA) dimensions and percentage contribution of fishing zones

Fishing Zones	Area Dimension (m^2)	% FA
Main Course	2, 491,310	50.71
OsS Strata		
Inlet	321,501	6.54
Tributaries		
Ikoyi arm (Agora axis)	58,487	1.19
Ikire arm (Minor trib. 1-Agora axis)	17,377	0.35
Ikire arm (major trib.1- Agora axis)	203,388	4.14
OyS Strata		
Inlet	1,643,168	33.45
Asala arm (Minor trib.2-koloko axis)	23,985	0.49
Asala arm (major trib. 2-koloko axis)	153,575	3.13
Total Fishing Area (FA)	**4,912,791**	**100**

- **Catchment Area (CA)=6,564,477 m^2**
- **Fishing Area (FA) = Catchment Area minus (-) Area covered by swamps**

Table 4: Area dimension and percentage area covered by man-made facilities at Asejire Lake

Site Strata	Area covered (m^2)	Contribution (% CA)
Pumping station (OyS)	128.79	0.002
Water treatment facility (OyS)	181.65	0.003
Pumping station (OyS)	57.83	0.0006
Total	**368.27**	**0.0056**

- **Total Catchment Area = 6,564,477 m^2**

4.2.2 Threats to fish abundance and diversity in Asejire Lake

The results on physical catchment condition with respect to potential threat to fish abundance and diversity revealed that watershed degradation, catchment fragmentation, losses in catchment area, spatial variation of physico-chemical parameters and frequency of opening of the gate valve of the dam were contributory to threats to fish abundance and diversity in the catchment. Results confirming these observations are presented in this section.

4.2.2.1 Watershed degradation

The satellite image of the catchment (Plate 3) shows that large portion of the adjoining watershed of the lake was undergoing deforestation. The degraded areas were linked with footpaths. Buildings that belonged to some companies that had their water pumps on the lake were physically observed near the dam on both strata but more extensively on O_YS. Farming activities and settlements were observed at the deforested areas at both strata. Estimates of areas of the adjoining watersheds of the lakes' strata that were under human activities are presented in Table 5. A total of 66.0% watersheds of the catchment have been put under human activities. Degradation was relatively higher at the O_YS compared to O_SS.

As for watershed forest degradation at the catchments fishing zones, the lowest (30.0%) occurred at O_YS trib. and highest occurred at O_YS dammed end (78.0%). Degradation ranged between 40.0 (inlet) and 45.0% (tributaries) at O_SS. These values followed different patterns at strata. On the O_YS, it followed the pattern: dammed end>inlet>tributary, while tributaries>dammed end>inlet was observed at O_SS. At tributaries, degradation of watershed was higher (45.0%) at O_SS tributary compared with O_YS (30.0%).

4.2.2.2 Catchment fragmentation

Asejire Lake showed evidence of fragmentation. The result of Asejire lake's catchments structure, presented in Section 4.2.1 (Plates 3-9), showed that water inlets of the lake receives water from separate and different rivers (Osun and Agbora). Structurally, the inlets had different shapes, while their area dimensions (Table 3) were different: 321,501 m^2 for O_SS water inlet compared with 1,643,168 m^2 for O_YS water inlet. The O_YS had one inlet and two tributaries, while O_SS had one inlet and three tributaries. The tributaries on the same stratum were parallel to each other. The distance between tributaries on the opposite stratum was wide: 1073±165 m apart. Graphical

comparison of area covered by the catchment's fishing zones presented in Figure 2, showed that the zones could be grouped by their areas into: two inlet fragments (one major inlet and one minor inlet) and five fragments of tributaries (one minor tributary on O_YS, one major tributary on O_YS, one minor tributary on O_SS, one minor tributary on O_SS and one intermediate tributary on O_SS.

4.2.2.3 Catchment shrinkage and loss of EAFA (Effective Area for Fishing Activities)

Assessment of Asejire lake's area dimension revealed evidence of shrinkage and reduction in available area for fishing activities (EAFA). Estimates of the area losses are presented in Table 6. The catchment had area coverage of 6,564,477 m^2, which is equivalent to 8.51% loss/shrinkage of the earlier reported catchment area. Swamps covered 25.16% CA. Marshes were tending towards being mono-flora with *Leersia hexandra* Sw, dominating. The grass harboured fish predators; threatened navigation and fishing activities (Plates 11- 12). The remaining 74.84% CA were available for fishing activities (FA). Altogether, 19.33% FA (14.46% CA) and 0.008% FA (0.005% CA) were respectively under siltation threat and man-made features. Only 60.37% CA were effective for fishing activities (EAFA). Plate 13 shows the digital image of the siltation threatened areas of the catchment.

4.2.3 Water quality of Asejire Lake

Results on seasonal and spatial variations of water quality parameters of the lake, patterns of variation, frequency of sites showing deviation from minimum and maximum values for healthy fish production and factors responsible for the variation pattern of the water quality parameters are presented in this section. Descriptive statistics of the spatial values of the parameters is presented in Appendix 3-.6.

Table 5: Percentage of Watershed Area under Human Activities at Asejire Lake

Strata	O_YS	O_SS
Tributaries	30.0	45.0
Inlet	75.0	40.0
Dammed end	78.0	42.0

*Total watershed under human activities=66.0%

Table 6: Losses in Catchment and Fishing Areas at Asejire Lake

Parameter	Present Study (m^2)	% Losses
Catchment area	6,564,477.00	8.51% CA
Swampy area	1,651,686.00	25.16% CA
Fishing Area (FA)	4,912,791.00	74.84% CA
Silted area	949,393.00	14.46% CA (19.33% FA)
Man-made features	368.27	0.005% CA (0.008% FA)

*** CA=Catchment Area**

Plate 11a

Plate 11b

Plates 11a and 11b: Migrating activity of *Leersia hexandria* (aquatic macrophytes) in Asejire Lake

(a) Macrophytes blocked navigation at tributary (b) Macrophyte mass migrating at main Lake course

- Macrophytes in a and b have potential of distrupting fishing and navigation activities

Plates 12a

Plates 12b

Plates 12a and 12b: Fish predator (*Varanus indicus*) resting on the aquatic macrophytes stalk while awaiting prey

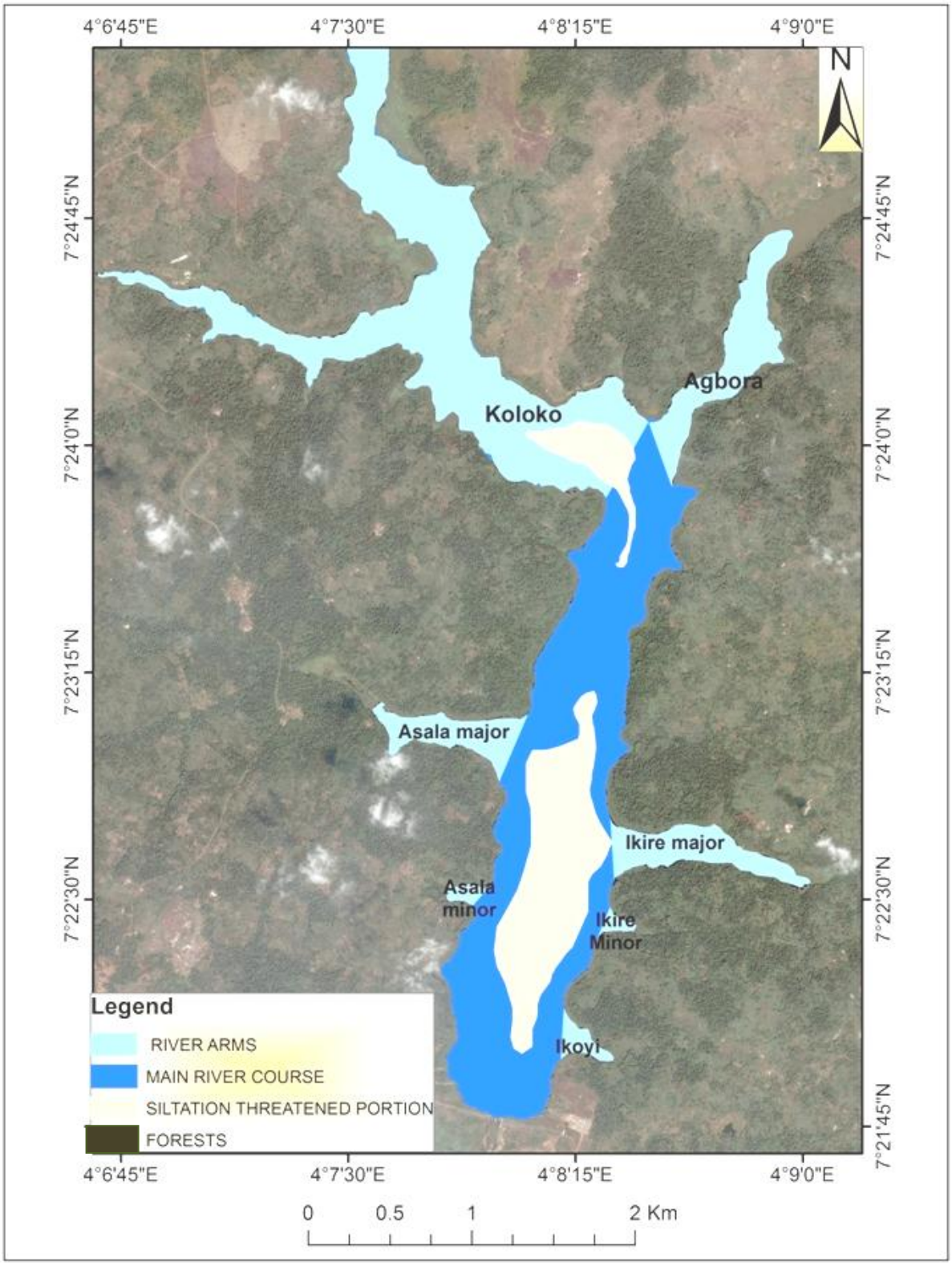


Plate 13: Map showing the siltation threatened portions of Asejire Lake
Adapted from www.google.com

4.2.3.1 Spatio-temporal values and variability in water quality at Asejire Lake

Mean spatial values of water quality in seasons and across strata are presented in Table 7.

The seasonal variations in WQP for wet seasons at O_YS and O_SS were:

- 27.4±3.2 and 30.0±2.5^oC (temperature)
- 6.1±1.8 and 5.0±2.1 mg/l (DO)
- 51.7±27.1 and 52.0±38.0 mg/l (TH)
- 55.3±43.7 and 134.00±89.5 mg/l (TA)

The WQP values of dry seasons at O_YS and O_SS were:

- 28.6±2.7 and 28.7±4.0^oC (temperature)
- 6.1±1.2 and 6.5±1.5 mg/l (DO)
- 52.7±6.2 and 51.7±38.3 mg/l (TH)
- 146.7±58.3 and 91.0±43.4 mg/l (TA)

Patterns of variation in the obtained values of water quality parameters across the sampling periods are presented in box forms (Figures 4-7). All parameters showed different box characteristics for the sampling period, indicating that the variation pattern for water quality parameters per sampling time were different, while some parameters showed possibility of limitation and extremely high values. The box diagram for temperature obtained across the sampling periods is presented in Figure 4. The diagram reveals that the values for each sampling period had different box characteristics. However, the boxes show decreasing trend along the wet season and an increasing trend along the dry season. The lowest and highest values, as revealed by the box-diagram, were obtained during the dry season (October/November and February/March, respectively). Considering the entire sampling periods, the lowest observed value was encountered during October/November sampling period.

Similarly, the box shapes for the sampling periods' dissolved oxygen values (Figure 5) showed that each sampling period had different patterns. Although, the wet season's boxes seemed to be similar, the dry season's boxes showed wide variations. The highest and lowest values were obtained during the dry season. The boxes also revealed that seemingly noticeable low dissolved oxygen content occurred during February/March sampling period, indicating that very low and probably limiting quantity of dissolved oxygen content was experienced at spatial site during the sampling period.

The box-plot of values of total hardness (Figure 6) showed decreasing pattern of boxes along wet seasons' sampling periods, while the dry seasons' boxes did not follow either increasing or decreasing pattern. The figure showed that variation in box shapes during sampling periods was more pronounced in total hardness than in the earlier reported parameters. The lowest and seemingly limiting value of total hardness and the value nearest to the highest were obtained during the August/September sampling of wet season. The highest and the lowest values obtained during the dry season were observed in February/March sampling. Similar to the situation observed in boxes for dissolved oxygen, the lowest value obtained during the wet season period was closest to the least value ever recorded for any parameter throughout this experiment, indicating high tendencies of having limiting values of these parameters at spatial sites during the sampling period.

Box shapes of alkalinity values (Figure 7) showed different shapes for each sampling period. Similar to the box pattern observed in total hardness, total alkalinity values showed a decreasing pattern of boxes along the wet season sampling period but increased trend occurred along the dry season. The boxes reflected compressed shapes indicating less within sampling period variation in mean values. Peak value was observed during the February/March sampling and this was distinctively high. The box shape for the period seemed to be different from all other shapes obtained throughout the experiment. Also similar to the pattern observed in hardness, the least obtained value seems to indicate limitation of alkalinity at spatial site and this occurred during August/September (wet season).

Table 8 shows the coefficient of variability (CV) of the studied water quality parameters. Coefficients of variability in Temperature, DO, TH and TA were 8.3-13.9 %, 19.6-42.0 %, 11.7-73.1 % and 39.7-79.0 %, respectively. HCV occurred in all parameters (CV>5%). During wet and dry seasons O_YS had greater CV compared to OsS with respect to DO, TH and TA. Also, O_YS had greater CV in temperature during the wet season.

In summary, the result indicated that HCV occurred in all parameters and all seasons in the catchment. O_YS was more vulnerable to variation than O_SS.

Table 7: Seasonal values of water quality parameters of Asejire Lake (January, 2010-December, 2011)

Parameters	Wet Season	Dry Season	O_YS	O_SS
Temperature (^oC)	27.4±3.2	30.0±2.5	28.6±2.7	28.7±4.0
DO (mg/l)	6.1±1.8	5.0±2.1	6.1±1.2	6.5±1.5
TH	51.7±27.1	2.0±38.0	52.7±6.2	51.7±38.3
TA (mg/l)	55.3±43.7	134.00±89.5	146.7±58.3	91.0±43.4

Legend:

DO= Dissolved Oxygen

TH= Total Hardness

TA= Total Alkalinity

O_YS= Oyo State Strata

O_SS= Osun State Strata

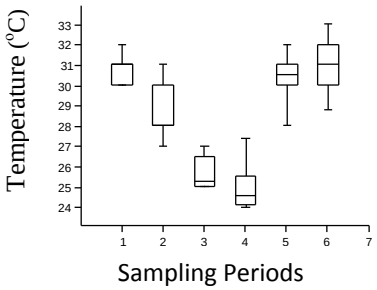


Figure 4: Pattern of Temperature (°C) values

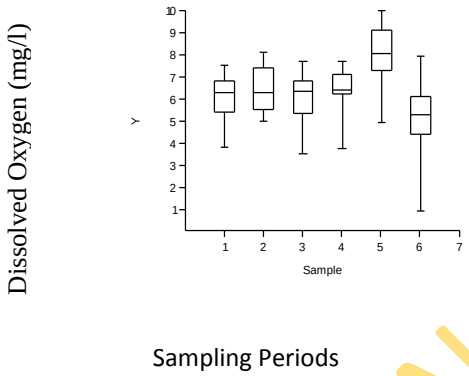


Figure 5: Pattern of DO (mg/l) values

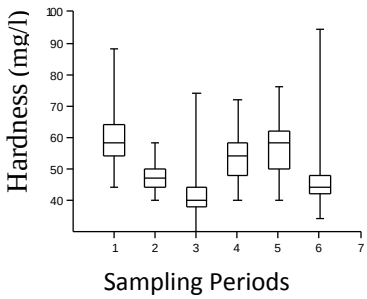


Figure 6: Pattern of TH (mg/l) values

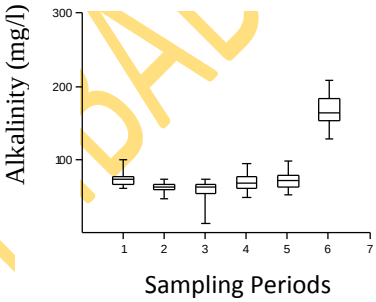


Figure 7: Pattern of TA (mg/l) values

Figures 4-7 Shows the box pattern of water quality parameters obtained from bimonthly sampling of 38 sites at Asejire Lake during January, 2010 to December 2011

Legend

- On X-axis, 1= April / May; 2= June / July; 3= August / September; 4= October / November; 5= December / January, 6= February / March
- DO= Dissolved Oxygen, TH= Total Hardness, TA= Total Alkalinity

Table 8: Coefficient of variability (% CV) of WQP data in seasons and strata (January, 2010-December, 2011)

	O_YS		O_SS	
Parameters	Wet Season	Dry Season	Wet Season	Dry Season
Temperature (^oC)	11.6	8.3	9.4	13.9
DO (mg/l)	29.5	42.0	19.6	23.1
TH	52.4	73.1	11.7	74.1
TA (mg/l)	79.0	66.8	39.7	47.7

Legend:

DO= Dissolved Oxygen

TH= Total Hardness

TA= Total Alkalinity

O_YS= Oyo State Strata

O_SS= Osun State Strata

4.2.3.2 Deviation of water quality parameters from standards

The result of assessment of number of spatial sites that deviated from recommended standards for healthy fish production (Table 9) revealed that deviations (LSV and EHSV) occurred across sites on strata and seasons.

During the wet season, deviation from minimum recommended values (LSV) occurred in all parameters except temperature. The affected sites ranged between 7.89 and 100 % of total sites (DO and TH, respectively). All parameters showed LSV during the dry season; the affected sites ranged between 2.63 and 84.21 % of total sites (TA and TH, respectively).

Deviation from maximum recommended values (EHSV) occurred across the wet and dry seasons. This occurred in temperature at 7.89 % of site during the wet season and 42.11% of sites during the dry season; in DO at 26.32 % of sites during the dry season. The digital map showing the sites with limiting values is presented in Plate 14. The map indicates that the deviation occurred across OYS and O_SS at both seasons.

4.2.3.3 Factors responsible for pattern of variability in WQP

Table 10 shows the result of extraction of number of principal factors contributing to variations in the water quality parameters at Asejire Lake. At Eigen Value of >1.0, two principal components were extracted. The components explained 62.67% of the total variance. On the first component, DO was high loaded, while temperature, TH and TA showed high loading on the second principal component.

Pattern of components matrix on the first component showed that DO was high loaded on the component. However, it had linear relationship with temperature (an abnormal matrix pattern). Inverse relationship existed between DO and temperature on the second principal component. Similarly, relationship between TH and TA followed different pattern on the two principal components. The components formed three iterations, indicating presence of a latent factor that links the two principal components.

Analysis of significant differences in water quality parameters of seasons and catchment's fragments (strata) as sources of variability (Table 11) showed that significant differences ($p<0.05$) occurred among data in wet and dry seasons. Similarly, data on O_YS and O_SS (strata) showed significance ($p<0.05$). O_YS was different from O_SS with respect to 50% of the parameters (Temperature and DO) during wet seasons. During the dry season, O_YS was only different from O_SS with respect to DO (25% of the water quality parameters).

Result on analysis of the relationship between the studied parameters at seasons and strata in order to detect the alliance of the season and strata with the extracted component (Table 12) revealed that the abnormal pattern as observed on the extracted component 1 occurred at the O_YS ($r= 0.44$; $p=0.05$) during the dry season, indicating that component 1 could probably be strata. Significant relationship ($p<0.05$) was not observed in any of the other tested cases, indicating that certain factor(s) are probably distorting the stability of normal pattern of relationships of the water quality parameters at the lake.

Table 9: Percentage sampled sited that had LSV and EHSV of WQP during wet and dry seasons at Asejire Lake (January, 2010 - December, 2011)

Parameter	Recom. Range	Wet Season				Dry Season			
		LSV		EHSV		LSV		EHSV	
		No.	% site	No.	% site	No.	% site	No.	% site
DO (mg/l)	4.00-9.00	3	7.89	0	0	7	18.42	10	26.32
Temperature (^{0}C)	25-31	0	0	3	7.89	20	52.63	16	42.11
Hardness (mg/l)	50-300	38	100	0	0	32	84.21	0	0
Alkalinity (mg/l)	50-300	5	13.16	0	0	1	2.63	0	0

- Total number of sites = 38
- Recom Range =Recommended range of values for fish health

Legend:

LSV= Limiting Spatial Values (values below the minimum recommended range for fish health)

EHSV= Extremely High Spatial Values (values above the maximum recommended range for fish health)

DO= Dissolved Oxygen

TH= Total Hardness

TA= Total Alkalinity

O_YS= Oyo State Strata

O_SS= Osun State Strata

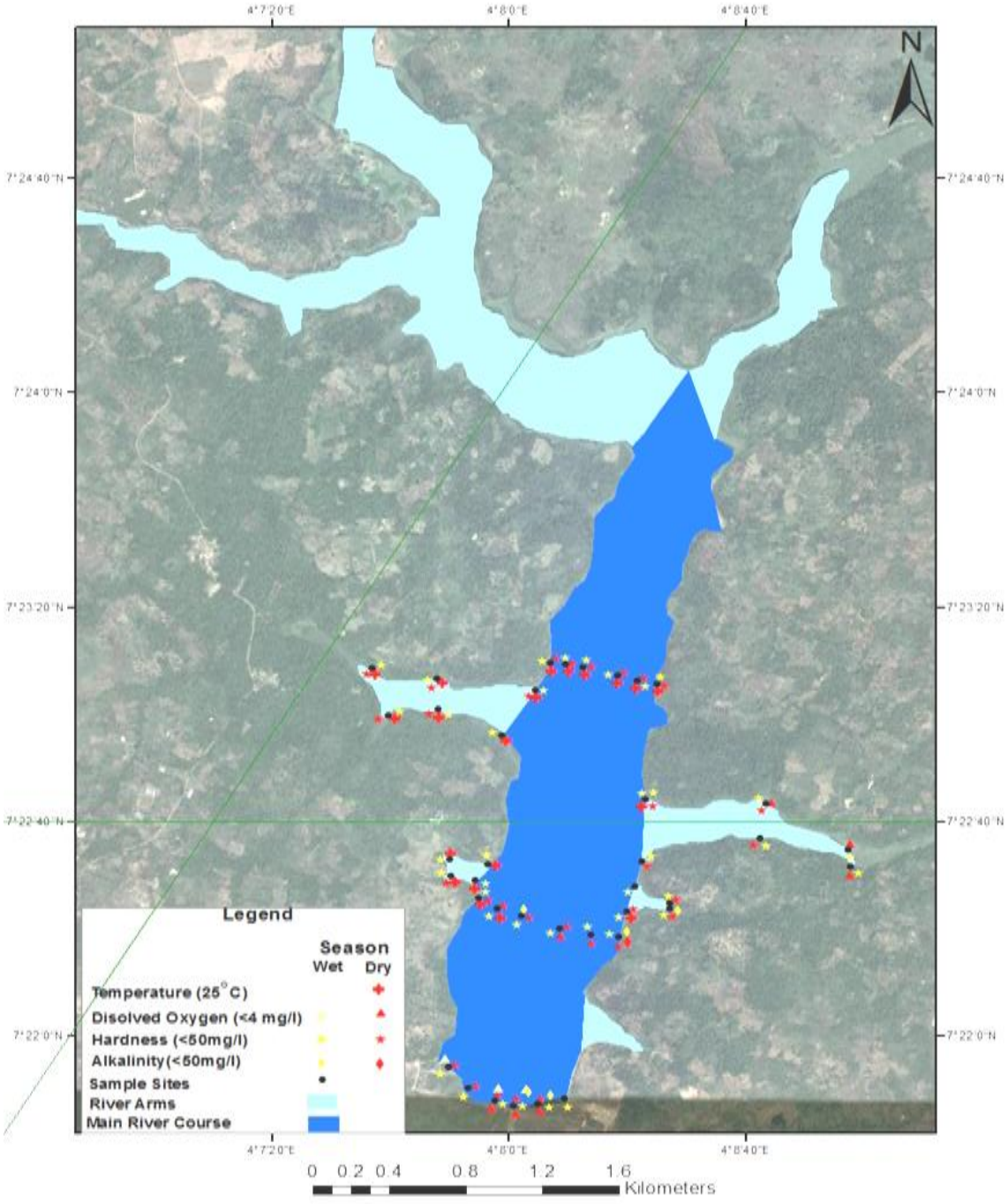


Plate 14: Map showing the sites that reflected limiting spatial values of water quality parameters in the wet and dry seasons at Asejire Lake during January, 2010 - December, 2011

Table 10: Factors, Factors Loading and Components Matrix of Water Quality Parameters

Variables	Principal Component	
	1	2
Temperature	0.046	0.**743**
DO	0.**840**	-0.034
T. hardness	-0.004	0.**720**
T. alkalinity	0.450	0.**621**
Eigen value	2.013	1.121
Variance (%)	40.258	22.419
Cumulative (%)	40.258	62.677

*Rotation converged in 3 iterations; *Bold values represent high loading

Table 11: Probability of difference (p-Values) in water quality parameters between O_YS and O_SS during wet and dry seasons during January 2010 – December, 2011 at Asejire Lake

Parameter	Wet	Dry
Temperature	0.001	0.40
Dissolved Oxygen	0.001	0.006
Total Hardness	0.13	0.74
Total Alkalinity	0.11	0.30

*Pooled wet seasons' data was significantly different from that of the dry season (p=0.03)

Table 12: Paired samples correlations of temperature and dissolved oxygen at seasons and strata during January, 2010 – December, 2011

Parameter	Correlation(r)	2-tailed (p-value)	Comment
Wet season			
O_YS	-0.31	0.19	Normal
O_SS	-0.12	0.62	Normal
Dry season			
O_YS	**0.44**	**0.05**	**Abnormal**
O_SS	-0.20	0.41	Normal

Significance taken at p=0.05

4.2.4 Frequency of opening of dam's gate

Table 13 shows the frequency of incidences of opening of the dams' gate monitored in the catchment during the 2010 – 2011 sampling period. Partial drawdown (PDGO) occurred between 1-7 times/Month (March and November, respectively) during the dry season. It was not observed in April but the frequency ranged between 15 and 18 times/month in other rainy season months (May-September). Complete drawdown (CDGO) was not observed in November. However, the value was between 1-2 times/month in both the wet and dry season months. Interval (days) in between a complete draw down (CDGO) and any other gate opening was between 3-17 days and 5-12 days (dry and wet seasons, respectively).

Water drawdown from the catchment was observed to result in exposure of underground pipes at Oyo and Osun strata of Asejire Lake catchment, exposure of expanse shore areas, high fish mortality at tributary and around impounded areas, exposed rock outcrop at shore area with trapped fresh water prawn, exposure of breeding sites in tributary and exposure of shore areas with destroyed set-net and catch. Pictures showing the effects of dam gate opening are presented in Appendix 5.

Table 13: Frequency of opening of dams' gate at Asejire Lake during the sampling period (January, 2010 – December, 2011)

Month	Frequency of Opening of Gate		Interval (Days) Of Gate Opening
	Partial	Complete	
Dry Season			
October	6	2	12, 15
November	7	0	NA
December	4	1	17
January	5	1	8
February	3	2	3,5
March	1	2	12, 9
Mean	7.50±3.55	2.33±1.03	
Wet Season			
April	0	1	12
May	15	1	6
June	18	1	6
July	18	2	6, 6
August	18	2	5, 6
September	16	1	6
Mean	30.17±7.39	2.33±1.36	

*Interval was taken at complete drawdown only *NA=Not applicable

4.3 Phenotypic variations of *Clarias gariepinus* population in Asejire Lake

Results of fish abundance and diversity as well as the phenotypic structure of the obtained *C. gariepinus* population at Asejire Lake are presented in this section.

4.3.1 Fish catch structure

4.3.1.1 Fish abundance and distribution at Asejire Lake

The fish abundance and relative proportion (composition) of the captured fisheries of the lake are presented in Table 14. The result showed that a total of 1,392 fish were caught during the sampling periods (January, 2010 – December, 2011).

Catch was higher in the wet season (53.16% total catch) compared to the dry season (46.84% total catch). Twelve families and 19 fish species were encountered. The most abundant family was *Claroteidae* and single species was encountered (*Chrysichthys nigrodigitatus)* and it constituted 49.78% of the total catch. This was followed by *Cichlidae* (42.46% of total catch).

The lowest catch was observed in the family *Latidae* (*Lates niloticus*-0.07%). *Cichlidae*, *Mormyridae* and *Clariidae* were species divergent; each of them, respectively constituted four species accounting for 42.46% catch, 3 species representing 3.59% catch and three species constituting 0.5% catch, respectively. Species composition in the total catch in the most divergent family (Cichlidae) was 34.55% (*Tilapia zillii*), 4.52% (*Oreochromis niloticus*), 3.52% (*Sarotherodon galilaeus*) and 0.14% (*Hemichromis fasciatus*). *Clariidae* was the least divergent family and *Clarias gariepinus* had the greatest composition in total catch (0.36 %) among members of the family. An equal proportion (0.07%) of *Heterobranchus bidorsalis* and *Clarias anguillaris* was encountered.

4.3.1.2 Fish species richness and dominance at spatial sites of Asejire Lake

Table 15a shows the fish abundance and species richness obtained for the 38 studied sites, while species dominance across sites and seasons and result of analysis of the data using diversity indices are presented in Table 15b. Digital map of sites and species that predominated is presented in Plates 15 and 16. The result on fish abundance and richness revealed that, during the dry season, the number of encountered species at spatial sites varied from zero (sites 9 and 26) to seven (site 23), while zero (sites 5, 9, 10) to 4 (sites 7 and 19) was obtained during the wet season. The highest value (7 species obtained at site 23) was closely followed by the value for sites 1 and 21 (5 species). No catch was obtained in site 9, which was located at the shore area of impounded end on the

same axis as site one. Most of the diversity indices (Table 15b) indicated that, despite the relatively higher fish catch during the wet season; the dry seasons catch showed higher species diversity. The dry season catch from sites ranged from 0 (site 9) to 126 (19.32 % catch) at sites 11, while the wet season catch range was 0 (sites 9 and 10) to 92 (12.43%catch) at site 21.

Clarias gariepinus was encountered at both strata: two were obtained at site 20 at O_SS tributary during the dry season, while three were obtained at site 31 at O_YS tributary (one during the wet season and two during the dry season).

Differences occurred in species that showed predominance at sites across seasons. Maps showing predominant species at their respective sites of predominance during the wet and dry seasons are presented in Plates 15 and 16. Eight species dominated their sites at one time or the other during the sampling period. *Chrysichthyes* species dominated more than half of the sites in all seasons. *Tilapia zillii* dominated 36.84% and 28.95% sites, while *Oreochromis niloticus* dominated 2.63% and 10.53% sites during the wet and dry seasons, respectively. *Mormyrus rume* and *Gnathonemus tamandua* showed dominance during dry seasons (10.53% and 2.63% sites respectively), while *Sarotherodon galilaeus*, *Parachanna* and *Macrobrachium species* showed dominance only in the wet season (2.63%, 2.63% and 5.26% sites, respectively). None of the members of the family *Clariidae* ever dominated any of the sites. A table showing the respective percentage sites of predominance of the species is presented in Appendix 6.

4.3.1.3 Analysis of differences and correlation of catches at seasons and strata

The total contribution of O_YS during the sampling period was higher compared with that of O_SS (812 and 580 fishes, respectively) (Table 15a). During the wet season, slightly higher catch (52.84%) was obtained at O_SS compared with O_YS (47.16%). In contrast, O_YS had higher catch with wider gap (71.01% catch on O_YS compared with 28.99% catch on O_SS) during the dry season. Variations of seasonal catches were not statistically significant. Similarly, catches from the strata were not significantly different.

The paired sample analysis for the catch data of seasons and strata (Table 16) showed that significant correlation did not exist between seasons, between strata during wet season and during the dry seasons. This indicates that pattern of catch did not follow the pattern of water quality, especially at the strata. However, the wet seasons catch showed a contrast, as negative correlation existed in catches from the O_YS and O_SS during the wet season, while positive correlation was observed between the strata during the dry season.

Table 14: Composition of captured fish at Asejire Lake (January, 2010 – December, 2011)

Family	Season					
	Dry		Wet			
	No.	%	No.	%	Total	% Total Catch
Clarotidae						
Chrysichthys sp.						
sub-total	**349**	**53.53**	**344**	**46.49**	**693**	**49.78**
Latidae						
Lates niloticus						
Sub-total	**0**	**0**	**1**	**0.14**	**1**	**0.07**
Alestidae						
Hydrocynus sp.						
Sub-total	**2**	**0.31**	**11**	**1.49**	**13**	**0.93**
Cichliidae						
Hemichromis sp.	2	0.31	0	0	2	0.14
Oreochromis niloticus.	52	7.98	11	1.49	63	4.52
Sarotherodon galilaeus	16	2.45	29	3.92	45	3.23
Tilapia zillii	153	23.47	328	44.32	481	34.55
Sub-total	**223**	**34.2**	**368**	**49.73**	**591**	**42.46**
Clariidae						
Clarias gariepinus	4	0.61	1	0.14	5	0.36
Heterobranchus bidorsalis	1	0.15	0	0	1	0.07
Clarias anguillaris	1	0.15	0	0	1	0.07
Sub-total	**6**	**0.92**	**1**	**0.14**	**7**	**0.5**
Palaemonidae						
Macrobrachium sp.						
Sub-total	**1**	**0.15**	**12**	**1.62**	**13**	**0.93**
Mochokidae						
Synodontis sp.						
Sub-total	**2**	**0.31**	**0**	**0**	**2**	**0.14**
Hepsetidae						
Hepsetus odoe						
Sub-total	**4**	**0.61**	**0**	**0**	**4**	**0.29**
Mormyridae						
Mormyrus rume	43	6.6	0	0	43	3.09
Gnathostomus tamandua.	3	0.46	0	0	3	0.22
M. macrophthalmus	4	0.61	0	0	4	0.29
Sub-total	**50**	**7.67**	**0**	**0**	**50**	**3.59**

Polypteriidae						
Polypterus endlicheri						
Sub-total	**5**	**0.77**	**0**	**0**	**5**	**0.36**
Channidae						
Parachanna obscura						
Sub-total	**6**	**0.93**	**3**	**0.41**	**9**	**0.65**
Clupeidae						
Sardinella sp.						
Sub-total	**4**	**0.61**	**0**	**0**	**4**	**0.29**
Grand total	***652***	**46.84**	***740***	**53.16**	***1392***	

Table 15a: Relative fish abundance and species richness at the sampled spatial sites during January, 2010 – December, 2011

	Dry Season			Wet Season		
Sites	Catch	% Composition	No. of *Species*.	Catch	%Composition	No. of *Species*
1	97	14.87	5	62	8.38	3
2	6	0.92	1	21	2.83	2
3	11	1.69	4	13	1.76	1
4	3	0.46	3	4	0.54	2
5	11	1.69	1	**0**	**0**	**0**
6	25	3.83	3	64	8.65	3
7	9	1.38	2	**11**	**1.48**	**4**
8	20	3.07	1	1	0.13	1
9	**0**	**0**	**0**	**0**	**0**	**0**
10	5	0.77	1	**0**	**0**	**0**
11	126	19.32	2	2	0.27	1
12	13	1.99	3	6	0.81	3
13	6	0.92	1	26	3.51	2
14	7	1.07	1	3	0.4	1
15	10	1.53	2	1	0.13	1
16	25	3.83	3	1	0.13	1
17	2	0.31	1	4	0.54	1
18	18	2.76	2	4	0.54	1
19	3	0.46	1	**50**	**6.75**	**4**
20	**6**	**0.92**	**2**	**21**	**2.83**	**2***
21	20	3.07	5	92	12.43	3
22	16	2.45	3	4	0.54	2
23	**16**	**2.45**	**7**	58	7.84	3
24	7	1.07	2	22	2.97	2
25	3	0.46	2	6	0.81	1
26	**0**	**0**	**0**	13	1.75	1
27	18	2.76	2	5	0.67	2
28	9	1.38	2	10	1.35	2
29	17	2.61	2	7	0.94	2
30	44	6.75	3	12	1.62	1
31	**13**	**1.99**	**4**	**10**	**1.35**	**3***
32	22	3.37	3	35	4.73	1
33	10	1.53	2	2	0.27	1
34	3	0.46	1	10	1.35	1
35	9	1.38	3	12	1.62	2
36	22	3.37	3	87	11.76	3
37	4	0.61	1	2	0.27	1
38	16	2.45	3	59	7.97	2
Total	**652**		**740**			

*Sites where *C. gariepinus* was encountered during sampling

Table 15b: Diversity of wet and dry seasons fish catch at Asejire Lake during January, 2010 – December, 2011

Diversity indices	Dry season	Wet season
Taxa	36	35
Individuals	652	740
Dominance	0.07823	0.06915
Shannon H	3.053	2.961
Evenness	0.5885	0.5519
Simpson index	0.9218	0.9309
Menhinick	1.41	1.287
Margalef	5.401	5.146
Equitability	0.8521	0.8328
Fisher alpha	8.204	7.635
Berger-Parker	0.1933	0.1243

Table 16: Paired Samples Correlations of Fish Catches from Seasons and Strata

Parameter	Correlation(r)	Comment
Wet season/Dry season	0.175	Chance occurrence
OyS at dry/ OsS at dry season	0.067	Chance occurrence
O_YS at wet/ O_SS at wet season	-0.193	Chance occurrence

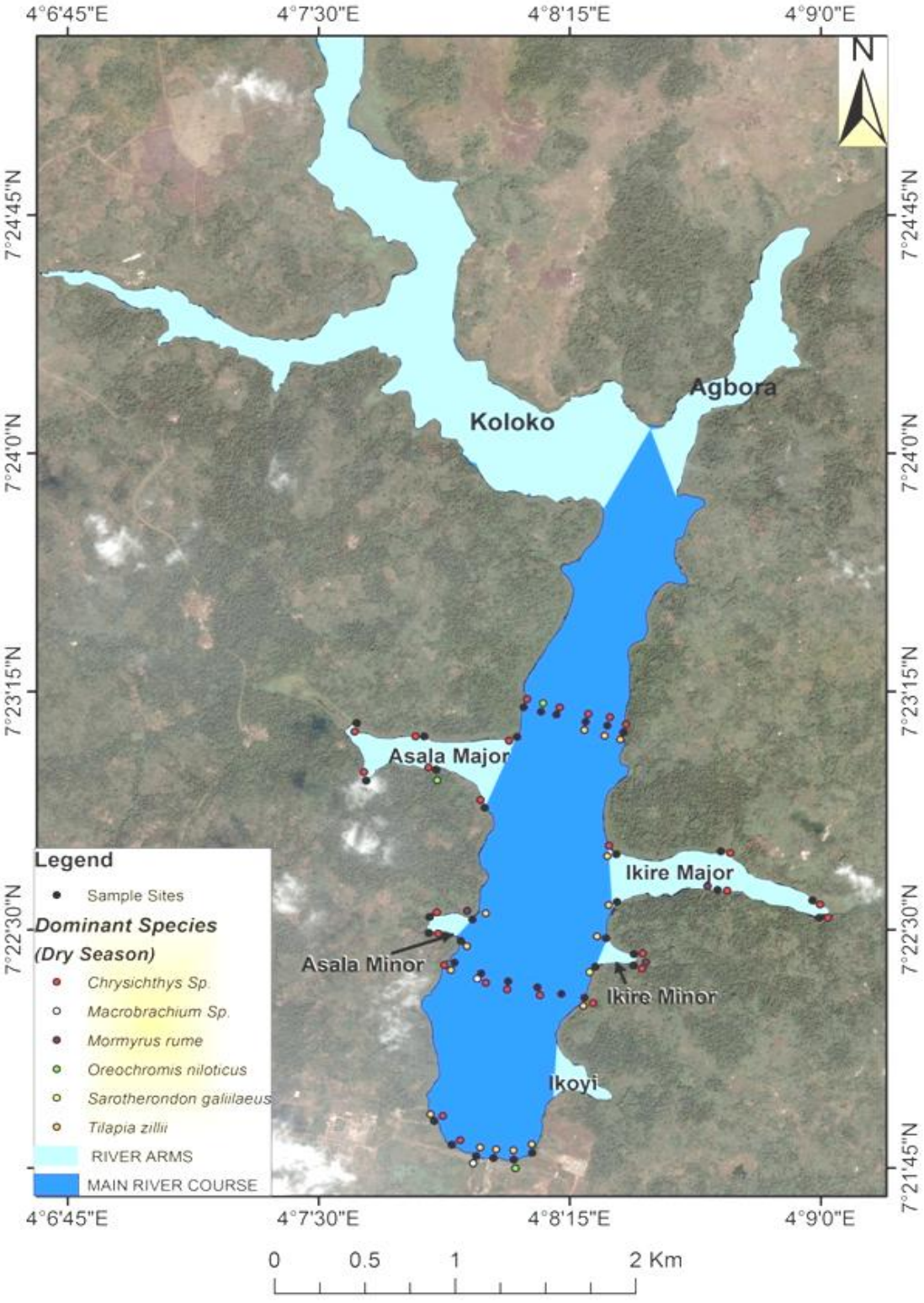


Plate 15: Map showing the dominant species and their sites of predominance (Dry Season)

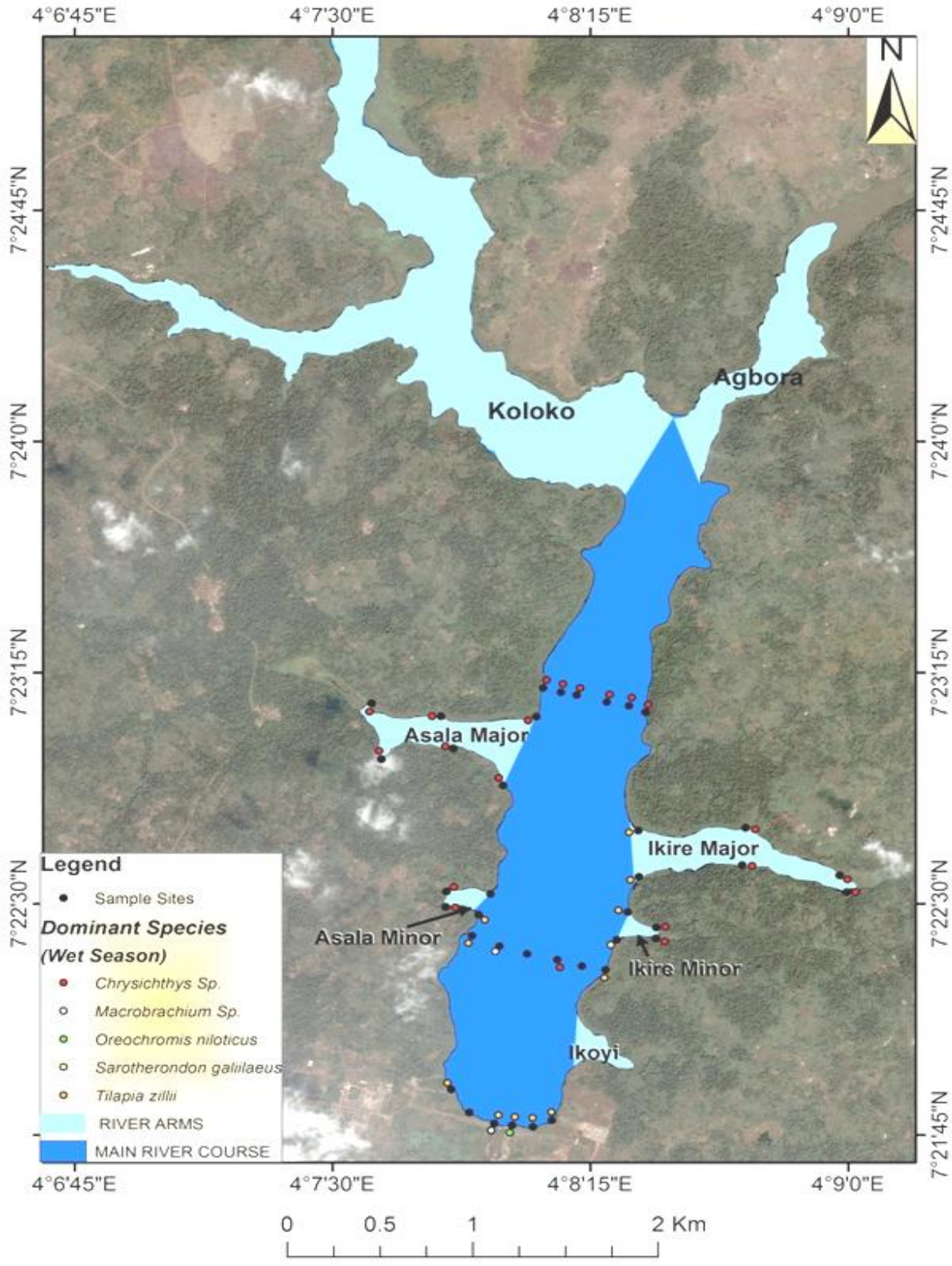


Plate 16: Map showing the dominant species and their sites of predominance (Wet Season)

4.3.2 Phenotypic variations of *Clarias gariepinus* population at Asejire Lake

Results of the phenotypic structure, most varied attribute and analysis of latent factors responsible for the structure, are presented in this section.

The descriptive statistics showing phenotypic values and the respective coefficient of variation of attributes of the studied *Clarias gariepinus* population is presented in Table 17. Results of factor analysis of the multiple mode attributes is presented in Table 18. Iteration of the attributes on the extracted factors are shown on Figure 8. The results revealed heterogeneity in phenotypes and this could be taxonomic. It also showed pectoral fin characters (PECSL and PESES) being the respective most varied morphometric and meristic characters.

Coefficient of variation in morphometric traits (Table 17a) ranged between 7.33 to 31.51 % (PECSL-L and PECSL-R, respectively). A total of 75 % of morphometric attributes were heterogeneous (CV >10 %), while all, except PECSL, had multiple modal values. This represented 91.67 % of the total sites. Pectoral Spine Length (PECSL) was the most varied morphometric attribute; CV was highest in it and the widest difference between left and right side values' variability occurred in it.

Phenotypic values of meristic attributes, their coefficient of variation and modes, as presented in Table 17b, showed that PESES-L (left) and PESES-R (right) and DR reflected heterogeneity. PESES was the most varied meristic trait; highest CV value and greatest difference between left and right values were observed in it. Also, all attributes had small and similar coefficient of variation (7.16-8.97%) except in PESES-L (64.79%) and PESES-R (68.12%). The widest variation between left and right values also occurred in PESES - L&R. The DR was the only meristic site that had multiple modes. The CV in meristic sites ranged between 7.16-68.12%. (PELFR-R and PESES-R, respectively).

Results of factor analysis of the multi-modal phenotypic data (Table 18) showed that 5 principal components were responsible, while component rotation (Appendix 7) revealed 16 different iteration of the different phenotypes. Skeletal view of the discovered PESES variants is presented in Plate 17.

Table 17(a): Phenotypic values (as %SL.) and Coefficient of Variation (CV) of morphometric attributes of the studied *Clarias gariepinus* population (N=37)

Phenotype	Minimum	Maximum	Mean± SD	CV (%)	Mode
HL	25.00	33.33	28.56±2.20	7.70	27.0a
BD MAX	6.11	16.05	10.95±2.12	19.36	8.92a
BDMIN	3.16	9.62	6.22±1.39	22.35	4.69a
PECFL-L	7.25	14.32	11.30±1.64	14.51	11.17a
PECFL-R	8.59	14.72	11.25±1.60	14.22	8.59a
PECSL-L	2.26	10.80	6.57±2.07	31.51	6.74a
PECSL-R	2.50	8.42	6.63±1.64	24.74	7.98
DFL	57.46	79.75	63.19±4.63	7.33	61.70a
PELFL-L	6.33	12.50	9.17±1.34	14.61	8.92a
PELFL-R	8.33	11.42	9.14±1.18	12.80	9.04a
AFL	34.47	58.33	42.24±3.54	8.38	40.43a
CFW	9.33	17.02	13.99±1.66	11.67	13.38a

a=Multiple modes, N= population size

Head length (HL), Maximum body depth (BD-MAX), Minimum body depth (BD-MIN), Pectoral fin length of left side fin (PECFL-L), Pectoral fin length of right side fin(PECFL-R), Pectoral spine length of left side fin (PECSL-L), Pectoral spine length of right side fin (PECSL-R), Dorsal fin length (DFL), Pelvic fin length of left side fin (PELFL-L), Pelvic fin length of right side fin (PELFL-R), Anal fin length (AFL) and Caudal fin width (CFW)

Table 18(b): Phenotypic values and Coefficient of Variation (CV) of meristic attributes of the studied *Clarias gariepinus* population (N=37)

Phenotype	Minimum	Maximum	CV (%)	Mode
PECFR-L	7.00	10.00	7.79	9.00
PECFR-R	7.00	10.00	7.57	1.00
PESES-L	0.00	1.00	64.79	1.00
PESES-R	0.00	1.00	68.12	1.00
PELFR-L	5.00	7.00	7.92	6.00
PELFR-R	5.00	7.00	7.16	6.00
DFR	**45.00**	**78.00**	**7.98**	**67.00a**
AFR	45.00	65.00	8.97	51.00
CFR	15.00	23.00	7.53	19.00

***a=Multiple modes, N= population size**

Pectoral fin rays count on left side (PECFR-L), Pectoral fin ray count on the right side (PECFR-R), Possession of anteriorly serrated spine on the left side (PESES-L), Possession of anteriorly serrated spine on the right side (PESES-R), Pelvic fin rays counts on left side (PELFR-L), Pelvic fin rays counts on right side (PELFR-R), Dorsal fin rays counts (DR), Anal fin rays counts (AFR) and Caudal fin rays counts (CFR)

Table 18: Extracted factors and matrix of multimodal attributes of the studied *C. gariepinus* population

	Principal Components				
Phenotypes	**1**	**2**	**3**	**4**	**5**
HL	0.175	-0.727	**0.624**	-0.080	-0.006
BD MAX	-0.125	**0.924**	0.093	-0.239	-0.057
BDMIN	0.487	0.178	-0.413	**0.734**	-0.088
PECFL-L	**0.959**	0.099	-0.194	0.073	0.085
PECFL-R	**0.879**	0.168	-0.339	0.014	0.186
PECSL-L	**0.649**	-0.539	-0.005	0.011	-0.468
DFL	0.162	0.134	**0.618**	**0.749**	-0.035
PELFL-L	**0.941**	0.171	-0.011	-0.225	0.015
PELFL-R	**0.779**	0.412	0.224	-0.394	-0.039
AFL	-0.115	**0.681**	0.549	0.183	0.286
CFW	0.393	-0.538	0.272	-0.030	**0.668**
DR	0.352	0.142	**0.808**	-0.093	0.319

Bold indicate high loading

Head length (HL), Maximum body depth (BD-MAX),Minimum body depth (BD-MIN), Pectoral fin length of left side fin (PECFL-L),Pectoral fin length of right side fin(PECFL-R), Pectoral spine length of left side fin (PECSL-L), Pectoral spine length of right side fin (PECSL-R), Dorsal fin length (DFL), Pelvic fin length of left side fin (PELFL-L), Pelvic fin length of right side fin (PELFL-R),Anal fin length (AFL) and Caudal fin width (CFW) and Dorsal fin rays counts (DR)

Plate 17: Skeletal view of Variations with respect to serrations in Pectoral Spine in *C. gariepinus*

(Mag. X 500)

4.4 Discriminant factors in sub-grouping *C. gariepinus* population of Asejire Lake

Phenotypic structure and result of analysis of canonical discriminant factors in subgroups of the studied *Clarias gariepinus* population are presented in this section.

4.4.1 Phenotypic structure of subgroups of *C. gariepinus* in Asejire Lake

This section presents the results on phenotypic structure, most varied phenotype, and assessment of the number of latent factors responsible for heterogeneity in each of the studied subgroups.

4.4.1.1 Phenotypic structure of sex sub-groups

Descriptive statistics with respect to size range of obtained sexually differentiated *C. gariepinus* populations in the study area is presented in Table 19. The population was female biased (Sex ratio was 3:7 for male and female individuals respectively. The sizes ranged between 17.9 and 41.20 cm SL (male) and 17.6 and 47.50 cm SL (female). The mean standard lengths (SL) of the sexes was not statistically different ($P>0.05$).

The descriptive statistics of the phenotypes in the studied female population of *C. gariepinus* is presented in Table 20. Coefficient of variation in morphometric traits (Table 20a) ranged between 6.08 and 39.12 % (HL and PECSL-L, respectively). The PECSL-R was next to the highest in variation. The widest difference in variability between the left and right of paired phenotypes and the highest variation values occurred in PECSL. Moreover, multiple modal attributes occurred in all morphometric traits except PECSL-R.

Variations in meristic attributes (Table 20b) ranged from 6.36 % (CFR) to 81.96 % (PESES-R). Next to the greatest was the PESES-L (71.64 %). Variations of phenotypes at the left and right sides of paired fins were similar. However, the widest difference occurred in PESES, while DR and AFR had multiple modes.

The result therefore showed similar trend in multi-modal morphometric and meristic attributes of female population and the entire population. However, additional multimodal attribute (AFR) occurred in the female sub-groups' phenotype. Factor analysis (Table 21) extracted five components in the multimodal attributes of the female sub-group, while the multi-modal phenotypes showed 5 iterations on the extracted components (Figure 9).

The morphometric and meristic characterization of the studied male *C. gariepinus* population in Asejire Lake is presented in Table 22. Coefficient of variation ranged between 4.17 % (DL) and 21.88 % (BD MAX) among morphometric phenotypes (Table

22a). Variation in PECSL-R (18.42%) was next to the highest. Similar values in left and right sides of the paired fins were observed in morphometric traits. However, the widest difference was observed in PECSL, while multiple modes existed in all morphometric attributes except in HL and PELFL-L.

Meristic traits (Table 22b) had variation range between 0.00 (PELFR-R) and 50.00 % (PESES-L). PESES-R (CV= 38.33 %) was next to the highest. PESES also had the widest difference between the left and right side values among paired meristic attributes. Modal values in meristic traits were multiple at DR and AFR, showing similarity with the female sub-groups.

Factor analysis extracted 4 principal components as responsible for the multiple modalities of data (Table 23). The attributes converged into 9 iterations after component rotation (Appendix 7).

Statistical examination of the difference in mean values of morphometric attributes between the separated sexes (Table 24) reflected that *P- values* ranged between 0.051(BD MIN) and 0.586 (PECSL-L) in morphometric attributes, while the meristic values ranged between 0.132 (PESES-R) and 0.98 (DR). Sexual dimorphism was, therefore, not confirmed at $p<0.05$ in the population.

Table 19: Sizes (SL) sex sub-groups of the studied population

	N	Size range (cm)	Mean	SD	t-value
Male	11	17.9-41.20	29.02	8.06	
Female	26	17.6-47.50	28.35	9.38	0.831

***N= Population size, SD= standard deviation,**

Table 20(a): Phenotypic values (as %SL.) and coefficient of variation (CV) of morphometric attributes of the female subgroup (N=26)

Phenotype	Minimum	Maximum	Mean±SD	CV(%)	Mode
HL	25.00	33.33	29.06±2.35	6.08	27.0a
BD MAX	6.11	16.05	10.85±2.30	21.19	8.92a
BD MIN	3.18	7.69	5.93±1.26	21.24	4.69a
PECFL-L	7.23	13.95	11.11±1.52	13.68	11.17a
PECFL-R	8.59	14.72	11.11±1.57	14.13	11.17a
PECSL-L	2.28	10.80	6.39±2.50	39.12	7.45a
PECSL-R	2.50	7.98	6.44±1.76	27.32	7.98
DFL	57.46	79.75	63.92±5.17	8.08	61.7a
PELFL-L	6.33	12.50	9.33±1.39	14.89	8.92a
PELFL-R	6.33	11.42	9.26±1.20	12.95	9.04a
AFL	34.47	58.33	42.54±4.07	9.56	40.43a
CFW	10.54	17.02	14.14±1.62	11.45	13.38a

a= multiple modes

Head length (HL), Maximum body depth (BD-MAX), Minimum body depth (BD-MIN), Pectoral fin length of left side fin (PECFL-L), Pectoral fin length of right side fin(PECFL-R), Pectoral spine length of left side fin (PECSL-L), Pectoral spine length of right side fin (PECSL-R), Dorsal fin length (DFL), Pelvic fin length of left side fin (PELFL-L), Pelvic fin length of right side fin (PELFL-R), Anal fin length (AFL) and Caudal fin width (CFW)

Table 20(b): Phenotypic values and coefficient of variation (CV) of meristic attributes of the female subgroup (N=26)

Phenotype	Minimum	Maximum	CV(%)	Mode
PECFR-L	7.00	10.00	8.19	9.00
PECFR-R	7.00	10.00	6.83	9.00
PESES-L	0.00	1.00	71.64	1.00
PESES-R	0.00	1.00	81.96	1.00
PELFR-L	5.00	7.00	8.83	6.00
PELFR-R	5.00	7.00	8.43	6.00
DR	45.00	78.00	9.16	69.00a
AFR	45.00	65.00	10.22	45.00a
CFR	15.00	20.00	6.36	19.00

a= multiple modes

Pectoral fin rays count on left side (PECFR-L), Pectoral fin ray count on the right side (PECFR-R), Possession of anteriorly serrated spine on the left side (PESES-L), Possession of anteriorly serrated spine on the right side (PESES-R), Pelvic fin rays counts on left side (PELFR-L), Pelvic fin rays counts on right side (PELFR-R), Dorsal fin rays counts (DR), Anal fin rays counts (AFR) and Caudal fin rays counts (CFR)

Table 21: Extracted factors and matrix of multimodal attributes of the studied female *C. gariepinus* sub-group

	Principal Components				
Phenotypes	1	2	3	4	5
HL	0.185	**-0.651**	-0.053	**0.630**	0.124
BD MAX	-0.344	-0.464	**0.725**	0.009	0.242
BDMIN	0.108	0.135	**0.956**	0.054	1.1E-005
PECFL-L	**0.921**	-0.196	0.016	-0.119	0.014
PECFL-R	**0.705**	-0.303	0.137	**-0.623**	0.093
PECSL-L	**0.560**	0.107	**-0.622**	0.131	0.379
DFL	0.385	**0.664**	0.025	**0.612**	-0.077
PELFL-L	**0.925**	-0.250	0.138	0.110	-0.077
PELFL-R	**0.946**	0.062	0.137	-0.110	0.135
AFL	0.380	**0.768**	0.081	-0.471	-0.038
CFW	**0.516**	**-0.792**	-0.002	0.180	-0.202
DR*	0.079	0.482	0.218	0.344	**0.729**
AFR*	0.383	**0.535**	0.207	0.452	**-0.528**

***Meristic attributes**

Head length (HL), Maximum body depth (BD-MAX), Minimum body depth (BD-MIN), Pectoral fin length of left side fin (PECFL-L), Pectoral fin length of right side fin(PECFL-R), Pectoral spine length of left side fin (PECSL-L), Dorsal fin length (DFL), Pelvic fin length of left side fin (PELFL-L), Pelvic fin length of right side fin (PELFL-R), Anal fin length (AFL) and Caudal fin width (CFW), Dorsal fin rays counts (DR), Anal fin rays counts (AFR)

Table 22(a): Phenotypic values (as %SL.) and coefficient of variation (CV) of morphometric attributes of male subgroup of *C. gariepinus* in Asejire Lake (N=11)

Phenotype	Minimum	Maximum	Mean± SD	CV	Mode
HL	25.33	29.60	27.18±1.30	4.78	25.33
BD MAX	8.75	14.57	11.18±1.68	15.0	8.75a
BDMIN	5.42	9.62	6.90±1.51	21.88	5.42a
PECFL-L	8.14	14.32	11.73±1.90	16.19	8.14a
PECFL-R	8.14	14.32	11.57±1.72	14.86	8.14a
PECSL-L	5.43	8.08	6.90±0.84	12.17	5.43a
PECSL-R	4.98	8.42	7.11±1.31	18.42	4.98a
DFL	59.11	67.68	61.52±2.51	4.17	59.11a
PELFL-L	6.79	10.80	8. 81±1.19	13.50	6.79a
PELFL-R	7.24	10.80	8.85±1.11	12.54	9.33
AFL	38.38	44.50	41.55±1.81	4.35	38.38a
CFW	9.33	15.08	13.63±1.79	13.13	9.33a

a= multiple modes

Head length (HL), Maximum body depth (BD-MAX), Minimum body depth (BD-MIN), Pectoral fin length of left side fin (PECFL-L), Pectoral fin length of right side fin(PECFL-R), Pectoral spine length of left side fin (PECSL-L), Pectoral spine length of right side fin (PECSL-R), Dorsal fin length (DFL), Pelvic fin length of left side fin (PELFL-L), Pelvic fin length of right side fin (PELFL-R), Anal fin length (AFL) and Caudal fin width (CFW)

Table 22(b): Phenotypic values and coefficient of variation (CV) of meristic attributes of male subgroup

Phenotype	Minimum	Maximum	CV	Mode
PECFR-L	8.00	10.00	7.00	9.00
PECFR-R	8.00	10.00	9.11	9.00
PESES-L	0.00	1.00	50.00	1.00
PESES-R	0.00	1.00	37.07	1.00
PELFR-L	5.00	6.00	5.07	6.00
PELFR-R	6.00	6.00	0.00	6.00
DR	65.00	73.00	38.33	67.00a
AFR	48.00	56.00	4.52	49.00a
CFR	16.00	23.00	9.97	19.00

a=Multiple modes

Pectoral fin rays count on left side (PECFR-L), Pectoral fin ray count on the right side (PECFR-R), Possession of anteriorly serrated spine on the left side (PESES-L), Possession of anteriorly serrated spine on the right side (PESES-R), Pelvic fin rays counts on left side (PELFR-L), Pelvic fin rays counts on right side (PELFR-R), Dorsal fin rays counts (DR), Anal fin rays counts (AFR) and Caudal fin rays counts (CFR)

Table 23: Extracted factors and matrix of multimodal attributes of the studied male *C. gariepinus* sub-group

	Principal Components			
Phenotype	1	2	3	4
HL	**-0.525**	**-0.797**	0.254	0.158
BD MAX	-0.093	**0.969**	0.229	-0.032
BDMIN	**0.934**	0.288	-0.168	0.131
PECFL-L	**0.937**	-0.197	-0.027	0.300
PECFL-R	**0.911**	0.301	0.281	-0.022
PECSL-L	0.336	-0.274	**0.850**	-0.300
PECSL-R	**0.647**	-0.225	**0.692**	-0.231
DFL	-0.261	**0.504**	**0.791**	0.229
PELFL-L	**0.976**	-0.175	0.121	-0.052
AFL	-0.277	**0.749**	0.398	0.451
CFL	-0.488	-0.475	**0.727**	0.088
DR*	**0.538**	**-0.571**	-0.017	**0.621**
AFR *	**0.980**	0.137	-0.091	-0.110

***meristic attributes**

Head length (HL), Maximum body depth (BD-MAX), Minimum body depth (BD-MIN), Pectoral fin length of left side fin (PECFL-L), Pectoral fin length of right side fin(PECFL-R), Pectoral spine length of left side fin (PECSL-L), Pectoral spine length of right side fin (PECSL-R), Dorsal fin length (DFL), Pelvic fin length of left side fin (PELFL-L), Anal fin length (AFL), Caudal fin width (CFW), Dorsal fin rays counts (DR), Anal fin rays counts (AFR)

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Table 24(a): Probability of heterogeneity in mean phenotypic values of morphometric attributes of the studied sexually differentiated populations of *C. gariepinus*

Phenotype	Male	Female	*P-(same)*
Morphometric			
HL	27.18±1.30	29.06±2.35	0.065
BD MAX	11.18±1.68	10.85±2.30	0.67
BDMIN	6.90±1.51	5.93±1.26	0.051
PECFL-L	11.73±1.90	11.11±1.52	0.304
PECFL-R	11.57±1.72	11.11±1.57	0.474
PECSL-L	6.90±0.84	6.39±2.50	0.586
PECSL-R	7.11±1.31	6.44±1.76	0.45
DFL	61.52±2.57	63.92±5.17	0.156
PELFL-L	8.81±1.19	9.33±1.39	0.288
PELFL-R	8.85±1.11	9.26±1.20	0.345
AFL	41.55±1.81	42.54±4.07	0.445
CFW	13.63±1.79	14.14±1.62	0.414

***Mean with the same superscript are not significantly different (p>0.05)**

Head length (HL), Maximum body depth (BD-MAX), Minimum body depth (BD-MIN), Pectoral fin length of left side fin (PECFL-L), Pectoral fin length of right side fin(PECFL-R), Pectoral spine length of left side fin (PECSL-L), Pectoral spine length of right side fin (PECSL-R), Dorsal fin length (DFL), Pelvic fin length of left side fin (PELFL-L), Pelvic fin length of right side fin (PELFL-R), Anal fin length (AFL) and Caudal fin width (CFW)

Table 24(b): Probability of heterogeneity in mean phenotypic values of meristic attributes of the studied sexually differentiated populations of *C. gariepinus*

Phenotype	Male	Female	*P-(same)*
PECFR-L	9.00±0.63	8.79±0.72	0.417
PECFR-R	9.00±0.82	8.78±0.60	0.398
PESES-L	0.82±0.41	0.67±0.48	0.372
PESES-R	0.89±0.33	0.61±0.50	0.132
PELFR-L	5.91±0.30	5.77±0.51	0.407
PELFR-R	6.00±0.00	5.81±0.49	0.361
DR	68.60±2.63	68.65±6.29	0.98
AFR	50.80±2.30	51.64±5.28	0.633
CFR	18.64±1.86	18.38±1.17	0.621

***Mean with the same superscript are not significantly different (p>0.05)**

Pectoral fin rays count on left side (PECFR-L), Pectoral fin ray count on the right side (PECFR-R), Possession of anteriorly serrated spine on the left side (PESES-L), Possession of anteriorly serrated spine on the right side (PESES-R), Pelvic fin rays counts on left side (PELFR-L), Pelvic fin rays counts on right side (PELFR-R), Dorsal fin rays counts (DR), Anal fin rays counts (AFR) and Caudal fin rays counts (CFR)

4.4.1.2 Phenotypic structure of sub-groups of size

Morphometric and meristic values in size sub-group 1 (10.1 - 20.00 cm) and their variation is presented in Table 25. Variation in morphometric traits (Table 25a) ranged from 3.53% in anal fin length (AFL) to 24.48 % in pectoral spine length of the left side (PECSL-L). Pectoral spine length (PECSL) was most varied with respect to the left and right values of paired fins' attributes. All morphometric attributes had mono-modal values.

Meristic attributes (Table 25b) varied from 0.00 % pectoral fin ray count (PECFR-R) to 49.40 % possession of anteriorly positioned serration on the right side (PESES-R). Possession of anteriorly positioned serration on the left side (PESES-L) had next to the highest value (44.19 %), while dorsal ray count (DR) (5.11%) was next to the lowest. Meristic traits had similar values for differences between the left and right side fins; however, the greatest variation value occurred in possession of anteriorly positioned serration (PESES). Compared with the earlier studied groups, higher number of attributes showed multiple-modality at pelvic fin ray count for left side, for the right side and for anal fin ray count (PELFR-L, PELFR-R and AFR). Anal fin ray count (AFR) was consistent as multiple mode attribute. Factor analysis revealed that all multiple attributes were on a common component.

The results of morphometric and meristic characterisation of size group 2 (20.1-30.0 cm) is presented in Table 26. Variation in morphometric traits (Table 26a) ranged from 3.24 to 27.29% in pelvic fin ray count of left side and pectoral spine length of the left side (PELFR-L and PECSL-L, respectively). Pectoral spine length of the right side (PECSL-R) was next to the highest value (24.16%). The widest difference in variation values from the left to right sides was observed in pelvic fin length of the left side (PELFL-L). However, this was nearly the same as the value in pectoral spine length (PECSL). The latter had higher variation values (27.29 & 24.16 % in the left and right sides, respectively). The values were higher than that of pelvic fin length (PELFL). Multiple modal values were observed in all morphometric traits except head length, pectoral fin length of the right side, dorsal length and pelvic fin length of the right side (HL, PECFL-R, DL and PELFL-R).

Variation in meristic traits of size group 2 (Table 26b) ranged from 0.00 % in pelvic fin ray count of left side (PELFR-L) to 66.20 % possession of anteriorly positioned serration on the pectoral spine at the left side (PESES-L). Possession of anteriorly positioned serration on the pectoral spine at the right side (PESES-R) was next to the

highest (57.14 %). Possession of anteriorly positioned serration on the pectoral spine (PESES) also had the widest difference between the left and right values among paired fins meristic attributes while dorsal ray count (DR) was the only meristic attribute with multiple modes. Factor analysis (Table 27) extracted 4 principal components. Attribute converged to seven iterations (Appendix 7) in which all attributes appeared central to anal fin ray count (AFR).

Table 28 shows the morphometric and meristic characteristics of size group 3 (30.1- 40.0 cm). The range of variation of the phenotypes of morphometric characterisation (Table 28a) range from 6.24 in PECSL-L to 39.84 % PECSL-R. Except in PECFL, paired fins were similar at the left and right sides in all morphometric traits. The PECFL had 6.24 % and 39.84 % in the left and right side values, respectively. Modes were singular in all morphometric attributes.

Meristic traits (Table 28b) varied between 5.95 % and 39.77 % (PELFR-R and PESES-L and PESES-R, respectively). Variations in meristic value on both sides of paired fins were similar. However, the greatest values were obtained in PESES. The PECFR-L was the only meristic attribute that had multiple modal values. Hence, factor analysis was not carried out.

The morphometric and meristic identity as well as coefficient of variability of individuals in size group 4 are presented in Table 29. The range of CV in morphometric traits (Table 29a) was 3.52 % (AFL) - 32.20 % (BD MAX). BD MIN was next to the greatest in terms of variation value. Paired fins varied in all paired morphometric traits. PECSL had the widest value, while PECSL-R and CFW had multiple modes.

Coefficient of variation in meristic attributes (Table 29b) ranged between 0.00 and 85.00 % (PELFR-R and PESES-R, respectively). The greatest variation value was closely followed by the CV of PESES-L. Paired fins' meristic attributes were equal in PECFR but differed at similar margin in PESES and PELFR. All meristic attributes had single modes, while factor analysis extracted only one component. Hence, attributes iterations on components was not generated.

Result of statistical test for difference in mean values of phenotypes of the different size groups is presented in Table 30. Probability ranged between 0.076 (CFW) to 0.939 (BD MAX) in morphometric attributes (Table 30a); 0.008 (DR) to 0.915 (CFR) in meristic attributes (Tables 30b). The populations were significantly differentiated ($p<0.05$) at only one phenotypic site (DR). Mean value of DR ranged between 63.43±8.76 (group 3) to 71.17±2.14 (group 4).

The graphical relationship of the mean values of DR in the groups is presented in Figure 8. The graph reflected an increasing mean DR count from groups 1 to 2; the greatest count in group 4 and a drop below all other values in group 3, indicating that it did not follow increase in size pattern.

Table 25(a): Phenotypic values (as %SL.) and coefficient of variation (CV) of morphometric attributes of size sub-group 1 (10.1-20.0cm SL) (N=8)

Phenotype	Minimum	Maximum	Mean	SD	CV	Mode
HL	26.42	32.45	29.36	2.43	8.28	32.45
BD MAX	8.95	14.13	11.15	1.52	13.63	11.17
BD MIN	5.00	6.70	5.7	0.62	10.75	5.32
PECFL-L	10.05	13.96	11.36	1.27	11.18	11.17
PECFL-R	9.05	13.40	11.30	1.56	13.81	11.17
PECSL-L	3.87	7.45	6.21	1.52	24.48	7.45
PECSL-R	6.63	7.98	7.53	0.78	10.36	7.98
DFL	57.46	65.83	61.64	2.26	3.67	81.70
PELFL-L	8.04	10.11	9.22	0.82	8.89	10.11
PELFL-R	7.54	9.78	9.09	0.71	7.81	9.04
AFL	39.38	43.55	41.64	1.47	3.53	40.43
CFW	14.07	17.02	15.25	1.17	7.67	17.02

Head length (HL), Maximum body depth (BD-MAX), Minimum body depth (BD-MIN), Pectoral fin length of left side fin (PECFL-L), Pectoral fin length of right side fin(PECFL-R), Pectoral spine length of left side fin (PECSL-L), Pectoral spine length of right side fin (PECSL-R), Dorsal fin length (DFL), Pelvic fin length of left side fin (PELFL-L), Pelvic fin length of right side fin (PELFL-R), Anal fin length (AFL) and Caudal fin width (CFW)

Table 25(b): Phenotypic values and coefficient of variation (CV) of meristic attributes of size sub-group 1 (10.1-20.0cm SL) (N=8)

Phenotype	Minimum	Maximum	CV	Mode
PECFR-L	8.00	10.00	9.11	9.00
PECFR-R	9.00	9.00	0.00	9.00
PESES-L	0.00	1.00	44.19	1.00
PESES-R	0.00	1.00	49.40	1.00
PELFR-L	5.00	6.00	9.82	5.00a
PELFR-R	5.00	6.00	9.82	5.00a
DR	66.00	77.00	5.11	67.00
AFR	47.00	63.00	10.08	47.00a
CFR	17.00	20.00	5.78	19.00

a=Multiple modes

Pectoral fin rays count on left side (PECFR-L), Pectoral fin ray count on the right side (PECFR-R), Possession of anteriorly serrated spine on the left side (PESES-L), Possession of anteriorly serrated spine on the right side (PESES-R), Pelvic fin rays counts on left side (PELFR-L), Pelvic fin rays counts on right side (PELFR-R), Dorsal fin rays counts (DR), Anal fin rays counts (AFR) and Caudal fin rays counts (CFR)

Table 26(a): Phenotypic values (as % SL.) and coefficient of variation (CV) of morphometric attributes of size sub-group 2 (20.1-30.0 cm SL) (N=15)

Phenotype	Minimum	Maximum	Mean	SD	CV	Mode
HL	25.00	31.60	28.15	1.98	7.03	28.05
BD MAX	8.70	16.05	11.11	1.88	16.92	8.70a
BD MIN	4.82	9.62	6.69	1.36	20.33	6.88a
PECFL-L	7.23	13.79	11.46	1.78	15.53	7.23a
PECFL-R	8.59	12.88	11.24	1.50	13.35	8.59
PECSL-L	3.98	8.33	6.12	1.67	27.29	3.98a
PECSL-R	3.98	8.42	6.25	1.51	24.16	3.98a
DFL	58.71	64.71	61.51	1.99	3.24	63.41
PELFL-L	6.33	12.50	9.13	1.57	17.20	6.33a
PELFL-R	6.33	10.40	8.92	1.22	13.68	9.06
AFL	37.50	45.18	41.64	2.28	5.48	37.50a
CFW	9.33	16.40	13.65	1.83	13.41	9.33a

a= multiple modes

Head length (HL), Maximum body depth (BD-MAX), Minimum body depth (BD-MIN), Pectoral fin length of left side fin (PECFL-L), Pectoral fin length of right side fin(PECFL-R), Pectoral spine length of left side fin (PECSL-L), Pectoral spine length of right side fin (PECSL-R), Dorsal fin length (DFL), Pelvic fin length of left side fin (PELFL-L), Pelvic fin length of right side fin (PELFL-R), Anal fin length (AFL) and Caudal fin width (CFW)

Table 26(b): Phenotypic values and coefficient of variation (CV) of meristic attributes of sizes' sub-group 2 (20.1-30.0 cm SL) (N=15)

Phenotype	Minimum	Maximum	CV	Mode
PECFR-L	8.00	10.00	5.27	9.00
PECFR-R	8.00	10.00	7.18	9.00
PESES-L	0.00	1.00	66.20	1.00
PESES-R	0.00	1.00	57.14	1.00
PELFR-L	6.00	6.00	0.00	6.00
PELFR-R	6.00	7.00	4.28	6.00
DR	63.00	78.00	5.73	66.00a
AFR	45.00	56.00	6.57	51.00
CFR	17.00	20.00	4.39	19.00

a=Multiple modes

Pectoral fin rays count on left side (PECFR-L), Pectoral fin ray count on the right side (PECFR-R), Possession of anteriorly serrated spine on the left side (PESES-L), Possession of anteriorly serrated spine on the right side (PESES-R), Pelvic fin rays counts on left side (PELFR-L), Pelvic fin rays counts on right side (PELFR-R), Dorsal fin rays counts (DR), Anal fin rays counts (AFR) and Caudal fin rays counts (CFR)

Table 27: Extracted factors and matrix of multi-modal attributes in sizes sub-group 2

	Principal Components			
Phenotype	1	2	3	4
BD MAX	-0.208	**0.928**	0.043	-0.122
BD MIN	**0.525**	**0.697**	-0.438	-0.045
PECFL-L	**0.844**	0.277	0.186	-0.353
PECSL-L	**0.852**	-0.364	-0.155	0.182
PECSL-R	**0.912**	-0.072	-0.261	0.274
PELFL-L	**0.819**	0.273	0.303	-0.321
AFL	-0.354	**0.644**	**0.543**	0.221
CFW	0.196	**-0.532**	**0.728**	-0.311
DR*	0.457	0.170	**0.554**	**0.640**

***meristic attributes, a= multiple modes**

Head length (HL), Maximum body depth (BD-MAX), Minimum body depth (BD-MIN), Pectoral fin length of left side fin (PECFL-L), Pectoral fin length of right side fin(PECFL-R), Pectoral spine length of left side fin (PECSL-L), Pectoral spine length of right side fin (PECSL-R), Dorsal fin length (DFL), Pelvic fin length of left side fin (PELFL-L), Pelvic fin length of right side fin (PELFL-R), Anal fin length (AFL), Caudal fin width (CFW) and DR

Table 28(a): Phenotypic values (as % SL.) and coefficient of variation (CV) of morphometric attributes of size group 3 (30.1-40.0 cm SL) (N=8)

Phenotype	Minimum	Maximum	Mean	SD	CV	Mode
HL	26.33	33.33	28.10	2.39	8.51	26.82
BD MAX	6.95	14.57	10.47	2.80	26.74	6.95
BD MIN	3.97	9.54	6.00	1.85	30.83	3.97
PECFL-L	8.41	14.32	11.09	2.19	19.75	11.58
PECFL-R	8.72	14.72	11.26	2.12	18.83	11.25
PECSL-L	6.95	7.73	7.21	0.45	6.24	6.95
PECSL-R	2.50	7.73	6.20	2.47	39.84	7.28
DFL	60.55	79.75	66.45	6.74	10.14	63.56
PELFL-L	6.85	11.42	9.02	1.70	18.85	9.93
PELFL-R	6.94	11.42	9.06	1.69	18.65	9.93
AFL	40.81	58.33	45.05	6.01	13.34	43.71
CFW	12.15	15.74	13.70	1.14	8.32	13.91

a= multiple modes

Head length (HL), Maximum body depth (BD-MAX), Minimum body depth (BD-MIN), Pectoral fin length of left side fin (PECFL-L), Pectoral fin length of right side fin(PECFL-R), Pectoral spine length of left side fin (PECSL-L), Pectoral spine length of right side fin (PECSL-R), Dorsal fin length (DFL), Pelvic fin length of left side fin (PELFL-L), Pelvic fin length of right side fin (PELFL-R), Anal fin length (AFL) and Caudal fin width (CFW)

Table 28(b): Phenotypic values and coefficient of variation (CV) of meristic attributes of size group 3 (30.1-40.0 cm SL) (N=8)

Phenotype	Minimum	Maximum	CV	Mode
PECFR-L	7.00	10.00	10.94	8.00a
PECFR-R	7.00	10.00	10.66	9.00
PESES-L	0.00	1.00	39.77	1.00
PESES-R	0.00	1.00	39.77	1.00
PELFR-L	5.00	6.00	8.00	6.00
PELFR-R	5.00	6.00	5.95	6.00
DR	45.00	67.00	12.72	67.00
AFR	45.00	57.00	10.06	57.00
CFR	15.00	23.00	13.57	19.00

a=Multiple modes

Pectoral fin rays count on left side (PECFR-L), Pectoral fin ray count on the right side (PECFR-R), Possession of anteriorly serrated spine on the left side (PESES-L), Possession of anteriorly serrated spine on the right side (PESES-R), Pelvic fin rays counts on left side (PELFR-L), Pelvic fin rays counts on right side (PELFR-R), Dorsal fin rays counts (DR), Anal fin rays counts (AFR) and Caudal fin rays counts (CFR)

Table 29(a): Phenotypic values (as % SL.) and coefficient of variation (CV) of morphometric attributes of size group 4 (40.1-50.0 cm SL) (N=6)

Phenotype	Minimum	Maximum	Mean	SD	CV (%)	Mode
HL	27.00	32.76	28.77	2.08	7.23	28.53
BD MAX	6.11	14.87	10.87	3.50	32.20	14.87
BD MIN	3.18	7.57	6.06	1.77	29.21	7.31
PECFL-L	10.97	11.98	11.48	0.46	4.01	10.97
PECFL-R	9.75	12.21	10.74	1.24	11.55	9.75
PECSL-L	6.10	10.80	7.45	1.96	26.31	6.10
PECSL-R	6.95	7.98	7.46	0.73	9.79	6.95a
DFL	59.22	69.68	63.05	3.57	5.66	61.71
PELFL-L	8.07	10.74	9.49	0.94	9.91	9.51
PELFL-R	9.39	10.74	9.89	0.49	4.95	9.76
AFL	40.98	44.63	42.34	1.49	3.52	40.98
CFW	13.38	14.91	14.29	0.65	4.55	13.39a

a=Multiple modes

Head length (HL), Maximum body depth (BD-MAX), Minimum body depth (BD-MIN), Pectoral fin length of left side fin (PECFL-L), Pectoral fin length of right side fin(PECFL-R), Pectoral spine length of left side fin (PECSL-L), Pectoral spine length of right side fin (PECSL-R), Dorsal fin length (DFL), Pelvic fin length of left side fin (PELFL-L), Pelvic fin length of right side fin (PELFL-R), Anal fin length (AFL) and Caudal fin width (CFW)

Table 29(b): Phenotypic values (as % SL.) and coefficient of variation (CV) of meristic attributes of size group 4 (40.1-50.0 cm SL) (N=6)

Phenotype	Minimum	Maximum	CV (%)	Mode
PECFR-L	8.00	10.00	7.00	9.00
PECFR-R	8.00	10.00	7.00	9.00
PESES-L	0.00	1.00	75.76	0.00
PESES-R	0.00	1.00	85.00	0.00
PELFR-L	5.00	7.00	10.50	6.00
PELFR-R	6.00	6.00	0.00	6.00
DR	69.00	73.00	2.49	69.00
AFR	49.00	65.00	10.41	56.00
I (CFR)	16.00	19.00	6.44	19.00

a=Multiple modes

Pectoral fin rays count on left side (PECFR-L), Pectoral fin ray count on the right side (PECFR-R), Possession of anteriorly serrated spine on the left side (PESES-L), Possession of anteriorly serrated spine on the right side (PESES-R), Pelvic fin rays counts on left side (PELFR-L), Pelvic fin rays counts on right side (PELFR-R), Dorsal fin rays counts (DR), Anal fin rays counts (AFR) and Caudal fin rays counts (CFR)

Table 30a: Probability of heterogeneity in mean phenotype values of morphometric attributes the studied size differentiated populations of *C. gariepinus.*

Phenotype	10.1-20.0	20.1-30.0	30.1-40.0	40.1-50.0	p-same
HL	29.36±2.43	28.15± 1.98	28.10 ±2.39	28.77± 2.08	0.540
BD MAX	11.15±1.52	11.11±1.88	10.47 ±2.80	10.87± 3.50	0.939
BD MIN	5.77±0.62	6.69±1.36	6.00± 1.85	6.06± 1.77	0.388
PECFL-L	11.36±1.27	11.46±1.78	11.09± 2.19	11.48± 0.46	0.727
PECFL-R	11.30±1.56	11.24±1.50	11.26 ±2.12	10.74± 1.24	0.884
PECSL-L	6.21±1.52	6.12±1.67	7.21± 0.45	7.45± 1.96	0.530
PECSL-R	7.53±0.78	6.25±1.51	6.20± 2.47	7.46± 0.73	0.509
DFL	61.64±2.26	61.51±1.99	66.45 ±6.74	63.05± 3.5	0.709
PELFL-L	9.22±0.82	9.13±1.57	9.02 ± 1.70	9.49± 0.94	0.798
PELFL-R	9.09±0.71	8.92±1.22	9.06 ± 1.69	9.89± 0.49	0.354
AFL	41.64 ±1.47	41.64± 2.28	45.05± 6.01	42.34± 1.49	0.294
CFW	15.25±1.17	13.65±1.83	13.70 ± 1.14b	14.29± 0.65	0.076

***Significant at (p<0.05)**

Head length (HL), Maximum body depth (BD-MAX), Minimum body depth (BD-MIN), Pectoral fin length of left side fin (PECFL-L), Pectoral fin length of right side fin(PECFL-R), Pectoral spine length of left side fin (PECSL-L), Pectoral spine length of right side fin (PECSL-R), Dorsal fin length (DFL), Pelvic fin length of left side fin (PELFL-L), Pelvic fin length of right side fin (PELFL-R), Anal fin length (AFL) and Caudal fin width (CFW)

Table 30(b): Probability of heterogeneity in mean phenotype values of meristic attribute of the studied size differentiated populations of *C. gariepinus.*

Phenotype	10.1-20.0	20.1-30.0	30.1-40.0	40.1-50.0	p-same
PECFR-L	9.00±0.82	9.00 ±0.63	8.50 ±0.93	8.92± 0.47	0.621
PECFR-R	9.00±0.00	9.00± 0.63	8.63± 0.92	8.92± 0.64	0.842
PESES-L	0.86±0.38 `	0.33± 0.25	0.88± 0.35	0.71± 0.47	0.313
PESES-R	0.83±0.41	0.77± 0.17	0.88 ± 0.35	0.77± 0.44	0.129
PELFR-L	5.50±0.54	6.00± 0.63	5.75 ± 0.46	6.00± 0.00	0.253
PELFR-R	5.50± 0.54	6.00± 0.00	5.88± 0.35	6.07± 0.26	0.190
DR	**68.88±3.52a**	**70.33±1.75c**	**62.57 ± 7.96b**	**69.93± 4.01abc**	**0.008***
AFR	51.38±5.18	54.83± 5.71	52.50 ±5.28	50.87± 3.34	0.431
CFR	18.50±1.07	18.17± 1.17	18.50 ± 2.51	18.50 ± 2.51	0.915

***Significant at (p<0.05)**

Pectoral fin rays count on left side (PECFR-L), Pectoral fin ray count on the right side (PECFR-R), Possession of anteriorly serrated spine on the left side (PESES-L), Possession of anteriorly serrated spine on the right side (PESES-R), Pelvic fin rays counts on left side (PELFR-L), Pelvic fin rays counts on right side (PELFR-R), Dorsal fin rays counts (DR), Anal fin rays counts (AFR) and Caudal fin rays counts (CFR)

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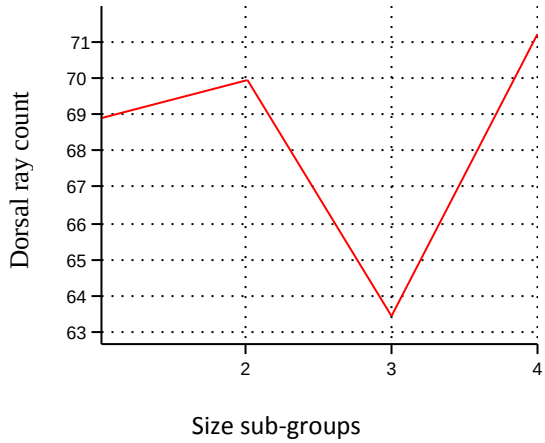


Figure 8: The relationship in mean values of dorsal ray counts (DR) in the size sub-groups

Subgroup 1= 10.1 - 20.0 cm standard length

Subgroup 2= 20.1 - 30.0 cm standard length

Subgroup 3= 30.1 - 40.0 cm standard length

Subgroup 4= 40.1 - 50.0 cm standard length

4.4.1.3 Phenotypic structure of pectoral spine variants sub-groups

Results on phenotypic structure, most varied attributes, extracted latent factors and assessment of significantly different phenotypes in subgroups of pectoral spine variants are presented in this sub-section. .

Table 31 shows the phenotypic value and variability of morphometric and meristic attributes of smooth pectoral spine individuals (S peses subgroup) in *C. gariepinus* population in Asejire Lake. Coefficient of variation ranged between 4.90 and 38.06 % in anal fin length (AFL) and pectoral spine length on left side (PECSL-L), respectively, in morphometric attributes, with 66.67 % of attributes being heterogeneous (Table 31a). All morphometric attributes were mono-modal, while the widest difference between values in paired fin attributes occurred in pectoral spine length (PECSL).

Variability among meristic attributes (Table 31b) was between 3.83% in pectoral fin ray count of right side to 12.35 % in pelvic fin ray count of left side ((PECFR-R and PELFR-L, respectively). With respect to coefficient of variation, PELFR-L was the only heterogeneous meristic attribute, while only AFR had multiple modes. The widest difference between values in paired fin attributes occurred in PELFR.

The morphometric and meristic attributes and their variation in partially serrated anterior portion of pectoral spine individuals (P peses subgroup) are presented in Table 32. The coefficient of variation in morphometric traits (Table 32a) was between 5.20 - 43.91 % (HL and PECSL-L, respectively). The difference between values on two sides of the paired fins was widest in PECSL, while multiple modes existed in all morphometric traits.

The coefficients of variation in meristic attributes (Table 32b) were between 0.00 (PECFR-L, PELFR-L and PELFR-R) and 10.97 % (PECFR-R). The difference between values on the two sides in the paired fins was widest in PECFR among meristic traits, while DR and AFR had multiple modes among meristic attributes. Factor analysis revealed that all the multiple mode attributes were on the same component.

Results on phenotypic variability in completely serrated pectoral spine individuals (C peses) of *C. gariepinus* population is presented in Table 33. The coefficient of variation values ranged between 5.59 (DL) and 27.09 % (PECSL-R) among morphometric traits (Table 33a). PECSL-L had the closest to the highest value (24.43 %). The values between left and right sides in paired fins values were similar in all

morphometric traits. However, the widest gap was observed in PECSL. All morphometric attributes had multiple modes.

The meristic attributes' variation values (Table 33b) ranged between 7.07 (PELFR-R) and 10.44 % (AFR). Values of paired fins were also similar in all meristic attributes. However, it was widest in PECFR. All meristic attributes had single modes.

Table 34 captures the result of statistical analysis of differences in mean values of attributes from the sub-populations. Morphometric attributes (Table 34a) had mean values ranging from 38.73±3.11 to 43.47±3.84 % of standard length. Significant difference existed between the groups at a morphometric site - AFL. The phenotypic values of AFL in the sub-groups followed the pattern C>S>P, indicating that completely serrated individuals (C) had highest, while the partially serrated (P) had the least; thus C had greater value than S. The meristic attributes were not different at $p<0.05$ (Table 34b). The dendrogram obtained from Euclidean similarity matrix of the subgroups values (Figure 9) revealed P as intermediate between S and C.

Table 31(a): Phenotypic values (as % SL.) and coefficient of variation (CV) of morphometric attributes of S-PESES (Anteriorly Smooth Pectoral Spine) Individuals in *C. gariepinus* Population of Asejire Lake (N=9)

Phenotype	Minimum	Maximum	Mean	SD	CV	Mode
HL	26.47	32.76	29.01	2.46	8.48	27.00
BD MAX	6.11	14.87	10.70	2.72	25.42	8.92
BD MIN	3.18	7.31	5.56	1.36	24.46	4.69
PECFL-L	8.41	13.79	11.13	1.52	13.66	11.27
PECFL-R	8.72	11.97	10.53	1.21	11.49	11.97
PECSL-L	3.99	10.80	7.83	2.98	38.06	10.80
PECSL-R	5.80	7.98	7.44	1.09	14.65	7.98
DFL	61.70	79.75	64.97	6.04	9.30	63.85
PELFL-L	6.85	12.50	9.19	1.65	17.95	8.92
PELFL-R	7.17	10.34	9.21	0.92	9.99	9.39
AFL	37.50	43.66	41.45	2.03	4.90	43.66
CFW	11.96	17.02	13.79	1.74	12.62	13.38

Head length (HL), Maximum body depth (BD-MAX), Minimum body depth (BD-MIN), Pectoral fin length of left side fin (PECFL-L), Pectoral fin length of right side fin(PECFL-R), Pectoral spine length of left side fin (PECSL-L), Pectoral spine length of right side fin (PECSL-R), Dorsal fin length (DFL), Pelvic fin length of left side fin (PELFL-L), Pelvic fin length of right side fin (PELFL-R), Anal fin length (AFL) and Caudal fin width (CFW)

Table 31(b): Phenotypic values (as % SL.) and coefficient of variation (CV) of meristic attributes of S-PESES (Anteriorly Smooth Pectoral Spine) Individuals in *C. gariepinus* Population of Asejire Lake (N=9)

Phenotype	Minimum	Maximum	CV	Mode
PECFR-L	8.00	10.00	5.89	9.00
PECFR-R	9.00	10.00	3.83	9.00
PELFR-L	5.00	7.00	12.35	6.00
PELFR-R	5.00	6.00	8.00	6.00
DR	63.00	74.00	5.43	69.00
AFR	45.00	57.00	7.61	49.00a
CFR	17.00	20.00	5.55	19.00

a=Multiple modes

Pectoral fin rays count on left side (PECFR-L), Pectoral fin ray count on the right side (PECFR-R), Pelvic fin rays counts on left side (PELFR-L), Pelvic fin rays counts on right side (PELFR-R), Dorsal fin rays counts (DR), Anal fin rays counts (AFR) and Caudal fin rays counts (CFR)

***PESES were removed from analysis being the subject of this grouping.**

Table 32(a): Phenotypic values (as % SL.) and coefficient of variation (CV) of morphometric attributes of P-PESES (Partially Serrated Pectoral Spine) sub-groups of *C. gariepinus* population of Asejire Lake (N=6)

Phenotype	Minimum	Maximum	Mean	SD	CV	Mode
HL	28.05	31.33	29.21	1.52	5.20	28.05a
BD MAX	8.75	13.10	10.41	2.03	19.50	8.75a
BD MIN	5.42	9.62	6.77	1.92	28.36	5.42a
PECFL-L	8.14	12.11	10.28	2.16	21.01	8.14a
PECFL-R	8.59	12.37	10.58	1.89	17.86	8.59a
PECSL-L	2.28	8.08	5.58	2.45	43.91	2.28a
PECSL-R	59.73	76.92	65.13	8.09	12.42	59.73a
DFL	59.73	76.92	65.13	8.09	12.42	59.73a
PELFL-L	6.79	9.97	8.53	1.31	15.36	6.79a
PELFL-R	7.24	9.97	8.21	1.22	14.86	7.24a
AFL	34.47	41.18	38.73	3.11	8.03	34.47a
CFW	10.54	14.81	13.09	2.09	15.97	10.54a

a= Multiple modes

Head length (HL), Maximum body depth (BD-MAX), Minimum body depth (BD-MIN), Pectoral fin length of left side fin (PECFL-L), Pectoral fin length of right side fin(PECFL-R), Pectoral spine length of left side fin (PECSL-L), Pectoral spine length of right side fin (PECSL-R), Dorsal fin length (DFL), Pelvic fin length of left side fin (PELFL-L), Pelvic fin length of right side fin (PELFL-R), Anal fin length (AFL) and Caudal fin width (CFW)

Table 32(b): Phenotypic values (as % SL.) and coefficient of variation (CV) of meristic attributes of P-PESES (Partially Serrated Pectoral Spine) sub-groups of *C. gariepinus* population of Asejire Lake (N=6)

Phenotype	Minimum	Maximum	CV	Mode
PECFR-L	9.00	9.00	0.00	9.00
PECFR-R	8.00	10.00	10.97	8.00
PELFR-L	6.00	6.00	0.00	6.00
PELFR-R	6.00	6.00	0.00	6.00
DR	66.00	73.00	4.47	66.00a
AFR	45.00	52.00	6.29	45.00a
CFR	18.00	20.00	5.12	18.00

a= Multiple modes

Pectoral fin rays count on left side (PECFR-L), Pectoral fin ray count on the right side (PECFR-R), Pelvic fin rays counts on left side (PELFR-L), Pelvic fin rays counts on right side (PELFR-R), Dorsal fin rays counts (DR), Anal fin rays counts (AFR) and Caudal fin rays counts (CFR)

***PESES were removed from analysis, being the subject of this grouping.**

Table 33(a): Phenotypic values (as % SL.) and coefficient of variation (CV) of morphometric attributes of C PESES (Completely Serrated Pectoral Spine) individuals of *C. gariepinus* population in Asejire Lake (N=22)

Phenotype	Minimum	Maximum	Mean	SD	CV	Mode
HL	25.33	33.33	28.79	2.25	7.82	25.33a
BD MAX	6.95	16.05	11.34	2.08	18.34	6.95a
BD MIN	3.97	9.54	6.46	1.33	20.59	3.97a
PECFL-L	7.23	14.32	11.43	1.72	15.05	7.23a
PECFL-R	8.59	14.72	11.65	1.64	14.08	8.59a
PECSL-L	3.87	7.73	6.10	1.49	24.43	3.87a
PECSL-R	2.50	7.98	6.35	1.72	27.09	2.50a
DFL	57.46	69.68	62.65	3.50	5.59	57.46a
PELFL-L	6.33	11.42	9.11	1.25	13.72	6.33a
PELFL-R	6.33	11.42	9.12	1.31	14.36	6.33a
AFL	40.43	58.33	43.47	3.84	8.83	40.43a
CFW	9.33	17.02	14.08	1.75	12.43	9.33a

a= Multiple modes

Head length (HL), Maximum body depth (BD-MAX), Minimum body depth (BD-MIN), Pectoral fin length of left side fin (PECFL-L), Pectoral fin length of right side fin(PECFL-R), Pectoral spine length of left side fin (PECSL-L), Pectoral spine length of right side fin (PECSL-R), Dorsal fin length (DFL), Pelvic fin length of left side fin (PELFL-L), Pelvic fin length of right side fin (PELFL-R), Anal fin length (AFL) and Caudal fin width (CFW)

Table 33(b): Phenotypic values (as % SL.) and coefficient of variation (CV) of meristic attributes of C PESES (Completely Serrated Pectoral Spine) individuals of *C. gariepinus* population in Asejire Lake (N=22)

Phenotype	Minimum	Maximum	CV	Mode
PECFR-L	7.00	10.00	9.67	9.00
PECFR-R	7.00	10.00	8.23	9.00
PELFR-L	5.00	6.00	7.07	6.00
PELFR-R	5.00	7.00	7.63	6.00
DR	45.00	78.00	9.91	67.00
AFR	45.00	65.00	10.44	51.00
CFR	15.00	23.00	8.14	19.00

a= Multiple modes

Pectoral fin rays count on left side (PECFR-L), Pectoral fin ray count on the right side (PECFR-R), Pelvic fin rays counts on left side (PELFR-L), Pelvic fin rays counts on right side (PELFR-R), Dorsal fin rays counts (DR), Anal fin rays counts (AFR) and Caudal fin rays counts (CFR)

***PESES were removed from analysis, being the subject of this grouping.**

Table 34(a): Analysis of significant differences in phenotypic values of morphometric attributes of S, P and C pectoral spine variant sub-groups

Phenotypes	Smooth	Partial	Complete	p-value
HL	29.01 ±2.46	29.21±1.52	28.79±2.25	0.7886
BD MAX	10.70±2.72	10.41±2.03	11.34±2.08	0.6228
BD MIN	5.56±1.36	6.77±1.92	6.46±1.33	0.2698
PECFL-L	11.13±1.52	10.28±2.16	11.43±1.0	0.5584
PECFL-R	10.53±1.21	10.58±1.89	11.65±1.64	0.0806
PECSL-L	7.83±2.98	5.58 ±2.45	6.10±1.49	0.4556
PECSL-R	7.44±1.09	65.13±8.09	6.35 ±1.72	0.9717
DFL	64.97±6.04	65.13±8.09	62.65±3.50	0.502
PELFL-L	9.19±1.65	8.53±1.31	9.11±1.25	0.066
PELFL-R	9.21±0.92	8.21±1.22	9.12±1.31	0.4296
AFL	**41.45±2.03^{ab}**	**38.73±3.11^{a}**	**43.47±3.84^{b}**	**0.01563***
CFW	13.79±1.74	13.09±2.09	14.08±1.75	0.5708

***Mean with different superscript along the rows are significantly different (P<0.05)**
Head length (HL), Maximum body depth (BD-MAX), Minimum body depth (BD-MIN), Pectoral fin length of left side fin (PECFL-L), Pectoral fin length of right side fin(PECFL-R), Pectoral spine length of left side fin (PECSL-L), Pectoral spine length of right side fin (PECSL-R), Dorsal fin length (DFL), Pelvic fin length of left side fin (PELFL-L), Pelvic fin length of right side fin (PELFL-R), Anal fin length (AFL) and Caudal fin width (CFW)

Table 34(b): Analysis of significant differences in phenotypic values of meristic attributes of S, P and C pectoral spine variant sub-groups

Phenotypes	Smooth	Partial	Complete	p-value
PECFR-L	9.00±0.53	9.00±0.00	8.79±0.85	0.7883
PECFR-R	9.13±0.35	8.75±0.96	8.75±0.72	0.05716
PELFR-L	5.75±0.71	6.00±0.00	5.80±0.41	0.7583
PELFR-R	5.75±0.46	6.00±0.00	5.90±0.45	0.7675
DR	68.75±3.73	69.50±3.11	68.11±6.75	0.9653
AFR	51.63±3.93	49.25±3.10	52.22±5.45	0.5949
CFR	18.75±1.04	18.75±0.96	18.55±1.57	0.889

***Mean with different superscript along the rows are significantly different (P<0.05).**

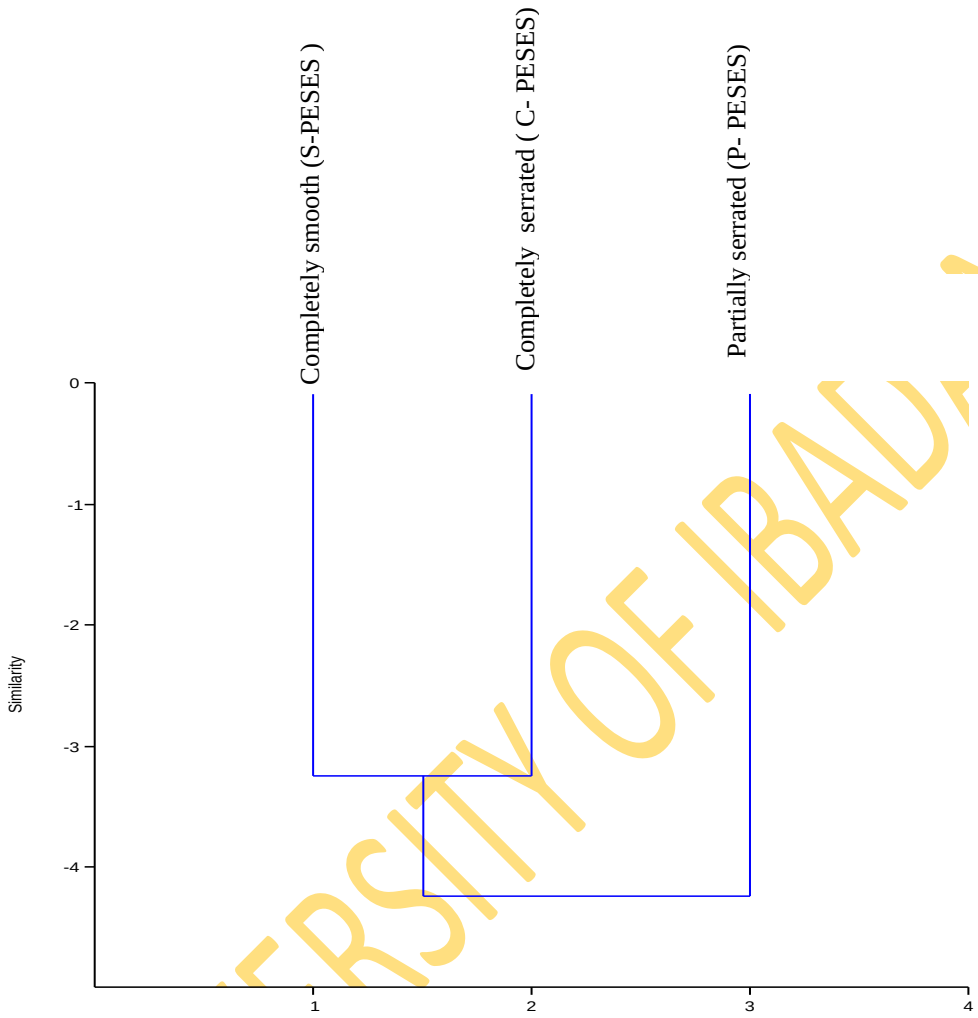


Figure 9: The similarity matrix of Anal Fin Length (AFL) in pectoral spine variant sub-groups (S, P and C) of *C.gariepinus*

S= Possession of completely smooth anterior portion of pectoral spine; P= possession of smooth anterior portion of pectoral spine at one of the two spines; C= Possession of anteriorly serration on the two pectoral spines

4.4.2 Analysis for canonically discriminant factors

Table 35 shows the summary of the morphometric and meristic phenotypes values and the attributes of significant differences among the studied sub-groups. With sex ratio of 3 males: 7 females, the population was sexually biased towards female. Phenotypes of the sexes were not significantly differentiated ($p>0.05$). However, minimum body width (BDMIN) was close to significance, having *p-value* of 0.051. Size groups were significantly differentiated at only one morphometric (CFW) and one meristic site (DR) at $p<0.05$. The values followed the pattern - group 1> 4> 3> 2 (did not follow pattern of size increment). Similarly, pattern of values of dorsal ray counts (DR) in groups was 2> 4> 1> 3; the highest value was obtained in group 2; the least occurred in group 3 (did not follow pattern of size increment); while comparison test showed significant difference ($p<0.05$) between groups 1, 2 and 3 at DR. The table also reveals significant difference ($p<0.05$) between the PESES groups at morphometric trait AFL (anal fin length), following the pattern C>S>P.

The canonical classification function of the size sub-group (Table 36) showed that 46.3% individuals of the original grouped cases were correctly classified. Plot of size groups and their territorial maps are presented (see Appendix 8). The plot showed separation of subgroups samples as the groups centroids were located apart.

Canonical classification function revealed that 50.8% individuals in the *a priori* group were correctly classified (Table 37) when possession of anteriorly position serration of pectoral spines (PESES) subgroups was analyzed without correction for size effect in data. Plots of the functions variables and the territorial map are presented (see Appendix 8). The plot showed significant separation of samples with group centroids located apart.

After correction for allometry (size / stage of life) effect in data, canonical classification test revealed 93.8 % classification success in the pectoral spine sub-groups (Table 38). The group's centroids were separated on territorial map and plots of their centroids on the extracted canonical functions (see Appendix 8).

Table 35: Summary of morphometric (as % SL., mean ± SD), meristic characteristics and the differentiating sites for the sub-groups of *Clarias gariepinus* population in Asejire dam

	Sex Groups		Size Groups				Pectoral Spine Groups		
Character	Male	Female	1	2	3	4	S	P	C
	(N=11)	(N=26)	(N=8)	(N=15)	(N=8)	(N=6)	(N=9)	(N=6)	(N=22)
Morphometric									
HL	27.18±1.30	29.06±2.35	29.36±2.43	28.15±1.98	28.10 ±2.39	28.77± 2.08	29.01±2.46	29.21±1.52	8.79±2.25
BD MAX	11.18±1.68	10.85±2.30	11.15±1.52	11.11±1.88	10.47±2.80	10.87± 3.50	10.70± 2.72	10.41±2.03	11.34±2.08
BDMIN	6.90±1.51	5.93±1.26[b]	5.77±0.62	6.69±1.36	6.00±1.85	6.06±1.77	5.56±1.36	6.77±1.92	6.46±1.33
PECFL-L	11.73±1.90	11.11±1.52	11.36±1.27	11.46±1.78	11.09±2.19	11.48± 0.46	11.13±1.52	10.28±2.16	11.43±1.00
PECFL-R	11.57±1.72	11.11±1.57	11.30±1.56	11.24±1.50	11.26±2.12	10.74±1.24	10.53±1.21	10.58±1.89	11.65±1.64
PECSL-L	6.90±0.84	6.39±2.50	6.21±1.52	6.12±1.67	7.21± 0.45	7.45±1.96	7.83±2.98	5.58±2.45	6.10±1.49
PECSL-R	7.11±1.31	6.44±1.76	7.53±0.78	6.25±1.51	6.20±2.47	7.46±0.73	7.44±1.09	65.13±8.09	6.35±1.72
DFL	61.52±2.57	63.92±5.17	61.64±2.26	61.51±1.99	66.45±6.74	63.05±3.50	64.97±6.04	65.13±8.09	62.65±3.50
PELFL-L	8.81±1.19	9.33±1.39	9.22±0.82	9.13±1.57	9.02±1.70	9.49±0.90	9.19±1.65	8.53±1.31	9.11±1.25
PELFL-R	8.85±1.11	9.26±1.20	9.09±0.71	8.92±1.22	9.06 ±1.69	9.89±0.49	9.21±0.92	8.21±1.22	9.12±1.31
AFL	41.55±1.81	42.54±4.07	41.64 ±1.47	41.64±2.28	45.05±6.01	42.34±1.49	41.45±2.03a	38.73±3.11a	43.47±3.84b
CFW	13.63±1.79	14.14±1.62	15.25±1.17a	13.65±1.83b	13.70±1.14b	14.29± 0.65ab	13.79±1.74	13.09±2.09	14.08±1.75
Meristics									
PECFR-L	9.00±0.63	8.79±0.72	9.00±0.82	9.00±0.63	8.50±0.93	8.92±0.47	9.00±0.53	9.00±0.00	8.79±0.85
PECFR-R	9.00±0.82	8.78±0.60	9.00±0.00	9.00±0.63	8.63±0.92	8.92±0.64	9.13±0.35	8.75±0.96	8.75±0.72
PESES-L	0.82±0.41	0.67±0.48	0.86±0.38	0.33±0.25	0.88±0.35	0.71±0.47	nd	nd	nd
PESES-R	0.89±0.33	0.61±0.50	0.83±0.41	0.77±0.17	0.88±0.35	0.77±0.44	nd	nd	nd
PELFR-L	5.91±0.30	5.77±0.51	5.50±0.54	6.00±0.63	5.75±0.46	6.00±0.00	5.75±0.71	6.00±0.00	5.80±0.41
PELFR-R	6.00±0.00	5.81±0.49	5.50±0.54	6.00±0.00	5.88±0.35	6.07±0.26	5.75±0.46	6.00±0.00	5.90±0.45
DR	68.60±2.63	68.65±6.29	68.88±3.52a	70.33±1.75c	62.57±7.96b	69.93±4.01abc	68.75±3.73	69.50±3.11	68.11±6.7
AFR	50.80±2.30	51.64±5.28	51.38±5.18	54.83±5.71	52.50±5.28	50.87±3.34	51.63±3.93	49.25±3.10	2.22±5.45
CFR	18.64±1.86	18.38±1.17	18.50±1.07	18.17±1.17	18.50±2.51	18.50±2.5	18.75±1.04	18.75±0.96	18.55±1.57

*** indicate attribute possessing significantly different mean value ($p<0.05$) in a group; Different superscript along the same row under same grouping indicate significant difference ($p<0.05$) among subgroups. Sample size is given in brackets.. While nd indicates not used for analysis. S= Possession of completely smooth anterior portion of pectoral spine, P= possession of smooth anterior portion of pectoral spine at one of the two spines, C= Possession of anteriorly serration on the two pectoral spines. Head length (HL), Maximum body depth (BD-MAX), Minimum body depth (BD-MIN), Pectoral fin length of left side fin (PECFL-L), Pectoral fin length of right side fin(PECFL-R), Pectoral spine length of left side fin (PECSL-L), Pectoral spine length of right side fin (PECSL-R), Dorsal fin length (DFL), Pelvic fin length of left side fin (PELFL-L), Pelvic fin length of right side fin (PELFL-R), Anal fin length (AFL) and Caudal fin width (CFW); Pectoral fin rays count on left side (PECFR-L), Pectoral fin ray count on the right side (PECFR-R), Possession of anteriorly serrated spine on the left side (PESES-L), Possession of anteriorly serrated spine on the right side (PESES-R), Pelvic fin rays counts on left side (PELFR-L), Pelvic fin rays counts on right side (PELFR-R), Dorsal fin rays counts (DR), Anal fin rays counts (AFR) and Caudal fin rays counts (CFR)**

Table 36: Results of Canonical Classification Analysis of the Size Sub-groups in *C. gariepinus*

		Predicted group membership				
	Subgroups' score	0.00	1.00	2.00	3.00	Total
Original						
Count						
	0.00	7	6	3	0	16
	1.00	0	13	6	0	19
	2.00	4	9	11	2	26
	3.00	2	2	2	0	6
Ungrouped Cases		2	2	2	0	6
%						
	0.00	43.6	37.5	18.8	0	100
	1.00	0	68.4	31.6	0	100
	2.00	15.4	34.6	42.3	7.7	100
	3.00	33.3	33.3	33.3	0	100

***46.3% original group cases correctly classified**

***Score legend**

0.00= Subgroup 1 (10.10 - 20.00 cm standard length)

1.00= Subgroup 2 (20.10 - 30.00 cm standard length)

2.00= Subgroup 3 (30.10 - 40.00 cm standard length)

3.00= Subgroup 4 (40.10 - 50.00 cm standard length)

Table 37: Results of Canonical Classification Analysis of the Pectoral Spine sub-groups phenotypes of *C. gariepinus* before Correction for Size Effects

		Predicted group membership			
Subgroups' score		0.00	1.00	2.00	Total
Original Count					
	0.00	7	6	3	16
	1.00	0	13	6	19
	2.00	6	9	11	26
Ungrouped Cases		2	2	2	6
%					
	0.00	43.8	37.5	18.7	100.0
	1.00	0.0	68.4	31.6	100.0
	2.00	23.1	34.6	42.3	100.0

***50.8% original group cases correctly classified for the Allometry uncorrected sample**.

***Subgroups score legend**

0.00 =S= Possession of completely smooth anterior portion of pectoral spine;

1.00= P= possession of smooth anterior portion of pectoral spine at one of the two spines;

2.00= C= Possession of anteriorly serration on the two pectoral spines

Table 38: Results of Canonical Classification Analysis of Pectoral Spine sub-groups Phenotype data after Correction for Allometry Effect

		Predicted group membership			
Subgroups' score		0.00	1.00	2.00	Total
Original					
Count					
	0.00	4	0	0	4
	1.00	0	2	0	2
	2.00	1	0	9	10
%					
	0.00	100.0	0.0	0.0	100.0
	1.00	0.0	100.0	0.0	100.0
	2.00	10.0	0.0	90.0	100.0

***93.8% original group cases correctly classified for the Allometry corrected sample.**

Subgroups' score legend

0.00 =S= Possession of completely smooth anterior portion of pectoral spine;

1.00= P= possession of smooth anterior portion of pectoral spine at one of the two spines;

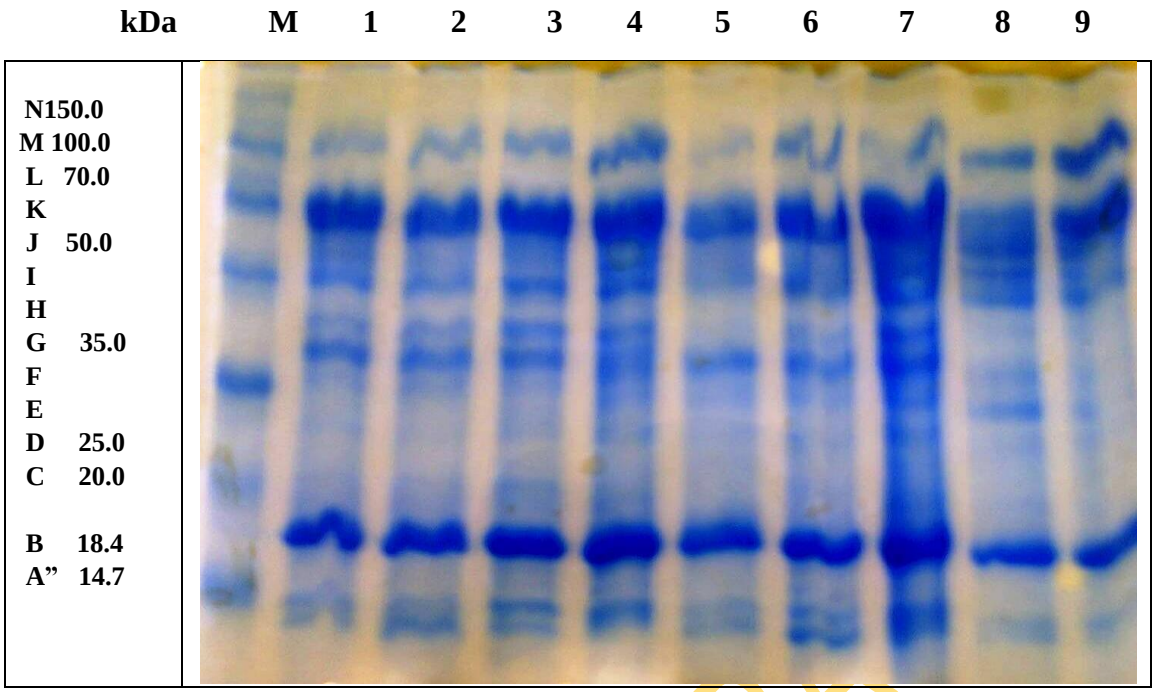
2.00= C= Possession of anteriorly serration on the two pectoral spines

4.5 Biochemical and genotypic structure of *C. gariepinus* population in Asejire Lake

The SDS PAGE electrophoresis profile of the populations is shown in Plates 18 and 19. Eighteen individuals were randomly selected from the population. Four individuals (13, 15, 17 and 18) were in the S sub-group, while the rest 14 were in C subgroup. Information on the subgroup of origin of the electrophoresed individuals are presented in Appendix 9. The profile revealed polymorphism of bands across groups. The banding profile revealed 14 bands of molecular weight range of <14.7 to 100KDa, obtained across all genotypes. Most of the bands were within 14.7 and 100 KDa except band A, with lower molecular weight (<14.7 KDa). Moreover, band A was distinctively inherited by 75% of the S pectoral spine group (individuals15, 17 and 18), while 100% of the C pectoral spine group individuals did not inherit the marker.

Band scores generated from the protein electrophoresed samples are presented in Appendix 10. Analysis of the band scores revealed that 66.67% of the 234 allelic sites had protein bands. A total of 78.57% of the bands were polymorphic (Table 39), while frequency of occurrence of each of the 14 bands was between the range of 0.17 - 1.00.

The dendrogram of the UPGMA (Unweighted Pair Group Method with Arithmetic mean) similarity matrix of the individuals is presented in Figure 10. At 0.63 coefficient of variation, 8 major clusters were identified. Relating the molecular characteristics with morphological sub-groups revealed that 75% of the S group members distinguished themselves by solely occupying the second cluster while, 100% of the other group separated. Moreover, canonical discriminant function, presented in Table 40, revealed that 100% of the originally grouped phenotypic cases were correctly classified.



Plates 18: Protein banding pattern of *C.gariepinus* population in Asejire Lake (Samples 1-9 belong to C subgroup – completely serrated anterior portion of pectoral spine)

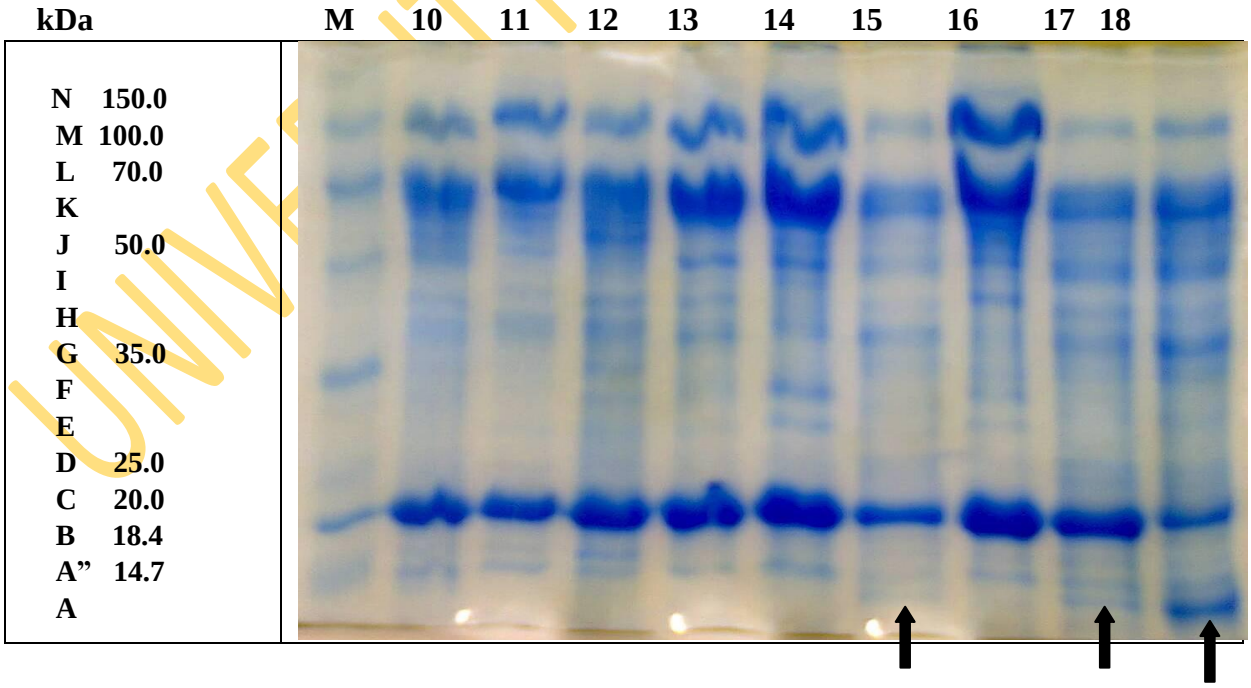


Plate 19: Protein banding pattern of *C. gariepinus* population in Asejire Lake (samples 10-18)

(13, 15, 17 and 18 were in the S subgroup while the rest 14 were in C subgroup)

Table 39: Distribution of identified 13 bands across the studied individuals (N=18)

Allelic bands	number of occurrence	Frequency
A	3	0.17
A”	15	0.83
B	15	0.83
C	10	0.56
D	18	1.00
E	9	0.5
F	12	0.67
G	12	0.67
H	10	0.56
I	8	0.44
J	16	0.89
K	8	0.44
L	18	1.00
M	18	1.00

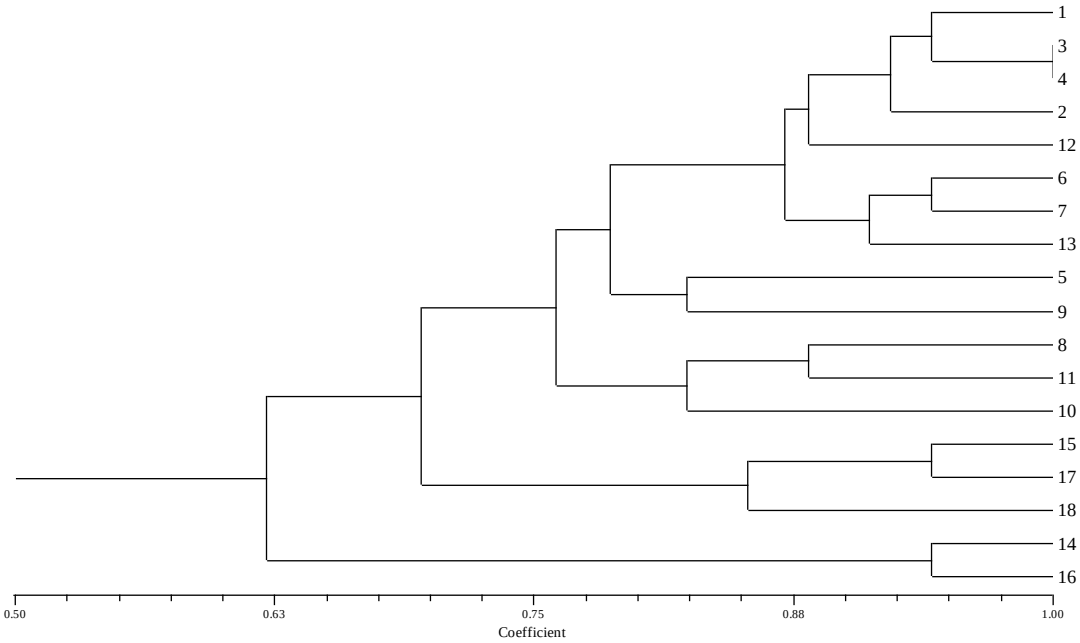


Figure 10: Similarity matrix of *C. gariepinus* samples genotypes after Sodium Dodecyl Sulphate Polyacrylamide Gel Electrophoresis using Unweighted Pair Group Method with Arithmetic mean (UPGMA)

Table 40: Results of classification analysis of genotypes of smooth and completely serrated pectoral spine (PESES) sub-groups in *C. gariepinus*

Score		Predicted Group Membership		Total
		.00	1.00	
Original Count	.00	4	.0	4
	1.00	0	14	14
%	0.00	100.0	0	100.0
	1.00	0	100.0	100.0

4.6 Genetic variability and inheritance of RAPD DNA markers

Information on subgroup of origin of the analyzed individuals is presented in Appendix 10. Attributes of the six selected RAPD Operon primers utilized in this study is presented in Table 41. The table shows that the primers were within 150 and 3500 base pairs. The obtained phenogram of the 6 primers are presented in Plates 20 - 25. The studied population contained 5 individuals of the non-peses group (13, 15, 17, 18 and 19), while the rest were in peses sub-group (Appendix 11). The gel profile of the studied sample showed that a unique allele was observed in OPAF-07 (Plate 25) and this was specific to individual 14 (a member of C group).

With respect to the studied population, characteristics of the selected primers are presented in Table 42. The table shows that RAPD primers were polymorphic and were able to detect private allele in the studied population. A total of 746 individual bands were obtained from a total of 63 detected loci, which gave 80.95% polymorphism. However, the highest number of amplified fragments (13) was produced by OPAF-07. The number of polymorphic bands per primer ranged between 7 (OPAE-04 and OPAE-05) and 11(OPAF-07). Polymorphic Information Content (PIC) ranged between 0.18 (OPAF-08) and 0.49 (OPAE-05).

Dendrogram constructed from the scored bands of the primers, presented in Figure 11 showed that they clustered into two groups with intra-and inter-group variations. Primers OPAD-09, OPAE-04 and OPAF-08 clustered and were differentiated from the rest of the three.

Table 43 showed information on occurrence of private allele by which the Pectoral Spine Sub-groups of *Clarias gariepinus* can be differentiated. Despite similar values of percentage polymorphic band, private alleles were encountered in both subgroups. However, bands were more polymorphic in the peses group than the non-peses (78 and 69.84 % PB, respectively). Specific homogeneous sites were obtained in 11 cases.

All individuals in both groups had allele j and k in OPAE-09. However, all loci were heterogeneous in OPAD-09 in the peses group, while 2 were homogenous in the non-peses group. Homogeneity of a particular allele in all members of a group could indicate its suitability as a marker for such group. OPAF-07 was differentially inherited by the two groups; it was uniformly inherited at one site (i) by all individuals in the peses group only. This makes it a potential differentiating site for the phena groups. Also, OPAD-09 showed no private allele in peses, indicating that the marker is not informative

for the category peses but had two (2) private alleles in the non-peses thus showing a sub-division or variant in this category.

The genetic analysis confirmed the morphological assignment of each of the *C. gariepinus* groups based on pectoral spine variation. It also highlighted subtle genetic intra-variability. The latter was able to give further information on genetic basis of morphologically divergence groups and show within-sub-group genetic variability pattern.

Dendrogram showing the cluster analysis of the individuals' genotype is presented in Figure 12. The UPGMA cluster diagram identified two major genotypic groups with inter-and intra-group relationships. It also confirmed genetic background for phenotypic separation of the population via pectoral spine; all individuals in the first cluster were from the peses group, while all the non-peses individuals were on the second cluster. However, all the groups had varied interrelationships, showing a highly heterogeneous population. Classification statistics (Table 44) revealed that the initial phenotypic grouping was 100% correct with the genotypic grouping obtained in this study (Appendix 12).

Table 41: Polymorphic RAPD operon primers in *C. gariepinus*: Code, sequence information and size ranges of the amplified products

S/N	Primer Code	Sequence	Size range (bp)
1	OPAD - 09	TCGCTTCTCC	200 - 3500
2	OPAE - 04	CCAGCACTTC	250 - 2500
3	OPAE - 05	CCTGTCAGTG	150 - 3000
4	OPAE - 09	TGCCACGAGG	200 - 3000
5	OPAF - 07	GGAAAGCGTC	250 - 3000
6	OPAF - 08	CTCTGCCTGA	150 – 3500

***bp= base pair**

M 1 2 3 4 5 6 7 8 9 10 1112 1314 1516 17 18 19 20

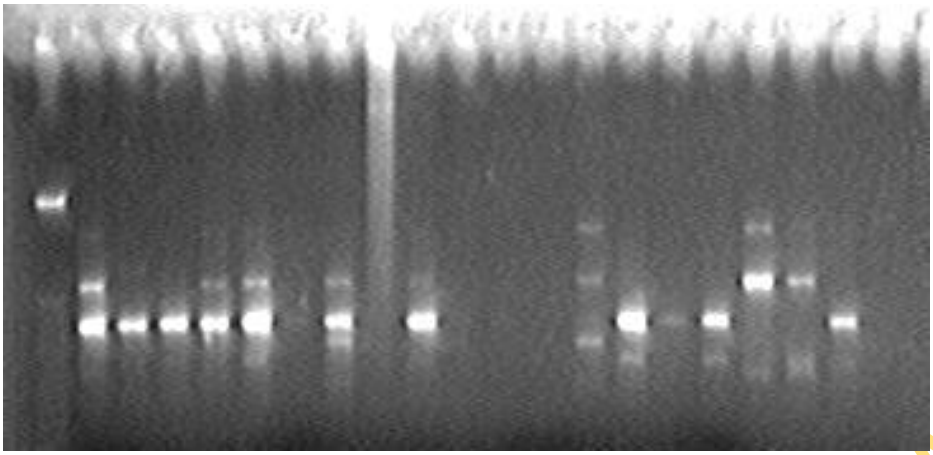


Plate 20: RAPD profiles of the *C. gariepinus* samples using OPAD – 09 (size = 200 - 3500 base pairs)

Samples 13, 15, 17, 18, 19 were smooth peses (S subgroup); samples 1-12, 14, 16, 20 were completely serrated (C subgroup)

M 1 2 3 4 5 6 7 8 9 10 1112 13 14 1516 1718 19 20

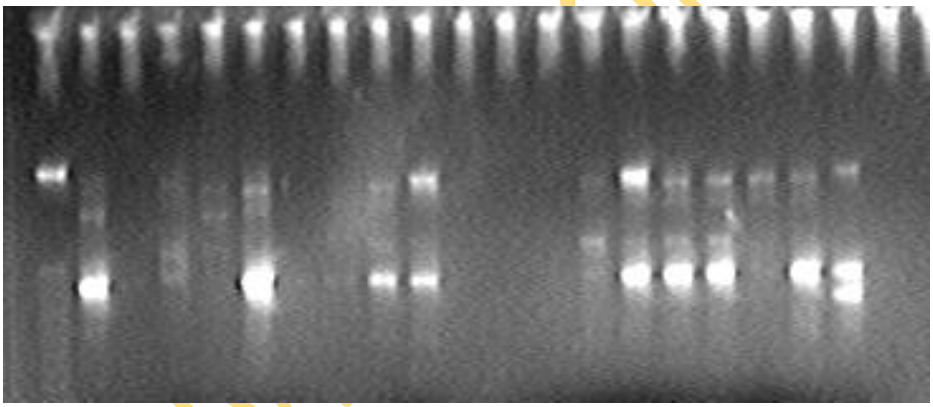


Plate 21: RAPD profiles of the *C. gariepinus* samples using OPAE 04 (size = 250 -2500 base pairs)

Samples 13, 15, 17, 18, 19 were smooth peses (S subgroup); samples 1-12, 14, 16, 20 were completely serrated (C subgroup)

M 1 2 3 4 5 6 7 8 9 10 1112 13 14 1516 1718 19 20

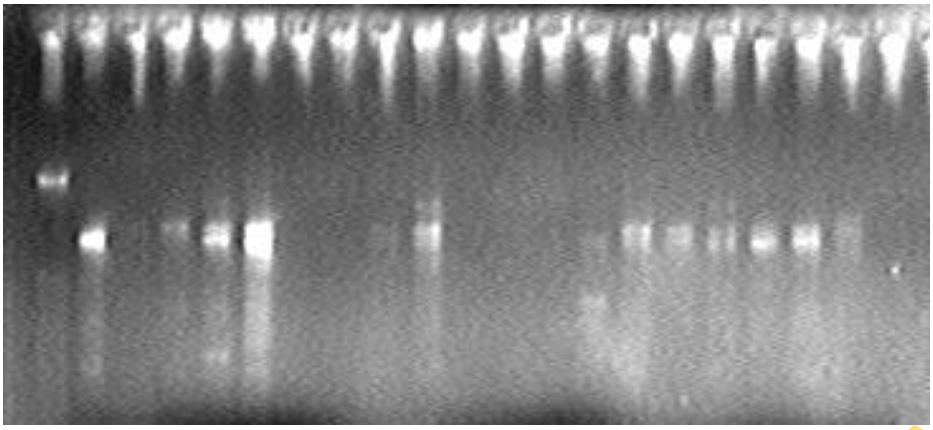


Plate 22: RAPD profiles of the *C. gariepinus* samples using OPAE- 09 (200 – 3000 base pairs)

Samples 13, 15, 17, 18, 19 were smooth peses (S subgroup); samples 1-12, 14, 16, 20 were completely serrated (C subgroup)

M 1 2 3 4 5 6 7 8 9 10 11 12 13 14 1516 1718 19 20

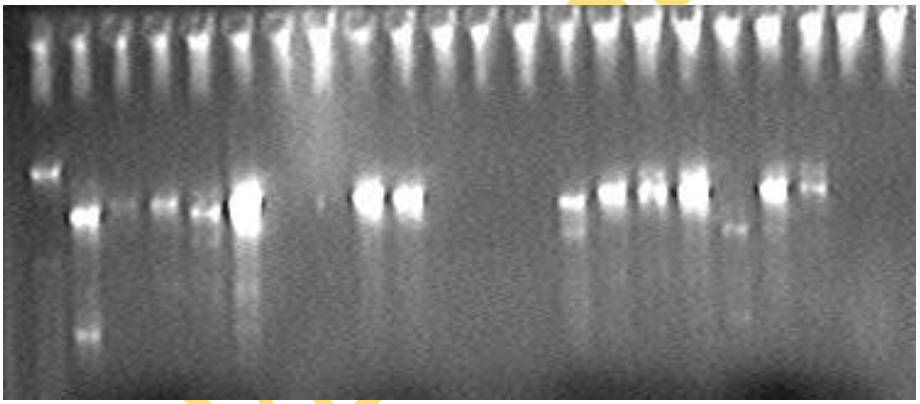


Plate 23: RAPD profiles of the *C. gariepinus* samples using OPAF -08 (150 -3500 base pairs)

Samples 13, 15, 17, 18, 19 were smooth peses (S subgroup); samples 1-12, 14, 16, 20 were completely serrated (C subgroup)

M 1 2 3 4 5 6 7 8 9 10 1112 1314 15 161718 19 20

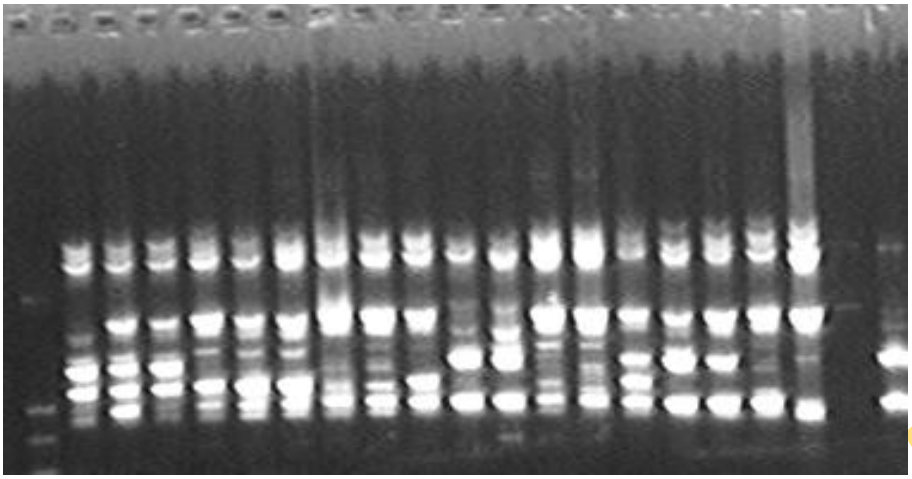


Plate 24: RAPD profiles of the *C. gariepinus* samples using OPAE-05 (150-3000 base pairs)
Samples 13, 15, 17, 18, 19 were smooth peses (S subgroup); samples 1-12, 14, 16, 20 were completely serrated (C subgroup)

M 1 2 3 4 5 6 7 8 9 10 11 1213 14 15 1617 18 19 20

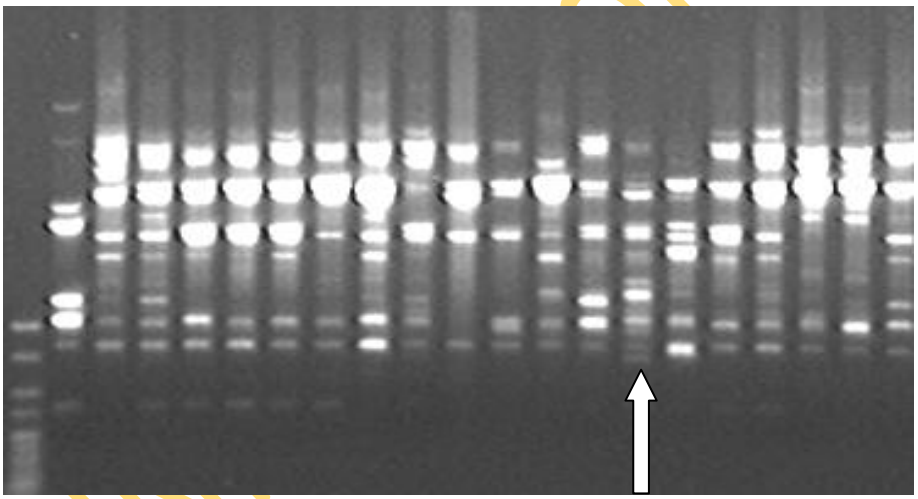


Plate 24: RAPD profiles of the *C. gariepinus* samples using OPAF -07 (250 – 3000 base pairs)
Samples 13, 15, 17, 18, 19 were smooth peses (S subgroup); samples 1-12, 14, 16, 20 were completely serrated (C subgroup)

- **Arrow indicates unique allele**

Table 42: Primer code, total number of band locus detected (NBL), number of polymorphic band (NPB), average polymorphic band (%PB), Polymorphic Information Content (PIC), Unique allele per primer, Total Number of Individual band per Primer (NIB) and Relative band frequency (BF) generated by the six RAPD primers

Primer Code	NBL	NPB	% PB	PIC	No. of unique alleles	NIB	BF
OPAD – 09	9	8	89.00	0.20	0	82	0.11
OPAE-04	9	7	77.78	0.3457	0	102	0.14
OPAE-09	11	9	81.82	0.2975	0	137	0.18
OPAF-08	10	9	90	0.18	0	104	0.14
OPAE-05	11	7	54.55	0.4959	0	137	0.18
OPAF-07	13	11	76.92	0.3551	1(14)	184	0.25
Total	63	51			1	746	

- NBL=number of band loci, NPB= number of polymorphic bands, % PB=percentage polymorphic band, PIC=polymorphic information content , NIB=Number of individual band,

Table 43: Occurrence of private allele and homogeneous sites by peses and non-peses pectoral spine sub-groups of *Clarias gariepinus* after RAPD primers analysis

	No. of homogeneous sites		
Primer Code	**peses**	**Non-peses**	**Differentiating allele**
OPAD–09	0	2 (b, i)	2(b, i)
OPAE-04	2(h, i)	4 (e, g, h, i)	2(e, g)
OPAE-09	2(j, k)	2 (j, k)	-
OPAF-08	1(j)	3(e, g, j)	2(e, g)
OPAE-05	6(c, d, g, h, I, j)	6(a, b, c, d, h, i)	4(a, b, g, i)
OPAF-07	3(c, d, i)	2(c, d)	1(j)
Total (MB)	14	19	11
%PB	78	69.84	

*MB= Monomorphic band, PB= Polymorphic band

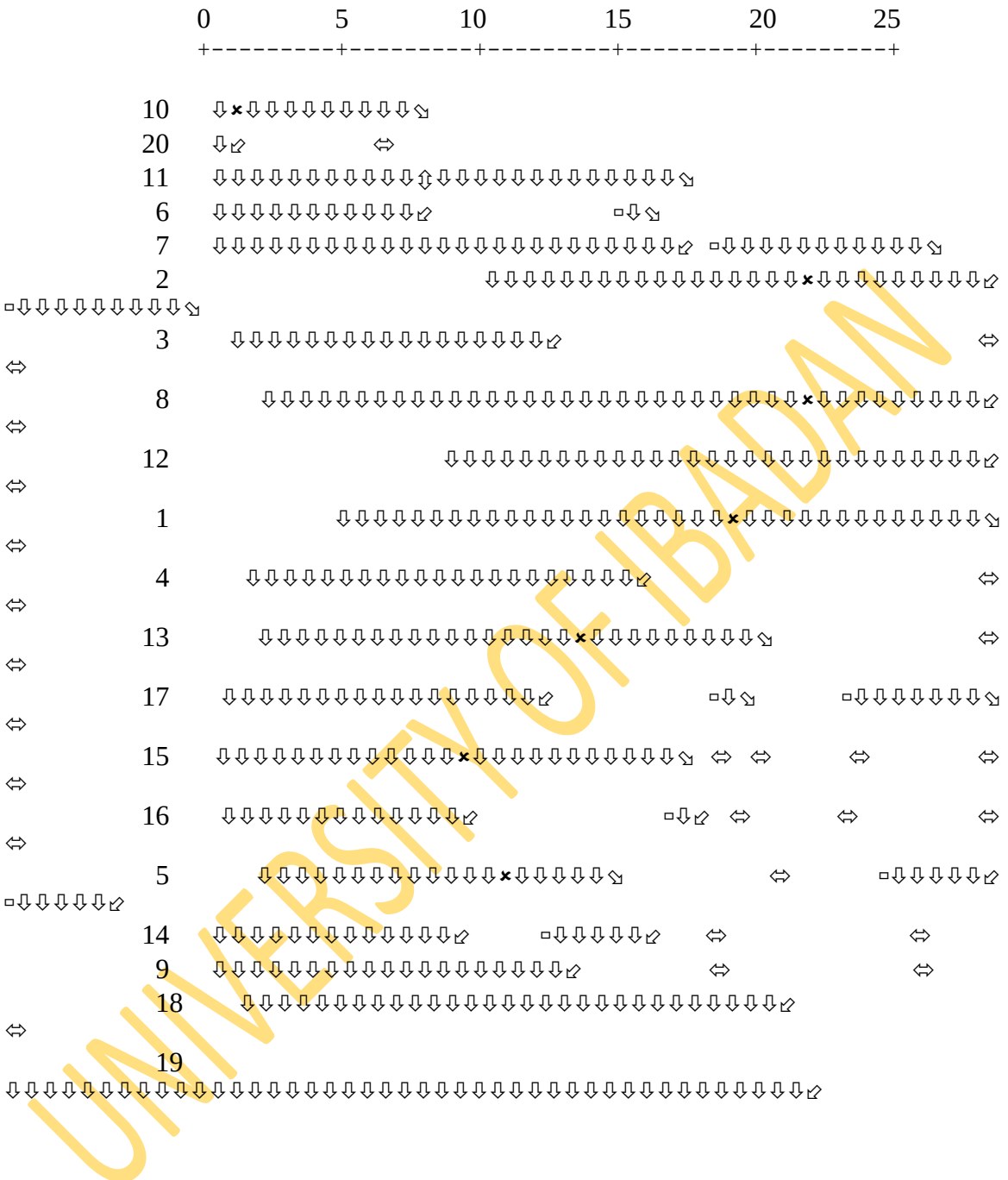


Figure 11: Dendrogram representing the inferred phylo-genetic relationship in *C. gariepinus* population based on RAPD analysis

- **Samples 13, 15, 17, 18, 19 were smooth peses (S subgroup);**
- **Samples 1-12, 14, 16, 20 were completely serrated (C subgroup)**

4.7 Inbreeding tendency and mean values of paired fins

Results of analysis of inbreeding tendency through assessment of bilateral asymmetry of paired phenotypes and the determination of mean values of the paired phenotypes of the studied population are presented in this section.

4.7.1 Paired fins analysis for inbreeding tendency in the population

Assessment of significant difference between phenotypes values of fins from the left and right sides of the studied *C. gariepinus* population revealed that bilateral asymmetry did not occur ($p>0.05$) in either pectoral spine variants or size sub-groups (Tables 44 and 45). *P-value* was not generated in PELFR count (partially serrated sub-group) in pectoral spine sub-groups, while p-value ranged from 0.1(completely serrated subgroups pectoral spine length) to 1.00 (completely serrated subgroups' pectoral fin ray count - PECFR and smooth peses subgroups' pelvic fin ray counts - PELFR). Moreover, p-value ranged from 0.26 (pectoral spine length - PECSL in size group 4) to 1.00 (pectoral spine length - PECFR in all size groups and pelvic fin ray count - PELFR in size groups 1 and 4).

4.7.2 Mean values of paired fins

Tables 46 and 47 show the descriptive values of pooled left and right sides attributes of the paired phenotypes of the population. The tables revealed the characteristic mean values of the paired phenotypes in the sub-populations when either pectoral spine sub-groups are separately considered and when considered in combination with size groupings.

As seen in Table 46, paired fins mean values in all the 3 studied morphometric attributes in PESES groups reflected heterogeneity (C.V. values <10%), with the greatest values obtained in pectoral spine length (PECSL); all sub-groups had similar values; however, S had the greatest, while the lowest was observed in C. The partially serrated subgroup was intermediate with respect to variation in pectoral spine length, while it had the greatest variation value in the other two attributes. In meristic attributes, pectoral fin ray count (PECFR) showed homogeneity in all sub-groups, but pelvic fin ray count (PELFR) was heterogeneous in all sub-groups and the values were similar.

All size groups in PELFR showed homogeneity (Table 47) thus indicating that the only heterogeneity observed in meristic attributes among PESES groups could be attributed to size effect (Allometry). Out of the 4 size groups in PECFR count, three (3) reflected homogeneity, while the fourth (4th) group had C.V. of 10.47 %. The

morphometric attributes values reflected that the pectoral fin attributes were the most varied. Heterogeneity was observed in 3 out of 4 size groups in PECSL and PECFL, while 2 out of 4 size groups in PELFL showed heterogeneity. The greatest and the lowest variation values were observed in PECSL, implying the attribute as the most varied.

Table 44: Probability of differences in mean phenotypic values (% SL) of paired fins of smooth (S), partial (P) and completely serrated (C) sub-groups of *Clarias gariepinus*

	Mean		
Attribute	**Left**	**Right**	***t-value***
Pectoral Fin Length (% SL)			
Smooth (7)	10.74±1.16	10.53±1.12	0.60
Partially serrated (3)	10.76±2.36	10.59±1.90	0.63
Completely serrated (20)	11.43±1.72	11.65 ±1.64	0.37
Pectoral Spine Length (% SL)			
Smooth (4)	8.26±3.26	7.44±1.09	0.54
Partially serrated (2)	6.76±1.87	6.70±2.43	0.91
Completely serrated (10)	6.15±1.56	6.66±1.34	0.1
Pelvic Fin Length (% SL)			
Smooth (8)	9.19±1.65	9.21±0.92	0.97
Partially serrated (4)	8.53±1.31	8.21±1.22	0.42
Completely serrated (20)	9.11±1.25	9.11±1.31	0.98
Pectoral Fin Ray Count			
Smooth (8)	9.00± 0.53	9.13±0.35	0.35
Partially serrated (4)	9.00± 0.00	8.75±0.96	0.64
Completely serrated (19)	8.79±0.85	8.79±0.71	1.00
Pelfic Fin Ray Count			
Smooth (8)	5.75±0.71	5.75±0.46	1.00
Partially serrated (4)	6.00±0.00	6.00±0.00	nd
Completely serrated (20)	5.80±0.41	5.90±0.45	0.16

***Significant differences taken at p<0.05.**

Table 45: Probability of differences in mean phenotypic values of paired fins of size sub-groups 1-4 (10.1-20.0, 20.1-30.0, 30.1-40.0, 40.1-50.0 cm SL) of *Clarias gariepinus*

	Mean		
Attribute	**Left**	**Right**	***t-value***
Pectoral Fin Length (% SL)			
10.1-20.0 (7)	11.29±1.35	11.30±1.56	0.9843
20.1-30.0 (12)	11.07± 1.76	11.23± 1.50	0.8109
30.1-40.0 (7)	11.02± 2.35	11.26± 2.29	0.8535
40.1-50.0 (5)	11.45± 0.41	11.18± 1.19	0.6455
Pectoral Spine Length (% SL)			
10.1-20.0(3)	6.26 ±2.07	7.53± 0.78	0.3746
20.1-30.0(8)	5.79± 1.66	6.16 ±1.58	0.6559
30.1-40.0(2)	7.34± 0.55	7.51± 0.32	0.7492
40.1-50.0(3)	9.45± 2.34	7.64± 0.59	0.2646
Pelvic Fin Length (% SL)			
10.1-20.0(8)	9.22± 0.82	9.09± 0.71	0.7368
20.1-30.0(15)	9.13 ±1.57	8.92± 1.22	0.6826
30.1-40.0(8)	9.03± 1.71	9.07± 1.69	0.9631
40.1-50.0(6)	9.39± 0.97	9.84± 0.54	0.3485
Pectoral Fin Ray Count			
10.1-20.0(6)	9.00± 0.89	9.00 ±0.00	1.0000
20.1-30.0(12)	9.00± 0.43	9.00± 0.60	1.0000
30.1-40.0(8)	8.50± 0.93	8.50± 0.93	1.0000
40.1-50.0(6)	9.00± 0.63	9.00± 0.63	1.0000
Pelvic Fin Ray Count			
10.1-20.0(8)	5.50± 0.53	5.50± 0.53	1.0000
20.1-30.0(15)	6.00± 0.00	6.07± 0.26	0.7557
30.1-40.0(8)	5.75± 0.46	5.88± 0.35	0.5538
40.1-50.0(6)	5.83± 0.75	5.83 ±0.41	1.0000

***Significant differences taken at p<0.05.**

Table 46: Mean phenotypic values of pooled left and right side attributes of pectoral spine sub-groups of *C. gariepinus* in Asejire Lake

Attribute	Minimum	Maximum	Mean±sd	Coefficient of Variation (CV)
Pectoral Fin Length (% SL)				
Smooth (14)	8.41	11.98	10.64±1.15	10.81
Partially serrated (6)	8.14	12.71	10.67±1.92	17.99
Completely serrated (40)	7.23	14.72	11.54±1.67	14.47
Pectoral Spine Length (% SL)				
Smooth (8)	3.99	10.80	7.85±2.29	29.17
Partially serrated (4)	4.98	8.98	6.73±1.77	26.30
Completely serrated (20)	3.87	7.98	6.41±1.44	22.47
Pelvic Fin Length (% SL)				
Smooth (16)	6.85	12.50	9.20±1.29	14.02
Partially serrated (8)	6.79	9.97	8.37±1.18	14.10
Completely serrated (38)	7.00	10.00	8.79±0.78	8.87
Pectoral Fin Ray Count				
Smooth (16)	8.00	10.00	9.06±0.44	4.86
Partially serrated (8)	8.00	10.00	8.88±0.64	7.21
Completely serrated (38)	7.00	10.00	8.79±0.78	8.87
Pelvic Fin Ray Count				
Smooth (16)	6.85	12.50	9.20±1.29	14.02
Partially serrated (8)	6.79	9.97	8.37±1.18	14.10
Completely serrated (40)	6.33	11.42	9.11±1.26	13.83

Table 47: Mean phenotypic values of pooled left and right side attributes of size sub-groups of *C. gariepinus* population in Asejire Lake

Attribute (CV)	Minimum	Maximum	Mean±sd	Coefficient of Variation
Pectoral Fin Length (% SL)				
10.1-20.0	9.05	13.96	11.29±1.40	12.40
20.1-30.0	7.23	12.88	11.17± 1.60	14.32
30.1-40.0	8.41	14.72	11.14 ±2.24	20.11
40.1-50.0	9.75	12.21	11.32 ±0.85	7.50
Pectoral Spine Length (% SL)				
10.1-20.0	3.87	7.98	6.89± 1.56	22.64
20.1-30.0	3.98	8.42	5.97± 1.58	26.47
30.1-40.0	6.95	7.73	7.42± 0.38	5.12
40.1-50.0	6.74	10.80	8.54± 1.82	21.31
Pelvic Fin Length (% SL)				
10.1-20.0	7.54	10.11	9.16± 0.74	8.08
20.1-30.0	6.33	12.50	9.03± 1.39	15.39
30.1-40.0	6.85	11.42	9.05± 1.64	18.12
40.1-50.0	8.07	10.74	9.69± 0.58	5.99
Pectoral Fin Ray Count				
10.1-20.0	8.00	10.00	9.00± 0.60	6.67
20.1-30.0	8.00	10.00	9.00± 0.51	5.67
30.1-40.0	7.00	10.00	8.50 ±0.89	10.47
40.1-50.0	8.00	10.00	9.00± 0.60	6.67
Pelvic Fin Ray Count				
10.1-20.0	5.00	6.00	5.50± 0.52	9.46
20.1-30.0	6.00	7.00	6.03± 0.18	2.99
30.1-40.0	5.00	6.00	5.81± 0.40	6.88
40.1-50.0	5.00	7.00	5.83 ±0.58	9.95

CHAPTER FIVE

DISCUSSION

5.1 Discussion

5.1.1 Climate, ecological and economic importance of the studied catchment

Background information on the climatic condition of a target environment is useful in a better understanding of the prevailing environmental challenges and enhances better explanation of the possible influence of natural phenomena on findings. Omoike (2004) gives an update on the meteorological information on Asejire Lake as presented by earlier scholars (Buchanan and Pugh, 1955; Elliott, 1986). The pattern of the obtained data on the climate of the study area by the above authorities and the current study showed variation in annual trend of values of climate parameters in Ibadan and its environments, including Asejire Lake. The range of values reported in Omoike (2004) and the result from the current study indicated variation in pattern of climate variables between the two periods which could indicate that there is a trend of changing climatic conditions in the study area. In the current report, the lowest temperature values occurred in different months and in different seasons in the years. It was observed in August (wet season) 2006; December 2007 (dry season) and January 2008 (dry season). The maximum values occurred in dry season months (March 2006 and February 2007 and 2008) in all the years. This implies that temperature pattern varied in the catchment and the variation was of comparatively higher magnitude than in 2007.

The pattern of rainfall condition as observed across the period of study indicated variation. Much variation was observed with respect to maximum rainfall values across the years. The highest values were not consistent with season. They occurred in wet and dry season months (September, 2006 - wet season, May, 2007 - wet season, and March 2008 - dry season). The value in 2008 was the least it was about two-third (2/3) compared with the rest. Moreover, the changes were similar with respect to relative humidity. Variable patterns of relative humidity, temperature and rainfall were observed in the years preceding this study in the locations around the studied catchment. This situation was most likely to be similar at the studied catchment as it is within Ibadan axis on the same geographic zone. The observed parameters are strong climatic factors.

The changing pattern of climatic condition has been reported as one of the greatest threats facing mankind today (IFAD 2007; World Bank, 2010). It also affects fish abundance and diversity IPCC (2007) observes that, although the consequences of

climatic change are often difficult to distinguish from the damage caused by overfishing and pollution, it has impacts on aquatic ecosystems. Climatic change results in reduction of primary productivity (FAO, 2006) it has strong effects on recruitment (Walther *et al*., 2002). Furthermore, climatic change induces vulnerability of stock to overfishing at levels of fishing effort that has been sustainable (Easterling *et al.,* 2007) and results in local extinction of freshwater and diadromous species and aids fish migration (IPCC, 2007). Changes in climatic condition may, in summary, be instrumental to changes in water quality, community composition, distribution and migration of fresh water aquatic species. For example, climatic change caused fall in primary productivity by 20% and fish catches by 30% in Lake Tanganyika (World Fish Center, 2007).

The observed pattern of climatic factors suggested that fish stocks in Asejire Lake might be under pressure owing to changing climatic condition. Its fisheries and water quality is under pressure (Omoike, 2004). This may reflect on the fish community structure and genetic pool of the fish resources including *C. gariepinus* in water body. Historical information obtained from the fisher-folk around the catchment and the reservoir management (Water Corporation of Oyo State) revealed that, since construction in 1972, Asejire Lake has served socio-economic and research purposes in South-western Nigeria. However, its ecological development is influenced by anthropogenic activities. (Obadara, 2006). These observations of climate variation and environmental challenges in the catchment would erode its significant role if the situation is not well managed. The changing climatic condition also affects genetic integrity of organisms, which will challenge the socio-economic and research relevance of the study area and its fisheries. Sustainable utilization of the catchment will therefore, involve management of its biotic and abiotic components in the face of the changing climatic condition.

5.1.2 Environmental condition of Asejire Lake

5.1.2.1 Digital map, catchment structure and area dimensions

McAllister *et al.* (1997) claim that ecosystem units could be mapped at the global, national and local levels. The digital mapping of Asejire Lake was done in this study. Also, current structure and area estimate of the catchment was successfully carried out. The generated shape of the catchment agreed with its analog map and its descriptions by earlier authors (Welcomme, 1985, cited in Omoike, 2004) with a little modification. It was observed that the swamps were gradually invading the water body and this was gradually re-shaping the catchment. Invasion by aquatic flora requires better management

skills to checkmate the situation. The image also showed the tendency of catchment fragmentation in Asejire Lake, which could have impact on genetic structure of the inhabiting fish populations. For instance, Bouza *et al.* (1999) observe that different tributaries in a river represents discrete habitats bearing genetically different populations in *Salmo trutta*.

The general outlook of the environment was characterized by two major water inlets that joined at the confluence to form one main lake course. Tributaries were located on both inlet axes and the axes were well separated. The tributaries could, therefore, be observed as fragments of the catchment which could contain genetically different populations. Also, the inlets would have different physic-chemical and biological characteristics. Owing to the large width of the main lake course, areas of the water media coming from the confluence that are close to shore along each inlet arm will present different physico-chemical and biological components while areas close to the middle of the water course will have a mix of the attributes of the water from the inlets. The inlets thus represent the upstream of the dam. Water masses from the inlets are mixed at confluence to form a main course which has series of branches after a long distance travel downstream. This feature of the dam could also be another source of heterogeneity in the catchment.

Pringle (1997) asserts that the upstream biological processes and upstream alterations impact the lower reaches rivers. The impacts can include phenomena at the generic, population, community, ecosystem and nutrient levels. Hence, the two inlet sources could generate water of different physico-chemical and biological properties which will reflect in the tributaries. The tributaries along each inlet axis may reflect divergence from each other as specific organisms and abiotic conditions may exist in the zones. This suggests that the catchment could represent a combination of different habitats and community structure. Habitat complexity and structural diversity are important components for ecosystems (EIFAC, 1984; Ryder and Scott, 1994 and McAllister *et al.,* 1997). Hence, each of the tributaries could represent separate fragments of the catchment.

It is expected that human influence on the hydrologic area of the catchment will increase with increasing age of the Lake coupled with population increase and industrialization. Observations of the water pumping facilities on the dam revealed that they were located on the hydrologic areas of the catchment while three out of the four (75%) identified facilities were located close to the shores near the impounded area of the

dam. Although multiple water use is a common global phenomenon, water pumping activities and water treatment procedures could constitute environmental challenges to both the physico-chemical and biotic components of the affected areas. However, the overall effect of such structures will depend on their relative size in relation to the entire catchment area and the environmental friendliness of their operation procedures. The impact of industrial activities will be felt with greater intensity on the O_YS than the O_SS. This will affect both the hydrologic areas and the watershed. This is because the majority of the man-made facilities were placed directly on the hydrologic zones of the O_YS stratum, while buildings were also observed on its watershed. These activities were at relatively low levels at the O_SS

Area characterization of the catchment showed that inlets and the main course of the Lake constituted a huge portion of the catchment. The man-made facilities are insignificant but they have tendency of adversely affecting water quality of the catchment. Inlets are a kind of upstream in freshwater lake ecosystem.

Area values indicated that the main course of the lake and the water inlets could be seen as the most important hydrologic zones of the catchment. Processes at the inlets could be traced at the main lake course, thus making the main lake course the most important hydrological zone in the catchment as far as area is concerned. However, its importance may not be elaborate with respect to fish production, genetic structuring and maintenance of the genetic integrity of the catchment biota. This is because the biotic and abiotic components in the zone will be transient. This will be conditioned by fluctuating water depth and flow rate due to flooding and especially water withdrawal during gate-valve manipulation of the Dam. Main Lake course would constitute a highly selective environment. Fluvial organisms will be selected while other species would either find their way to the tributaries or be flushed out of the system when the dam is opened.

Benthic organism will develop phenotype that allows firm grip on the floor, attributes for quick walk-away from the shore and or phenotype that allows quick body maneuvering. Migration from the main dam course to the tributaries will be a surviving strategy for organisms in the main dam course. This will be important especially during dam-gate valve opening. Some of the migrants may come back when the situation gets better. This suggests that phenotypic diversity could be hypothesized as survival strategy in the main dam course. Species diversity may also be limited based on this described physical condition of the catchment. However, fish population at the impounded area will

be more than in other zones of the main course because organisms that do not inhabit the zone will be flushed to it when dam-gate valves are opened.

The remaining small area of the Lake is claimed by network of tributaries. Withthe discussed challenges at the main dam course, the tributary appears to be the major salvage area for aquatic organism of the Lake. However, the relatively limited area of this salvage zone seems to be a major challenge to fish abundance, diversity and community structure in the catchment. The little area allocated to the tributaries is subdivided to five (5) fragments. The discussion on catchment structures has hypothesized that these zones could represent catchment fragments. The fragments have different shapes and areas. Species diversity in the fresh water catchment was inferred to have been a product of basins area or its correlates (Welcomme, 1985, cited by Akinyemi, 1987 and quoted in Omoike, 2004). Species diversity may, therefore, differ at individual tributaries. Bagenal (1978) avers that the shape of basin and characteristics of the water are central to fish distribution and operation of gear. Hence, efficiency of gear for fish catch and water quality at the zones in the catchment may also be different.

The relatively small fragments of the individual tributary are separated on different strata and the stratums are wide apart. This separation, coupled with the unstable main dam course would encourage inbreeding as organisms are restricted to breeding within limited area. This would be felt more on the O_SS, as it contained comparatively greater number of tributaries.

Fragmentation and degradation of habitat, as observed in this study, may be major causes of biodiversity loss and can endanger the genetic identity of a species (Wu *et al.*, 2003), interrupting gene flow and consequently modifying population structure and diversity (Horreo *et al.*, 2011). Saunders *et al.* (1991) observed that habitat loss and habitat isolation caused by landscape fragmentation not only affect ecological processes, but also exert an influence on genetic structure and genetic variation of species, which will make a difference to their adaptability. Inbreeding tendencies in these zones could be challenged by migrating species that may not be doing so at will but are moved along the water current from the inlets and the main dam course during flooding and especially during dam water withdrawal. This implies that heterogeneous population and phenotypic structure could be hypothesized in the catchment. Similarly, resource polymorphism resulting from different food condition at different fragments could also be hypothesized.

Man-made facilities covered a relatively insignificant proportion of the total hydrologic area. However, the facilities could constitute ecological challenge if not

properly managed. This is because some of them were made of metallic materials which could be prone to rusting and corrosion.

5.1.2.2 Environmental threats

(i) Watershed characteristics

Management of watershed is important in ensuring sustainability of its adjoining aquatic environment. Riparian vegetation filters lateral inflows, shades the water, prevents bank erosion, provides woody debris, and inputs insects and leaves to stream food chain (McAllister *et al.*, 1997).

Output of the produced digital map revealed that the watershed is currently undergoing degradation of the initial forested watershed habitat. The watershed vegetation, as revealed in the digital map, showed expanse deforested areas that were linked with footpaths. Actual measurement of degraded forested area was not carried out in this study. However, an estimate of watershed area under human activities was obtained from the satellite image of the catchment. More than half of the watershed was under human activities. Settlements (buildings belonging to companies and individuals) and farming activities were physically observed in the deforested areas of the catchment. Omoike (2004) has noted that the Lake's catchment was surrounded by villages comprising mostly farmers and the fisher folk. However, the current situation suggests that the number of settlement and farming activities might have increased over time. Hence, the pronounced attendant deforestation. Increased deforestation and farming activities in the watershed could have been influenced by population increase at the watershed and or increasing number of the fisher folk who now engage in farming as a result of poor and frustrating catch and or poor socio-economic situations. Population increase in riverine settlements may be as a result of national population rise, urban-riverine area migration because of increased poverty level in the cities and the increase in industrialization at catchment areas.

Buildings that belong to some companies and personal houses were linked by footpaths, while water pump facilities were observed on the water catchment. This situation may be showing the link between the increased water catchment area use and settlements with level of industrialization in the watershed. These three parameters are indices of increased human activities at the watershed which would put forested zones under the pressure of de-forestation with negative effects on valuable wetlands of the catchment. These effects may be in line with the observation of McAllister *et al.* (1997)

that wetlands are subject to drainage or landfill from farmlands and other forms of developments. Goulding (1980) claims that forested wetlands are spawning and nursery habitats; more earth materials will be washed to the shore as more land is opened to erosion as a result of deforestation thus exposing these habitats to destruction. Hence, shore filling could be suspected while hydrologic areas of the catchment will be reducing. Hence, the physical and biotic quality of the habitat may be compromised.

Wang *et al.* (1997) observed that habitat quality and biotic integrity were significantly positively correlated with the amount of forested land and negatively correlated with the amount of agricultural land in the entire watershed. High urban land use was associated with poor biotic integrity and was weakly but significantly associated with poor habitat quality, while the overall watershed land uses clearly had strong effects on habitat quality and biotic integrity. Watershed degradation will heighten aquatic environmental degradation and a consequential alteration of biotic and genetic structure of the catchment. Degradation of habitat is the main causes of biodiversity loss and can endanger the genetic identity of a species (Wu *et al.*, 2003). The watershed land use will have to be planned and controlled in order to ensure biotic diversity in the catchment. This is because unplanned and uncontrolled settlements and land conversion constitute challenges to fish biodiversity (www.nepadst.org/sanbio/fish_biodiversity/index.php).

The O_YS had relatively higher portion of its watershed area being degraded. The relatively higher degradation at this stratum followed the observed trend of human activity that was discussed in the precious section. Degradation followed different pattern at different stratums. On the O_YS, it followed the pattern: dammed end>inlet>tributary, while tributaries>dammed end>inlet was observed at O_SS. The dammed end of O_YS was more degraded probably because most of the industrial activities observed at the Lake were being carried out at this area. The observed anthropogenic activities at the stratum were diverse. They included industrial, agricultural, demographic and chemical utilities. Human activities on the O_SS were biased toward agriculture. On the O_SS, greater degradation occurred at the tributaries. The observed human activities at the watersheds adjoining the tributaries were farming and agriculture based. This also supported Omoike (2004), who reported agricultural processing activities as an environmental issue at its littoral zone.

The presence of micro-climatic zones was also observed in the watershed. This could be conditioned by relief structure of the catchment. Rocky areas were observed in

the catchment and even in hydrologic areas of the catchment. This would influence micro-climatic conditions.

(ii) Catchment fragmentation, catchment shrinkage and losses in effective area for fishing activities in Asejire reservoir (EAFA)

Catchment fragmentation was confirmed in this study. The effects of fragmentation on biota, including the genetic structure of fisheries in water body have been earlier discussed under section 5.1.2.1. The loss in catchment area observed in this study might be one of the major reasons for catch structure observed by Omoike (2004). The reduction might have been conditioned by dam age and shore filling. Increases in deforestation of the watershed would result in the exposure of land areas to erosion which carries materials to the neighbouring water bodies to fill the shores. The reduction would affect fish abundance and species composition of the catchment. Welcomme (1985), cited by Akinyemi (1987), observes that considerable difference in the number of species inhabiting the various river systems in Zaire, Nigeria and Ghana are due to a difference in basin area or some correlation of it. Basins difference could be measured in length of the main channel or stream order. The larger the basin area, the greater the potential for habitat diversity and increasing number of species in African lakes and rivers. The difference in the values after some years of usage has correlation with Welcomme (1985), who argues that rivers tend to decrease in number of fish species as they increases in age.

Some portions for fishing activities in Asejire Lake were observed to be lost to siltation, man-made facilities, and loss of flora diversity in wetland. Also, man-made features were observed to cover insignificant portion of the hydrologic area. Owing to its relatively small percentage contribution to the total catchment area, man-made facilities might not be considered as independent factor of importance. However, two out of the four man-made features were directly placed on the water body. All of them were constructed with metallic materials and placed on the water course near the impounded area. Some of the facilities were already rusting. There is likelihood of heavy metal contamination especially with respect to iron in this area and this will vary in space owing to the effect of uneven distribution of the man-made facilities in the catchment. However, dam drawdown would limit such effects as the materials will be washed away.

The results indicated that some portions of Asejire Lake is currently threatened by siltation. Increased siltation reduces fish production and diversity (Berkman and Rabeni, 1987). Siltation has negative effects on fish by clogging their gills, altering movement and migration, decreasing their resistance to disease, impairing feeding for visual feeders,

engendering poor eggs and fry development and having fatal impact on small aquatic fish food and habitat destruction for bottom-dwelling organisms (Fisheries and Ocean Canada, 2010). Sources of siltation in the catchment could be erosion activities at the watershed, increased flooding condition by unpredictable rainfall as a result of global climate change and shore erosion as a result of water withdrawal. The geographic survey showed that Asejire shore was characterized by extensive sandy but silty shore; this will be susceptible to erosion when water current is generated. Current will increase in the catchment when the adjoining potential wind breakers (forest) are being reduced. Flood and water drawdown will remove particles and carry sediments which are deposited when the currents are reduced. Rainfall is a major source of flooding. However, flushing during water withdrawal from the Lake could create artificial flooding condition.

Poor flora diversity was observed at the swamps of Asejire Lake. This is contrary to the expected flora characteristic of fresh water marshes. Freshwater wetlands are characterized by diversity of fish and shellfish and are generally vegetated by a diverse group of plants. Flora abundance and diversity are also highly dependent on the particular characteristics of the habitat.

The studied area was gradually becoming a nearly mono-species environment, with *Leersia hexandra* dominating the area. The aquatic macrophytes belong to the *poaceae* family. It is a climbing perennial aquatic grass with long rhizomes that root at the nodes. It has round, low branching stems with stiff dense hairs at the nodes, it has ascending zig-zag branches bearing overlapping spikelets. Akobundu and Agyakwa (1998) note that it is a common weed of river banks, lakes and lowland rice that can reproduce from seeds as well as from rhizomes. The aquatic macrophytes which dominate the swamps, influence navigation, limit fishing activities, damage gears and harbour fish predators.

The area covered by the swamp seems large and could be seen as an advantage of large wetland area. However, the observed flora characteristics tend to suggest that it may be viewed as disadvantageous to fish abundance and diversity. The catchment might have lost its swamps flora diversity over time as a result of some of the earlier discussed factors such as siltation.

(iii) Spatial values of water quality parameters of Asejire Lake

The need to manage water resources for quality, quantity and safety have become a major issue in biological studies. Growth and survival, which together determine the ultimate yield in fisheries are influenced by ecological parameters and management

practices (Boyd and Tucker, 1998). Identification of sources of threat to living organisms in an environment is a strong instrument in designing management strategy for sustenance of the organisms. The environment influences expression of genetic potential as organisms adapt to prevailing environmental conditions. A comprehensive knowledge of the limnological features of a lake or any environment in which fish live is imperative for assessing its productivity and suitability for fish.

The aquatic environment of the studied Lake revealed poor water conditions at spatial sites despite normal mean values. Water quality parameters followed abnormal patterns of relationship, water quality at the sampling periods and strata also showed variations. The studied parameters are important components for fish development and reproduction. For instance, temperature and dissolved oxygen are of importance to aquatic life. Dissolved oxygen and the factors affecting it are of critical importance to aquatic organisms**.** Dissolved oxygen plays vital roles in the biology of organisms including the cultured organisms (Thunjai *et al.*, 2001). Boyd (1979) and Boyd and Lichtkoppler (1985) identify 5.68-5.7 mg/l as optimum range of dissolved oxygen for fresh water organisms. Saloom and Duncam (2005) opine that the minimum dissolved oxygen should be 5 mg/l for tropical fish. Omitoyin (2011) notes that 4-9 mg/l would be better for fish health management. However, Fafioye *et al*. (2005) recorded values as low as 1.4 - 4.8 mg/l range in a water body in south-western Nigeria. The minimum mean value of dissolved oxygen content obtained in both wet and dry seasons in the catchment in this study was below the minimum values reported in the literature for optimum conditions in tropical fresh water (Boyd, 1979; Saloom and Duncam, 2005). This implies that oxygen challenges occur in the catchment and this is not seasonally biased. Moreover, range of individual values revealed that values as low as 0.9mg/l was obtainable in the catchment. This value is similar but lower than that reported by Fafioye *et al.* (2005) in another water body in the same region. However, maximum mean values were within recommended ranges. The greatest mean value was obtained in the dry season and value as high as 9.6 mg/l was recorded during the season.

Dissolved oxygen concentrations are greatest at 0^0C and decrease with increases of temperature (Boyd, 1979). The high value in dry season could be linked with low temperature obtainable during harmattan periods in dry season. The pattern of the box-plot revealed that each sampling period had different patterns although wet season patterns were comparatively similar. Dry season's patterns showed differences in box patterns and wide variations. This implies that the highest and the lowest values obtained

throughout the experiment were obtained during the dry season. Natural waters are never completely quiescent and oxygen transfer is regulated by the amount of turbulence (Welch, 1968). Boyd (1979) argues that diffusion of oxygen into natural waters is slow, except under conditions of strong turbulence. The amount of turbulence in the wet season would be more regular in the wet season going by rainfall with associated flooding and dam gate opening. This could be responsible for the less variation pattern in dissolved oxygen content during the wet season. Turbulence in dry season will be minimal and dependent probably on the frequency of dam gate-valve opening. This is because rainfall and its associated sources of turbulence including gate-valve manipulation will be reduced during dry season. Dissolved oxygen pattern at each sampling will therefore, depend on the prevailing situation of dam with respect to dam gate opening and minimal flow rate as at sampling time.

The dissolved oxygen content pattern seems to reflect limited quantity during February/March sampling period. This period coincides with the end of the season. During this period, water condition at dam assumes a seemingly stagnant form as influx of water to the dam is reduced. Even the management of the dam usually shuts gate in order to maximize the available water till rain starts. Temperature will be rise and dissolved oxygen will drop in value. Temperature may be more influenced by insolation rather than air temperature (Boyd, 1995). Hence, its values will decrease as wet season advances and insolation decreases giving rise to high relative humidity; and decrease as dry season advances owing to increasing level of insolation in the catchment. Dry seasons are characterized by relatively high temperature and this would increase up to the end of the season. This situation indicates that fish distribution will be influenced at both seasonal and spatial sites at the catchment. This is because seasonal temperature places broad distribution limits on tropical fishes, while local distribution patterns are much more affected (Omoike, 2004).

Box shapes were different within and between the sampling periods. The between-sampling time variation, as reflected in the differences in box types, could be as a result of differential climatic condition and or variation as a result of varied water environment at different sampling periods. Climatic change has been earlier reported in this study for the catchment areas vicinity. Adeyeye and Abuludi (2004) note that temperature could vary at different portions of a dam and this can be attributed to decomposition of organic effluents Omoike (2004) reported presence of sites of organic deposition in Asejire dam. However, the site for organic deposition, which was observed in this study, was so

minimal that this factor may not be completely responsible for the variation despite spatial sampling employed in this study. This variation could be linked with climatic change effect. The box shape indicated that less variation was observed in the wet season values compared to those of the dry season. This could be attributed to the possibility of greater mixing of water during wet seasons in wet seasons. Transfer of heat from upper to lower layers of water depends largely upon mixing of water by wind (Boyd, 1979). The pattern of wet season mixing could be due to high amount of rainfall, flooding and subsequent high frequency of dam-gate opening. However, the lowest and highest values are obtained in the dry season. This indicates that temperature varies more in dry seasons. This could be traced to less frequent mixing. Boyd (1995) observesd that water depth could also influence water temperature. This could occur in the catchment as a result of dams water draw down. Egorge, (1970) reported that temperature elevation was observed after closure of dam gate in Asejire dam. A reverse of this could occur at dam-gate opening.

Total hardness is a measure of concentration of calcium and magnesium ions expressed as equivalent of calcium carbonate. Hence, the presence of inorganic salts such as magnesium chloride, calcium chloride, magnesium carbonates and calcium carbonates, in water can cause water to be hard. Total alkalinity is the total concentration of bases in water expressed as mg/liter equivalent of calcium carbonate ($CaCO_3$); it normally results primarily from bicarbonate (HCO_3) and carbonate (CO_3) ions (Boyd, 1979).

The obtained range of alkalinity values in this study implies softness. Moyle (1945) and Mairs (1966) consider alkalinity value of < 40 mg/l as indicative of soft water. In this study, the wet season values were higher in values compared to dry season. The higher value in wet seasons could be as a result of more quantity of ionic material being brought into the catchment through runoff during rainfall. However, Parker (1995) claims that fish does best at alkalinity between 20 to 30 mg/l. The ranges of alkalinity values obtained in this study were above the ranges. Mean values of alkalinity was higher in the dry season than the rainy season.

The result also revealed that higher mean values were obtained in alkalinity than in hardness. When the total alkalinity of a water sample exceeds its total hardness, some of its bicarbonates and carbonates are associated with potassium and sodium ions (Boyd, 1979). These indicate that the alkalinity measured in this study could have estimated carbonates and bicarbonates of sodium and potassium ions along with calcium and magnesium. Despite this, minimum alkalinity values as low as 12.00 mg/l were obtained

during wet season while similar low values were also observed in both wet and dry seasons in the hardness values of certain sites. These indicate that major nutrients, such as calcium, magnesium, sodium and potassium, could be of limited quantity at some sites within the catchment, especially during wet seasons.

The sites with the limited values were all located along Agora axis (O_SS) of the main dam course. This shows that the inlet axis could be different by physico-chemical conditions, thus supporting the concept of catchment fragmentation. These sites may be composed of rock materials which contribute less quantity of inorganic salts in solution or they may be less prone to mineralization. High alkalinity may be due to carbonate contents of rocks and soils of water sheds and bottom mud (Boyd, 1979). The condition of the watershed could also be instrumental. However, the digital map and observations during geographic survey revealed that the Agora inlet had more muddy condition; however, mud accumulation at these sites could equally have been challenged by flushing during draw downs.

Moreover, the box pattern showed that alkalinity and hardness had similar patterns supports the report of Mair (1966). The wet season samples showed limitation while the dry season values showed wide variation in values obtained within the same sampling period. Apart from bedrock attributes, dam-gate valve opening is most likely to be responsible for this type of variation pattern. The target ions will be flushed out of the catchment along with other dissolved nutrients; the situation will be more frequent during the wet season. However, standing of dam water for a relatively longer period will build up nutrient and this would be more frequent during the dry season when the water level drops and takes relatively longer time to build up.

The highest and lowest values of alkalinity were obtained during the same sampling time (February/March) at different sampling years could be as a result of different environmental situations as at times of sampling. This could also be linked with water condition with respect to the dam's water period of standing after water has been drawn or rainfall condition. The higher value observed in the dry season, when compared with the wet season values in the catchment reflected that the current result disagreed with Mair (1966), who claims that high value of hardness is expected in wet seasons due to runoff. The tested ions could be obtained in natural waters through mineralization and dissolution of basal materials to form solution. The more static the water body is all things being equal, the more ionic concentration in the water body will be, and vice-versa. Extremely low value could however be observed if nutrient concentrated water is

removed and there is not enough time allowance for re-concentration. The February/March alkalinity value was the highest and was distinctively higher and different from all other shapes obtained throughout the experiment. This period could coincide with the period of standing dammed water for a relatively abnormally longer period and the standing water gets highly concentrated in the process, which could be due to power outage or mechanical challenges that took longer time to be fixed or insufficient water inflow owing to rainfall pattern.

These results indicated that nutrient ions availability in the aquatic environment could be limiting during wet seasons and fluctuate during dry seasons as a result of dams water condition controlled by dam gate-opening. Omoike (2004) found insufficient nutrient availability in Asejire dam catchment. This study supported the idea and provided information on the possible source of the problem for better management. These parameters are usually affected by flow conditions.

Limiting (deviation from minimum recommended) values occurred in hardness in all and nearly all sites in the wet and dry seasons respectively. The Value of Calcium and Magnesium ion expressed as equivalent of Calcium Carbonate (Hardness) is a measure of presence of inorganic salts such as the chlorides and carbonate salts. The cations involved (Calcium and Magnesium) are associated with metabolic activities and their deficiency could result in metabolic imbalance in fish. The entire sites reflected this trend, indicating that all sites could be limited of the cation. This implies that there is no hiding place for organisms during such periods. The intrinsic ability of individuals in surviving the challenge and the frequency of such situation set selection pressure in the catchment while the fittest organisms will survive.

(iv) Factors responsible for variability in water quality parameters

The extraction of two principal components which interacted in three forms indicated that the variable condition could be grossly caused by two independent factors. Going by the significant differences observed in seasons and the catchment fragments, it can be deduced that these factors were probably the principal components responsible for the variation. Season was possibly the component 2. This is because seasonal variations in values of water quality parameters do not change the pattern of relationship between these parameters. Temperature and DO will normally have inverse relationship (Boyd, 1985). This relationship was maintained on component 2. However, deviation from this pattern was observed on component 1. Strata were significantly different and abnormal correlation of temperature and DO was observed on one of the strata. This indicates that

catchment strata (fragmentation) were the component 1. Meanwhile, the significant abnormal correlation was observed at O_YS. The abnormal pattern thus correlates with the strata that reflected the highest level of human activities in the catchment. Wang *et al*. (2008) note that significant relationship exists between urbanization and surface water quality. Level of urbanization has positive correlation with clearing of forest as observed in the differential extent of degradation and human activities at the studied strata of the catchment. Hence, the water quality at the strata showed differences.

Potential influences of natural processes and anthropogenic activities on spatio-temporal variations in water quality has been reported in Pillsbury and Byrne (2007), Mendiguchı´a *et al.* (2007) and Kannel *et al*. (2008). Studies investigating the spatial and seasonal variability of water quality have reported that water quality issues are highly dependent on land use patterns and influence from watershed runoff discharge (Caccia and Boyer, 2005). The abnormal pattern of relationship between water quality parameters in this study could emanate from unpredictable interruption of human activities, especially from the watershed. O_YS was more affected. This stratum had higher level of human activities, reflecting in forest degradation, demographic structure and industrial activities at its watershed. Its fishing zone also contained a greater number of man-made facilities when compared with the O_SS.

From the analysis of water quality of the catchment, the two factors responsible for water quality variation could be seasons and strata. It will be of interest to understand the factor that will cause variability irrespective of season or strata in the catchment. Such factor will also affect fish distribution and genetic structure of fish population of the Lake. Human activities will occur at any season or strata and it is possibly the responsible factor.

(v) Frequency of opening of dam's gate

Partial drawdown was minimal during dry-season months. However, partial flow was maintained for longer periods in all the rainy-season months except April The values were greater or equal to half of the days of a month (15-18). A higher frequency of partial drawdown during the rainy season may be due to dam structure maintenance to prevent collapse as a result of flooding via gate-valve manipulation. Influx of flood water from watersheds after rainfall depends on rainfall pattern and this may influence frequency of dam gate manipulation. Annual rainfall range of the Asejire area was within 102-104cm in the wet season and 13-39cm in the dry season (Elliot, 1986 and Omoike, 2004). Gate

opening will therefore, be manipulated at more frequency in the rainy season in the study area.

The result on frequency of complete drawdown showed that human influence in gate opening could be suspected in the catchment. Complete drawdown is expected to be a means of releasing long-standing water for refreshing. This is most expected to occur during the dry seasons. However, the desire to increase catch by fishermen could motivate human influence on gate manipulation during the rainy season and at odd times in the dry season. This is because low water level would be desired for better catch during the rainy periods, as shallower water correlates with species clustering (Maravelias, 2011, Duttemann *et al.*, 2012). Uiblein *et al*. (2006) also observe that water depth affect length and weight of fish caught.

It is also expected that the interval between complete drawdown and another dam opening should take longer time during dry season than rainy season owing to the reduced water in-flow and high rate of water loss normally experienced during this period. This was the trend in March and October. However, an abnormal situation was observed in February. The gate was completely opened twice. The interval between openings were extremely short at both periods (3 and 5 days post-drawdown). Situations like this cannot be as a result of flood or long-standing foul water but a human factor which is most likely out of the drive to have better catch. This result indicates that the catchment is highly dynamic with respect to water depth and flow. This may have multiplier effect on nutrient availability and nutrition and edaphic, geographic and biological structure of the catchment. There will be natural selection for versatile organisms while others go into extinction. High heterogeneity of sites relevant for adapting to the physical condition in the versatile organisms of the catchment could be hypothesized.

Migration within the upper dam across its axes (O_YS and O_SS) may be disturbed by the frequency and flow-rate during drawdowns. This may limit organisms that inhabit different tributaries from exchanging genetic materials (gene-flow) by migrating to the other strata, thus reducing survival strategy in small populations and resulting in genetic depression of such population via inbreeding.

Assessment of the environment indicated that watershed degradation, catchment fragmentation and shrinkage, loss of flora diversity and siltation of hydrologic area, unstable and limiting quality of water parameters were the main challenges of Asejire Lake. Apart from structural issue of fragmentation, other factors had link with either dam management practice of opening of the dam's gate as well as anthropogenic activities at

the watershed were the main challenges in Asejire Lake. Studies have revealed that the identified challenges would reflect in genetic structure as well as abundance and distribution of the fishery resources of the Lake.

5.1.3 Genetic structure of *C. gariepinus* population in Asejire Lake

5.1.3.1 Phenotypics' structure of *Clarias gariepinus* population in Asejire Lake

The catch structure from spatial sampling and phenotypic structure of the obtained *C. gariepinus* population is discussed in this section.

(i) Fish catch structure of Asejire Lake

Biological surveys provide specimens needed for taxonomic and genetic research (McAllister *et al.,* 1997). The spatial sampling of fish was carried out to obtain samples for genetic studies, compare catches with the earlier trends and set standards for combined monitor of catch, environment and the genotype. Fish catch from this study was of greater quantity compared to Omoike (2004). A total of 1,392 fish were caught during the sampling period compared with the 520 fish caught by Omoike (2004). *Chrysichthys nigrodigitatus* was the most abundant single species totalling 30.5% proportion in catch in Omoike (2004); its superiority in catch was also retained in the current study (49.78%**).** Higher number of individual fish catch during the current study may be as a result of gear selectivity and the intensity of sampling. Gura trap was used in this study and 38 sites were sampled compared with fleets of gillnet set at the back of reservoir, littoral area, middle of reservoir and industrial effluent discharge sites reported by Omoike (2004). The number of species (19) and families (12) observed in this study was similar to the respective 18 and 12 reported by Omoike (2004). However, these were lower compared to 41 species and 14 families found in Akinyemi (1987) and 23 species and 13 families observed by Elliot (1986). This showed decline in species diversity within fish families in Asejire Lake. Despite differences in gear used and intensity of sampling, there were similarities between the current finding and the reported species diversity by Omoike (2004). These indicate that this study also confirmed the reported loss of species diversity as observed by the scholar.

Claroteidae (formerly *Bagriidae*) family was the most abundant species in the catchment, which is also similar to the observations of Omoike (2004). However, greater proportion in catch was observed in this study (49.78 %0 compared with the 30.5 % found in Omike (2004). This could be linked with the selectivity of the gear used. The catch structure with respect to the most abundant single species, the most divergent

family and the trend of species richness and reduced diversity used by Omoike (2004) was similar to the observations in this study. Dominance of the *Cichlidae* family as the most divergent in lake system has been noted by Daddy *et al.* (1991) who found *Cichlidae* to be the dominant family in Tatabu Lake in Niger State of Nigeria. It also agreed with Olaniran's (2000) finding on International Institute of Tropical Agriculture (I.I.T.A) Lake, in Ibadan, Nigeria.

The least composition among the species divergent families was observed in the *Clariidae* family. This may implies that the family is currently the most threatened divergent family in the catchment. *C. gariepinus* had the greatest proportion in catch among the members of the family. Omoike (2004) obtained only this specie in the family *Clariidae* and 0.6 % was its composition in the total catch. The obtained lower catch proportion despite more intense search, a generally higher total catch and benthic habitat focused gear suggests a gradual species decline in the catchment. This is further supported by the field observation that this specie, which is one of the most important aquaculture candidates, was becoming scarce and obtaining wild samples for research is becoming more challenging. This trend of results on the *Clariidae* family suggests the need for a strict management and conservation approach on the fishery at Asejire Lake. This is achievable through legislation provided relevant data on the species and the catchment are generated. ICN (1988) asserts that among populations at risk of imminent extinction, there was diversity in population structure, selective pressures of the environment, modes of adaptation to the environment and causes for population decline.

The target species did not dominate any site though captured in low quantity at both OyS and O_SS strata. This indicates that it can survive any of the strata despite their present situation but some factors that probably affect the catchment irrespective of strata affect its abundance. Lintermans (2007), Olden *et al*. (2007) and Jelks, *et al*. (2008) claim that many freshwater fish species around the world are threatened or endangered as a result of habitat degradation, altered hydrology, invasive species and disease. However, over-exploitation has also been responsible for decline (Limburg and Waldman, 2009). Introduction of invasive species has been linked with disease and this has been discussed above with respect to the study area. Over-exploitation in the catchment has been insinuated by Omoike (2004), also reported changed values of physico-chemical parameters compared with earlier studies. However, altered hydrology due to dam water drawdown and fragmented habitat were not included. Whereas, alteration of river course in dam system could be a strong factor in species sustainability. WWF, (2010) avers that

Mekong giant catfish will be driven to extinction if Mekong river is dammed. Santos *et al*, (2011) opine that, because species morphology is somehow linked to habitat use and its performed niche, alteration in the environment, such as those from dam construction, may restrict the permanence of certain previously existing species. The depleting state of Asejire fisheries, especially the *Clariidae* family, could be as a result of alteration in the environment as observed in earlier studies.

The alteration especially opening of the gate of the dam, could also be instrumental to the pattern of catch that was obtained in the strata. Analysis of catches from the strata indicated that O_YS had greater contribution to total catch compared to the O_SS. The relatively higher catch in this zone despite its level of industrial development and watershed degradation pointed to an interruption to normal relationship between human activities and aquatic life as highlighted in the previous discussions. Moreover, catches from strata were negatively correlated during one season and positively during another. This pattern was different from that of water quality parameters, suggesting that the controlling factor for catch structure variation across strata was probably independent of the factor affecting the water quality.

It is expected that strata with higher level of human activities would have lower catch due to higher fishing pressure. However, inverse situation was observed in the studied catchment. Apart from human activity at the watershed, another factor that could alter fish distribution pattern and differentially affect strata at seasons is the opening of the dam's gate. The opening will come erratically and have differential effect on the strata. The differential effect of water withdrawal on the catch from strata could be as a result of the depth of each stratum. This is because water depth will influence quantity of fish catch. Low depth shores would be exposed while relatively high shore have less effect. Behavioral adaptation for fish in situations of low water is to deeper areas and if well adapted to walk, they migrate to nearby swamps through different adaptive features. Gunder, (2004) notes that, in such situation, *C. gariepinus* would migrate to the swamp by walking using its pectoral spine. Other organisms could colonize a small but safe micro-habitat in the catchment and inbreed.

(ii) Phenotypic structure of *Clarias gariepinus* population in Asejire Reservoir

Different characters were observed to possess different variability in the studied population. This results supports of the idea that each character may show a different degree of variability within a single population (Mayr, 1969). The revealed phenotypic values implicated within population heterogeneity with pectoral fin characters PECSL

(pectoral spine length) and PESES (possession of anteriorly serrated pectoral spine) being the respective most varied morphometric and meristic characters of the *C. gariepinus* population in the study area.

The character of great concern with regard to variation in this population was the PECSL. It had the greatest coefficient of variation, the greatest difference in the left and right side values and it was the only trait with single mode in value from one side and multiple modes at the other side of the body. Its mono modal value at the left side, contrary to other attributes, showed indicates the unison of the population at this site, and the suitability of the morphometric value as a potential population's representative. This agrees with the conventional use of left side morphometric traits in morphometric studies. However, the disparity between modal values in-between the sides supported the need to assess both sides. It also indicated another index of a highly heterogeneous morphometric site. The heterogeneity at this site and some other morphometric traits was in supported Gunawickrama, (2007), who observed that some morphological characters of fish were useful in generating heterogeneity in morphology. The variation pattern observed in this study might have emanated from changing structure evolving as a result of complex interactions of biotic and abiotic factors in the environment. Species morphology is somehow linked to habitat use and its performed niche and alteration in the environment, such as those resulting from dam construction (Santos *et al*., 2011). This may evolve and diversify owing to competition, predation or other biotic interactions (Bock, 1990).

The greatest variation among morphometric traits observed in PECSL could be community-based and or habitat-induced. This is because morphometric value, especially with reference to walking attributes like pectoral spine, could vary based on level of use in the habitat. Pectoral spines serve locomotory and protective roles in *C. gariepinus*. The spines are extended while crawling through shallow pathways (Gunder, 2004). The variation pattern observed could indicate that the greatest operation in the habitat has to do with the use of this trait; hence, all individuals expressed it at different levels. This reflects more in the right spines, as most right sides tend to be more active than the left even in human. Species like *C. gariepinus* occupies the swamp, and would react to exposed shore by taking walk to the nearest favourable site via its pectoral spine. This could be the surviving strategy against the effect of environmental variation and walking attitude necessitated by dam drawdown frequency in the catchment. This result agreed with Santos *et al*. (2011) whoclaims that it is expected that morphology would reflect fish adaptation to reservoir condition.

Multiple modal attributes in the rest morphometric traits indicated heterogeneity. Bimodality in phenotypic traits has been observed between morphological types in fish (Eastman and Devries 1997; Guiger *et al*., 2002). Morphometric trait in *Clarias gariepinus* could be influenced by sex and or size; Skelton (1993) observes that males grows larger than females of the same species, while Gunder (2004) recognizes metamorphosis as part of its attributes. These factors may have effect on the fish morphology because variation at different stages of life is to be expected in situations of metamorphosis. This phenomenon can, however, be differently expressed in the sexes.

With respect to variation pattern in meristic attributes, PESES and DR were the significant traits. All meristic traits had variation value below 10%, except PESES-L&R, and all meristic traits had single mode except DR. This indicated heterogeneity at these meristic loci while all others were homogeneous. Meristic characters like number of spines and fin rays permit greater accuracy than linear measurements and are favoured in the systematic populations of fishes and reptiles (Mayr, 1969). They are discrete, serially repeated, countable structures that are fixed in embryos or larvae (Turan, 2004).

The variation pattern in PESES of the studied *C. gariepinus* population was similar to that of morphometric trait PECSL; however, the values did not differ in modal attributes of left and right sides. High coefficient of variation with mono-modal value implies that high variability at this site is a general trend in the population. Multiple modes may indicate presence of morphologic type (Guiger *et al*., 2002). The presence of strong pectoral fins with spines that are serrated on the outer side referred to as PESES in this study, has been reported in *C. gariepinus* (Teugels, 1986). However, the trait was observed at three different levels in this study (completely absent -smooth, partial possession one spine possession; and completely serrated-two spines possession). This indicates the possible source of high coefficient of variation as observed in the population's phenotypes and could constitute a major source of systematic challenges with respect to the population. A similar trend of phenotypic variation in pectoral spine was observed to be related with some other traits and morphologic types of *Pimelona chagressi*; further analysis of the population confirmed presence of haplotypes (Martin and Birmingham, 2000). Hence, presence of taxonomic sub-group based on this trait could be hypothesized. In particular, heterogeneity at the PESES site occurred concurrently with heterogeneous DR and heterogeneity of most of the morphometric traits.

The observation could have taxonomic and or genetic implications. This is because DR is a strong taxonomic trait. According to Holden and Reed (1978), the most vital external characteristics for identifying fish are fin ray counts, especially those of the dorsal and anal fins. Mayr (1969) opines that precise measurements sometimes display bi-modal characteristics and there are differences in the number or structure of the chromosomes. The presence of taxonomic sub-group with genetic source of variation could be suspected. However, establishing the relatedness of the traits would be important. Factor analysis revealed that the variables were related having 19 iterations with DR and HL showing relatedness on a common factor (component 3). The genetic basis of the variation pattern could be achieved through molecular genetics approach. Detection of within population morphotypes has taken genetic approach in concluding phenotypic variation patterns (Mayr 1969; Carvalho and Hauser, 1992, Turan *et al*., 1998; Shaw *et al.,* 1999). Turan *et al*. (2005) assert that high phenotypic differences observed in *C. gariepinus* may be due to the presence of other taxa and suggest application of molecular genetics technique to confirm the detected phenotypic variation pattern.

Within population heterogeneity could be caused by both non-genetic and genetic sources. Apart from ecologically induced variation, allometric growth and sex have been mostly considered in morphometric analysis of populations (Elliot *et al.,* 1995; Turan *et al*., 2005; Gunawickrama, 2007; Arbour *et al*., 2011). Although studies were not encountered on the use of PESES for population sub-grouping, the trend discussed in Martin and Birmingham, (2000) on the trait and the classes of expression observed in the current study suggests that this may also have influence on the divergent traits in this study. Analysis of the role of the highlighted possible sources of phenotypic heterogeneity prior to molecular studies may be necessary in order to confirm the source of heterogeneity in this versatile specie.

5.1.3.2 Phenotypic structure and Discriminant factors in sub-groups of the studied *Clarias gariepinus* population

Results on phenotypic structure and discriminate factors are separately discussed in this section;

(i) Phenotypic structure of sub-groups of sex of sex in *Clarias gariepinus* population

Significant difference in morphometric and meristic attributes was not observed between male and female populations. This implies that sexual dimorphism was not obtained. However, comparatively higher degree of body depth was obtained in males

compared with females. The insignificant difference could be due to certain conditions of the catchment. The comparatively higher depth in males as observed in this study agreed with Kutano *et al*. (2012), who observed that males tended to have deeper bodies than females but the magnitude of sexual dimorphism was reduced in stream-resident forms of *Gasterosteus aculeatus.* This implies that habitat forms influence degree of sexual dimorphism and this could be responsible for the observed trend. Previous studies on the environment have indicated heterogeneity of the catchment. Skelton (1993) reported sexual dimorphism in *Clarias gariepinus* using growth pattern, whereas this study focused on some other different traits. BDMIN was nearly significantly different between the sexes (p=0.051). The sexual ratio of the population may have influenced the phenotypic structure. Sex ratio obtained in this study was 3:7 (male: female) showing a female biased population. This attribute seems to be potential site for sexual dimorphism in the population.

The relatively smaller head in males along with deeper body depth at the caudal peduncle observed in this study may be indicative of habitat use effect. Santos *et al*. (2011) link relatively larger head, longer caudal peduncle and mouth to morphological diversification in order to explore different habitats. With the established environmental condition characterized by limiting nutrients and unpredictable food chain as a result of frequent flushing, flexible organisms would adjust to explore available resources per time. The sexual and morphometric structures obtained in this study could be a product of differential phenotypic expression in response to the prevailing habitat condition in the catchment. Morphological changes among species reflect at least, in part, the differentiated use of resources and ecological differences, with a parallel between morphological and ecological similarity (Santos *et al.,* 2011). The smaller head along with reduced proportion in male population may imply that the they were less phenotypically plastic.

Higher coefficient of variation was observed in female population at HL while BDMIN values were similar. Low genetic variability often reduces the capacity to adapt to changing environmental condition resulting in inability to cope with abiotic and biotic stresses in habitats (Valen, 1965). Habitats are the main causes of biodiversity loss and can endanger the genetic identity of a species (interrupting gene flow and consequently modifying population structure and diversity (Horreo *et al.,* 2011). The better plastic female population may have therefore been less influenced by the habitat compared with the male population; hence, the female-biased population and the morphometric structure

obtained. Habitat characterization as observed in this study revealed habitat loss and possibility of fragmentation to which the sexes may be differentially affected. Taxonomic group, species, and populations may be differentially threatened by habitat fragmentation; however, organisms with plastic life history are likely to be less susceptible (Horreo *et al.*, 2011).

Size structure might have also reduced the probability of sexual dimorphism in the analyzed sample. Closely associated set of traits that showed sexual dimorphism in growth was positively allometric in males when size range 31-91mm was analyzed in *Oreochromis niloticus* (Oliveira and Almeida, 2005). This suggests the need for deciphering the population by different size groups. However, HL and BDMIN were observed as potential morphologic sites for sexual dimorphism in *C. gariepinus* population in the study area. Similar to this observation, Gunawickrama (2007) obtained sexually biased population in which none of the recorded morphometric characters was significantly different between sexes; hence, ignored sex in further analysis.

Coefficients of variation were reduced when different sexes were separated. However, all morphometric traits reflected heterogeneity having greater than 10% coefficient of variation with the exception of HL, DL and AFL in both sexes. This implies that, although sex differences would reduce level of heterogeneity, they did not outright solve the problem of taxonomic complexity. Heterogeneous mode occurred in all traits in both sexes; however, PELFL-R (male) and PECSL-R (female) were homogeneous. The sexes therefore differentiated themselves in terms of the attribute that was homogeneous in each case. Moreover, the multiple modes in nearly all the traits concurrently occurred with heterogeneous coefficient of variation in nearly all the traits indicating a strong pointer to possibility of complexity in morphology, which could require further deciphering of the population.

Pectoral fin attributes were still the most dynamic morphometric traits in the sexually differentiated populations, indicating the central position of the attribute with respect to phenotypic variability in the catchment. Also, differentiating the sexes did not remove heterogeneity of the sample. For example, variability in phenotypes of the sexually differentiated population still reflected multiple modes of DR in both sexes as it was observed in the sexually undifferentiated populations' phenotypic structure. DR is a strong taxonomic trait. A meristic attribute (PESES) was heterogeneous (CV >10). It had the widest difference between L&R values and was not multiple modal in both sexes. Concurrently, a morphometric attribute (PECSL) showed similar pattern. These two

attributes were pectoral fin based and their variation pattern seems correlative. The presence of heterogeneous site which correlates with other sites could indicate presence of morphologic sub-group (Mayr, 1969).

Heterogeneity (CV>10) was observed at DR in both sexes, while AFR had multiple modes. Therefore, that the pattern of variability that was reported with respect to DR in the entire population was confirmed in both sexes. This suggests that the variability in DR as observed in the population was controlled by the presence of non-sex associated factor. Non-Sex linked variation could either be continuous or discontinuous (Mayr, 1969). The presence of individual variation due to slight genetic differences between individuals of a population constitutes continuous variation while polymorphism (non-continuous variation) occurs when a population can be grouped into very definite classes, determined by the presence of certain conspicuous characters. Meanwhile, presence of polymorphic forms has been reported in fish populations based on morphometric and meristic traits (Sandlund *et al*., 1992; Martin and Birmingham, 2000; Beland, 2004; Turan *et al.,* 2005).

(ii) Phenotypic structure of sizes' sub-groups in *C. gariepinus* population of Asejire Lake

The ultimate goal of morphometric studies is to quantify shape differences within the context of a particular set of questions or hypotheses in ecological and evolutionary studies (Straus and Fuiman, 1985). Many fish species transform in body shape during growth-allometry (McHenry and Lauder, 2006) and, thus, a population containing fish of different stages of life could have heterogeneous phenotypic structure. This study identified allometry (size variation) as an independent factor in attributing level of divergence of characteristic variability at phenotypic sites. The size groups were significantly differentiated in at least one of the studied sites (DR). Allometric growth has been attached to significantly differentiated morphometric data (Turan *et al.,* 2005; Gunawickrama, 2007). Kassam *et al*. (2004) observed statistically significant body shape differences among species but not between sexes among co-existing species of Petro-tilapia. Nearly significant difference between sexes but significant difference between size groups thus agreed with Kassam *et al*. (2004). The reasons for the insignificant sex differences have been provided in the earlier discussion at the section on sex sub-group.

Size sub-groups showed significant difference with reference to DR in this study. Significant ray count difference has been reported in *Pterogogus auriganus* with males possessing larger first and second spinal rays in dorsal fin than females (Park *et al.*,

2005). However, DR increased from group1 to 2, dropped below either 1 or 2 in group 3 and was highest in the largest sized group (4). This presupposes that DR initially increased with size of fish and reached peak at the largest size group a depression in value at size group 3 is, however, an unexpected trend. It is impossible for an increased number in a biological trait at an earlier stage of life to be lost at an intermediate stage of the same individual and improve beyond earlier values at an adult stage. It could, therefore, be inferred that a sub-population possessing lower DR range could be present and dominating the size group 3, thus responsible for the drop in the mean value. Moreover, groups 1 and 3 had equal proportion of individuals in the sample. The minimum DR count obtained in group 1 (47) was greater than the minimum obtained in group 3 (45). Group 3 had greater maximum value. These buttressed the idea that there could be a group possessing relatively smaller DR count which could probably be detected at size group 3 of the sampled population. The presence of polymorphic form in this population could therefore, be implied based on the observed trend. No two individuals (except mono-zygote twins) in a population of sexually reproducing animals are exactly alike, genetically or morphologically. However, when such variation results in members of a population that can be grouped into definite classes, determined by the presence of certain conspicuous characters, such discontinuous individual variation is called polymorphism (Mayr,1969).

The pattern of phenotypic variation in the size groups revealed that PECSL was morphometrically central to groups 1-3. It was the site that was most varied, while BD (MAX) had the greatest coefficient of variation among morphometric traits in group 4. Earlier studies revealed that PECSL was the most varied morphometric trait in the population. It had a similar position in heterogeneity ranking in size groups as in the entire population except in group 4 in which it was next to the highest. Therefore, size did not erode its variability ranking except in the advanced stage (group 4). The less variation in PECSL in group 4 could indicate that these traits are less plastic at advanced stage being less susceptible to environmental sources of phenotypic variation such as wearing away owing to its ecological role. Pectoral spine is utilized in walking movement (Gunder, 2004) and would be more flexible at early stage but become more hardened or adapted to the environmental condition at adulthood; hence the less variability. This result is similar to the report of Strauss and Fuiman (1985), who observed that larvae are relatively more variable at a given size than adults and adults are relatively more variable among species because of divergence during development in Pacific Sculpins. The greater

variation in BDMAX in group 4 could, therefore, be as a result of a more varied growth and development of individuals with respect to body depth at adulthood.

PESES was the most varied meristic trait in all sub-groups and it had a singular mode in all. However, complexities of modal values were observed in PELFR-L&R and AFR, DR and PECFR-L (groups1, 2 and 3, respectively) while all traits in group 4 were mono-modal. The mono modal meristic traits in group 4 suggested homogeneity at this stage of life. However, heterogeneity at most of the sites in groups 1-3, especially with AFR and DR included implies that variation in the sub-groups may be taxonomic. This is based on the importance attached to these traits in taxonomy (Holden and Reed, 1978). The consistent heterogeneity of the PESES with other heterogeneous meristic traits in groups 1-3 also points to the possibility of PESES sub-division to be playing central role in the development. Delineating the population by this meristic trait could be helpful in solving the bottleneck.

(iii) Phenotypic structure of pectoral spine variants sub-groups of *C. gariepinus* population in Asejire Lake

Pectoral spine variations sub-grouping seems to be potential for deciphering the studied population and solving the observed taxonomic complication. The disappearance of the multiple modes in DR in all subgroups except the intermediate (partially serrated pectoral spine subgroup) is a strong indicator of the possibility. The DR was not multimodal in the two distant groups but was present alongside AFR-a covariant normally used in taxonomy of fish.

None of the completely serrated spine subgroups' meristic phenotypes reflected multiple mode or heterogeneity with respect to coefficient of variability. The observed multiple modes in morphometric phenotypes in this subgroup could be as a result of intra sub-groups variability. This indicates that the morphological heterogeneity did not have correlation with any meristic attribute. Unification of all the heterogeneous sites upon factor analysis could indicate that the variation must have been initiated by a common factor and this could be habitat-related. Langerhans *et al.* (2003) asserts that intra-specific morphological divergence has been associated with habitat use. Hence the observation in the present study may be linked with differential habitat use resulting from presence of biomes in the catchment and or variation of the entire catchment.

Earlier observations on the catchment structure and dam management revealed that the catchment is fragmented and variations in water level are potential environmental threats to fisheries. These factors will influence differential resource use and individual

flexibility in coping with the situation. These may be responsible for the morphometric variability in the population. Moreover, omnivorous fishes have broad morphological variations probably related to lack of specialization (Horn, 1998). *Clarias gariepinus* is an omnivore. Being versatile, it can occupy diverse environments and is able to conveniently undertake walk when swimming becomes difficult. Its habitat use in a flexible environment will be reflected in most attributes as observed in this group. Hence, the heterogeneity of most traits in this group could be linked with habitat structure and variability.

PECSL was the most varied morphometric attribute in this group. This indicates that the environmental challenges were mostly felt by the trait. Pectoral spine is a walking and swimming feature. Greatest variation at the site could imply that it is a relatively plastic site. It could also indicate that habitat variation is taking greater effect on the walking and swimming activities in the catchment to which individuals were responding to at different levels. This trait could be mostly associated with habitat use in the catchment. Morphometric measures have been performed in order to reflect traits associated to habitat use (Watson and Balon, 1984; and Santos *et al*., 2011).The other paired traits were also heterogeneous and the values were similar in left and right sides. This pattern might have been equally induced by the habitat condition in the catchment.

The intermediate position of the partially serrated group was confirmed. DR and AFR were multiple-modalled despite low CV (4.47 and 6.29 %, respectively) alongside all morphometric traits. This indicates that this subgroup could be a crossbreed of the other two groups which were phenotypically distant. However, the placement of all the attributes that had multiple modes on the same principal component upon factor analysis showed that the heterogeneity in all the traits were controlled by a common factor. This might be the earlier observed size variation effect (allometry). The individuals in the sub-group belonged to groups 2 and 3 in size sub-groups. These groups were statistically different at DR. However, AFR and DR values are always considered together in developing identification keys in fish (Holden and Reeds, 1978). This indicates that they are possibly covariant. Variation at a taxonomic site will be along with some morphometric traits, depending on the taxonomic weight of the phenotype. Hence, heterogeneity at DR as a result of allometric growth pattern could have occurred alongside AFR and this could be responsible for the multiple modes in the morphometric traits. However, removal of size effect in data for assessment of morphometric heterogeneity will be relevant in ascertaining the role of size in this respect.

The pectoral fin attributes- PECSL and PECFR- were the most varied morphometric and meristic traits respectively. The PECSL maintained its most varied attribute as observed in the previous groups. The high coefficient of variability in PECFR despite being monomodal showed that the variation did not have any link with the variation in AFR and DR. Hence, the heterogeneity was independently attained. This could be linked variation in environmental condition of the catchment. Pectoral fin ray variation could be linked with demand on the fishery to swim, especially for manoeuvering, steering and fast movements. Hence, heterogeneity of the morphometric traits could be linked with variations in sites.

Resource polymorphism was reported in *Salvelinus alpines* from lake Hazen by combining morphometric variation in head, body and fin shape (Arbour, *et al*., 2011). McHenry and Lauder (2006) observed that hydrodynamic changes resulted in disproportionately increased span of fins. Variation from left and right sides was widest in PECFR 0.00-10.97 % (in left and right, respectively), the left being homogeneous, and the right heterogeneous. This could signal possibility of bilateral asymmetry in the population. Meanwhile, bilateral asymmetry-unbalanced meristic counts on the right and left halves of the body in fishes can be linked with inbreeding (Dunham, 2004). The earlier discussed environmental challenges of the catchment could necessitate the situation.

All attributes, except AFR, had multiple modes in the completely smooth pectoral spine sub-group. This was not in association with any other trait among either morphometric or meristic attributes. This situation indicates that heterogeneity in the AFR must have been independently attained due to environmental condition of the catchment. The reason could also be extended to most of the morphometric traits that were heterogeneous. PECSL and PELFR were the most varied thus indicating their relevance in monitoring within population attributes variation in morphometric and meristic traits in the catchment. The wide difference in coefficient of variation values between left and right in the traits could indicate inbreeding tendencies. However, similar mean values on both sides suggest that each side of the fin attained variation values independently. This may be as a result of differential response of the attributes to varying environmental conditions. Going by the variation pattern, the mean of pooled value of the attributes will be needed for proper identification. Also, statistical test of difference between the left and the right side values will be necessary to assess inbreeding depression because this will consider the mean values and the amount of variation.

Phena identification plays a vital role in fisheries management, aquaculture and evolution studies. Poor understanding of fish and fisheries can lead to traumatic changes in the biological attributes and productivity of a species (Smith *et al.*, 1991). The three pectoral spine sub-groups had different phena identities and could be morphological types which can be differentiated by AFL. Results indicated that C individuals had longer anal fin (AFL) than P and C. The C and S were distant, while P was intermediate. This shows an intergrading sets of individuals which can be grouped by a conspicuous character (AFL) It indicates that the PESES groups are polymorphic forms of *Clarias gariepinus* in the catchment. *Clarias gariepinus* has been described with the presence of external serration of pectoral spine (p). However, a sub-group possessing a smooth anterior spine projection (S) was discovered in this study with an intermediate between the groups (P). The discovered variety(S) was less varied at the distinguishing site (AFL). C had the greatest frequency of individual in the population, followed by S and P was the least. The relative abundance of C could be because it is relatively ancient and has established itself for a long time S will be a more recent group which may have evolved or introduced. However, the intermediate (P) could be intra-specific cross between the two varieties. This development has great biological importance because it proves the existence of selective differences between apparently neutral characters (Mayr, (1969). The polymorphic forms were morphologically divergent and could have different aquaculture potential which will be of importance in enhancing productivity.

Confirming polymorphism will requires a more precise molecular genetics back-up. This is because conspicuous characters in polymorphic individuals are frequently controlled by a single gene. The pectoral spine variation could be a product of introduction or sympatric morphs. Arbour *et al*. (2011) observe that, without an examination of the genetic relationships of morphs, the role of factors such as phenotypic plasticity and genotypic composition in determining morphological differences cannot be fully resolved. Therefore, establishing genetic relationship between the groups will be necessary.

The groups were morphometrically differentiated at anal fin length. The relevance of this attribute in differentiating morphs is mentioned by Arbour *et al*. (2011) when discussing sympatric morphs of Arctic char of *Salvelinus alpines.* Anal fin is a median fin. Lauder and Drucker (2004) note that these fins play an important role in acceleration in swimming. Long anal fin contributes to fast starts and manoeuvres by increasing thrust-producing surface area of the caudal peduncle region while small anal fin would be

beneficial in improving flow regimes across the caudal peduncle. This morphologic sub-group might have evolved as a result of necessity of adjusting to fast start and manoeuvres in swimming as demanded by flow condition of the dam catchment. Flow will be determined by dam gate-opening frequency and its dynamics. This supports the hypothesis earlier propounded when discussing dam dimension, that dam management practice of gate-opening will have effect on the fish phenotype in the catchment.

Among the vertebrates, phenotypic variability is considered to be greatest in fish which have relatively higher within-population coefficients of variation of phenotypes (Carvalho, 1993). This variability is likely to have arisen from the great phenotypic plasticity of fishes in response to changes in environmental factors (Wimberger, 1991, cited in Gunawickrama, 2007). This study also revealed that, after population delineation using pectoral spine attribute, within-population coefficient of variation of phenotypes were high in all sub-groups morphometric traits. Altogether, 75%, 83.33% and 66.67% of phenotypes in C, P and S, respectively, were heterogeneous, based on their coefficient of variation values. PECSL was the most varied attribute. This implies that phenotypic variability was recorded in the population sub-groups of most phenotypic traits in the population with PECSL being the most varied attribute. Phenotypic plasticity is an environment-induced phenotypic change that occurs within an organism's lifetime. It is likely to play an important role in the process of diversification. Fluctuating environment may have favoured phenotypic plasticity in the population

Phenotypic plasticity is involved in forming adaptive variations and resource polymorphism which may have a genetic basis (Skulason and Smith, 1995; Smith and Skulason 1996, cited in Svanback and Eklon, 2006). It is therefore, important to establish the genetic variation of the population. This would aid an understanding of the genetic nature of the population. The information will be useful for future referencing, establishing genetic link between the observed morphologic groups and genetic variation pattern of the population for management and conservation purposes.

PECSL was observed to be the most varied morphometric trait in nearly all cases. This implies indicating that the variation in this trait will not be taxon-specific (should the groups be confirmed to be genetically differentiated) but environmental factor could be implicated. This attribute is a locomotive trait, a variation of which could be as a result of hydrodynamic condition in the catchment.

McHenry and Lauder (2006) observe that locomotors in zebrafish (*Danio rerio)* disproportionately increase in span owing to hydrodynamic changes. This could be

mostly felt by this versatile and important locomotory trait. According to Gunder (2004), *C. gariepinus* possesses versatile locomotory behaviour being capable of migrating overland to another water source by sculling with its tail as it elbows along on its spines. It has versatile adaptive features and can adapt to interspecific competition and predation pressures through body size, shape, head protection, pectoral spines and piscivorous habits. This enables it to survive almost all conditions (Bruton, 1979; De Moor and Bruton, 1988). The high variation at this site may, therefore, indicate survival strategy against variably catchment condition with respect to quick start swimming and walking behaviour. *C. gariepinus* occupies marshes and swamps. Its ecological role there is discussed by Na-nakorn *et al*. (2004). Complete dam drawdown, as reported earlier in this study, might have necessitated fast quick move by *C. gariepinus* either along the draining water or a fast walk away from the draining area of the swamp as shore lines are drained. This implies adjustment of anal fin due owing the need for fast quick start swimming; and pectoral spine length to walking through distance to the hinter-land.

The effect of these on individual fish is, however, dependent on the prevailing situation of individuals' location going by the catchment structure. The Asejire catchment observed in this study was fragmented. Individual fish could therefore present individual phenotypes attained from its isolation mechanism in the fragmented area over a long time. The fragmented groups thus formed sympatriates; hence, the group could indicate sympatriates morphs. However, establishment of canonical significance of the differences between the supposed morphs will be important. It is also necessary to note that the differences between the left and the right values in the subgroups and the allometric growth pattern observed in this study further necessitates documentation of the mean of values from both sides of the body with respect to the principal factors.

(iv) Discriminant analysis: canonical basis of phenotypically discriminate subgroups

Delineating heterogeneous population by factors that may have contributed to the development is important and it could reveal evolutionary trend in species. However, identifying important discriminate factors is primary in accessing this advantage in populations. *S*ex was excluded from discriminant analysis, being an insignificant factor as its subgroups were not differentiated at any of the assessed phenotypic traits. Classification function confirmed that PESES had strong implication as a discriminant factor for the studied population. Its influence was stronger than that of size. It also had significant classification success when size effect was removed. This pattern of result

agreed with the observed trend in phenotypic studies in which size groups were differentiated by DR. Moreover, delineating the population by PESES grouping resulted in disappearance of significant difference in DR. This implies that these groups could be the major contributory factor to the observed complex DR pattern that was earlier observed in size subgroups. Identifying this attribute as a strong discriminate factor agreed with the earlier observation that this attribute is similar to that reported in Martin and Birmingham (2000) and Beland (2004). The authors discovered that pectoral spine variation in *Pimeloda chagressi* had genetic basis, as the subgroups were found to be subspecies (haplotypes). The significant grouping of the PESES group may be confirming that the groups are morphotypes (variants) of the population. Morphs could either be based on resources (environment) or genotypic polymorphism. Mayr (1969) suggests biochemical/ electrophoresis differentiation tests in assessing morphs genetic basis.

5.1.3.3 Biochemical and genotypic structure of pectoral spine sub-groups *of C. gariepinus*

Biochemical analysis of total protein and isozyme markers has revealed better diagnostic genetic potential and is usually free from genotype X environment interactions (Lombard *et al.*, 2001; Torkpo *et al.*, 2006). This was confirmed in this study. Polymorphism of bands across groups as observed in this study showed the usefulness of the SDS PAGE as a biochemical methodxa of genotyping with respect to the studied populations.

Although most of the generated bands were within 14.7 and 100KDa, band A" with lower molecular weight (< 14.7KDa) was inherited by 75% of members of the S group, the C subgroup did not show the band. This was also supported by the result of the canonical classification which showed that the phenotypic subgroups were completely different from each other as observed in the phenotypic characterization.

Nucleic acid molecules are size-separated with the aid of an electric field where negatively charged molecules migrate toward the anode (positive) pole. The migration flow in electrophoresis is determined by the net charge density (the ratio of charge to molecular weight). Small weight molecules migrate faster than larger ones (Sambrook and Russel, 2001). The S subgroup individuals were also grouped by similarity matrix and canonical classification to be distinctively different from the other subgroup. Analysis of genetic relationship in morphological divergence groups is a kind of characterization that could generate varieties or breeds in fish stocks. It could be of importance in genetic

improvement, management and conservation, especially when markers for subspecies identity are available. Based on the result of the protein electrophoreses, the subgroups were observed to be genetically discriminant groups, which can be differentiated by allele A. This allele could, therefore, be observed as a potential marker for deciphering the morphologic subgroups, as the allele A tend to be controlling the absence or presence of the pectoral spine attribute (PESES). This knowledge could be of use in genetic improvement of the *C. gariepinus* species via Marker-Assisted Selection. Omitogun *et al*. (2001)haveobserved that genes controlling each character can be mapped and isolated to complement and hasten the work of breeders for genetic improvement.

Electrophoresis is a sieving process for proteins and this is based on molecular weight of nucleic acids. Allele A" had the lowest molecular weight. The low molecular weight allele could be linked with α-amylase inhibitor. Gatehouse (1979) and Machuka (2001) determined the position of proteins using standard low and high molecular weight markers in Kilodalton, such as: phosphorylase B,94; bovine serum albumin, 67; ova-albumin, 43; carbonic anhydrase, 30; trypsin inhibitor, 20.1 and α-amylase inhibitor, 14.4. All the proteins reported by these authors were within medium range proteo-ladder (14.7-100 kDa). The position of allele A" was observed in this study to be the closest to 14.4 which corresponds to the molecular weight of α-amylase inhibitor.

Alpha-amylases is a family of enzymes that hydrolyse α-D-(1,4)-glucan linkages and plays an important role in the carbohydrate metabolism of many autotrophic and heterotrophic organisms (MacGregor *et al.,* 2001). It is primarily used in heterotrophic organisms to digest starch in their food sources (Silva *et al*., 2000). Alpha-amylase activities have been reported in pancreatic tissues, liver and heart of fish species. Froystad *et al*. (2006) reported low amylase activity in Atlantic salmons' intestinal content; the activity was about half of the activities measured in Atlantic cod while activities in rainbow trout was fourteen times higher. Alpha-amylase would also be active in *C. gariepinus* but report on this was not encountered.

However, α-amylase and proteinase inhibitors are attractive candidates for the control of starch-dependent organisms and have been used in control of seed weevils (Franco *et al*., 2000). Protein inhibitors of α-amylase are believed to make plants less palatable, even lethal to insects (Sasikiran *et. al.,* 2002); they are starch blockers, preventing dietary starches from being digested and absorbed by the body (McEwan *et. al*., 2010). Ali *et al*. (2006) note that it could be useful in treating obesity and diabetes mellitus resulting from defects in insulin secretion. This information is relevant in

nutrition and medicine because inhibitory activity of amylases in food source could cause a marked decrease in the availability of digested starch in the consumers and in diabetic patients.

Detection of α-amylase inhibitor in almost all the members of the S group could therefore, indicate that although the subspecie may not have comparative advantage of being highly palatable and efficient in digesting and absorbing starches when compared with the C sub- group; they will however, be of potential use in treating obesity and diabetes mellitus in humans. Extensive research has been conducted on the properties and biological effects of these inhibitors in plant physiology, animal and human nutrition because of their possible importance (Garcia-Olmedo *et al.,* 1987, Silano, 1987). Alpha-amylase inhibitors could be manipulated through genetic engineering (Wang *et al*., 2006) and could be isolated and purified from specimens (McEwan, 2010).

Separation of the species by the presence of a proteinase inhibitor may have evolutionary basis. Such evolutionary trend could come from pressures of various kinds and may be phylogenetically related. Proteinase inhibitors are a potential model system that is used to study basic evolutionary processes, such as functional diversification (Christeller, 2005). Morphological studies had earlier observed existence of functional disparity in the subspecies. In conclusion, pectoral spine subgroups in *C. gariepinus* were biochemically separated by the presence or absence of alpha-amylase inhibitor, which is of nutritional and medical importance to consumers. However, the groups could have developed into these sub-species as a result of evolutionary factors. McAllister *et al.,* (1997) aver that the global number of proportion of species-level biota, animal, plants and micro-organisms that occur in fresh water is not precisely known. This study has therefore increased knowledge with respect to sub-species level in *C. gariepinus* (the most important aquaculture species in freshwater ecosystems in Nigeria.

5.1.3.4 Genotypic variability and inheritance of RAPD DNA markers by pectoral spine sub-groups of *C. gariepinus*

Presence of genetic diversity as well as morphological characteristics in strains proffers easy and quick isolation method for research and industrial analysis (Lather *et al.,* 2010). Knowledge on genetic variation in *genus Clarias* is important as it will facilitate better identification (Teugels, *et al*., 1992; Agnese *et al*., 1997; Rognon *et al*., 1998) as well as assist in detection of introgression and hydridization with other species (Billington *et al*., 1996).

The result of the investigation on genetic variability of the studied population using RAPD-DNA marker revealed variation in both within and between sub-groups of *C. gariepinus*. This suggests that the population expressed genetic heterogeneity. This agreed with the earlier reported observation of heterogeneous phenotypic structure of the population.

The RAPD primers were polymorphic in the population and its sub groups It also established pattern of intra-and inter-group variations, thus showing the efficiency of the RAPD primer in molecular genetics studies in the populations It also supported the usefulness of the RAPD primer in genetic studies in *Clarias gariepinus* as discussed by Ali *et al.* (2009) and in genetic variability studies as reported in Almeida and Sodre (2002), Quibai *et al*. (2006) and Hung *et al.* (2005). Although similar percentage band frequencies were obtained in the two PESES subgroups the PESES subgroup individuals were more polymorphic than the non-PESES.

Canonical classification analysis of the genotypic data showed 100percent differentiation of the subgroups' genotypes, presence of private alleles and the subgroups can be differentiated using OPAF-07. These indicate a potential advantage in marker assisted selection for these potential *C. gariepinus* varieties. This observation may have implications apart from taxonomy; Saad *et al.* (2009) note that generated RAPD-DNA markers may be associated with DNA regions which affect economic characters. Moreover, earlier studies on biochemical differentiation of the sub-groups revealed a differentiating marker that has nutritional and medical importance. The identified locus in this study may be confirming that the earlier observations has DNA basis and their differences will be heritable. The UPGMA dendrogram agreed with the phena classification of the pectoral spine groups thus indicating that the sub-groups are genetically different.

Within-population variation was observed in both groups. This indicates that the populations were genetically heterogeneous. Earlier phenotypic studies on the population revealed that the *Clarias gariepinus* population obtained from the Asejire dam was heterogeneous and that within phena groups variation existed. The current result may, therefore, be confirming that the pattern has genetic basis.

However, genetic variability of the stock will have to be maintained in order to sustain the fishery. This is because of the reported decreasing population size of *C. gariepinus* in Asejire dam coupled with expanding pressure on its use for research and mass propagation (FAO, 2012). Smallness of population in fragmented catchment, like

the study area, will facilitate in-breeding and its attendant depression in the future. However, the variability pattern, as documented in this study, would be useful in monitoring and maintenance of C. *gariepinus* genetic pool in the catchment. Maintenance of genetic variability of broodstock will involve minimizing mating of closely related individuals (Boliver and Newkirk, 2002). Saad *et al.* (2009) note that failure to maintain stocks genetic variability in *Oreochromis niloticus* families could be attributed to uncontrolled mating of closely related individuals. However, minimizing mating of closely related individuals in the study area may not be feasible going by its observed fragmented structure, as earlier presented, and *C. gariepinus* declining stock in the catchment (Omoike, 2004, and the present study). Moreover, this will be heightened by the pressure on its fisheries as major source of wild broodstock for research and mass propagation (FAO, 2012), hatchery stock improvement, coupled with its reproductive versatility (Nukwan *et al.*, 1990) and the sporadic growth of hatcheries in the region. However, collections from the capture environment could be isolated in a special hatchery with a scientific breeding programmes and produced through rotational mating selection (RMS) method (PNGS, 2007) but this has to be done under restricted management in order to achieve the desired objective (Saad *et al*., 2009).

In conclusion, the pectoral spine variants are genetic variants and are potential varieties for *Clarias gariepinus*, the RAPD primers are suitable genetic markers establishing variability in the populations, while the detected markers will be useful especially in planning breeding programmes based on marker assisted selection (MAS) and cloning specific genes in the sub-species. Bowditch *et al.* (1993) aver that detection of genetic variation is essential to a wide range of comparative genetic research endeavours, which include gene mapping, individual identification, parentage determination, population genetics and molecular phylogenetics. The findings in this study has have wide application in utilization and management of genetic resources in *C. gariepinus*.

5.1.3.5 Inbreeding tendency and mean values of paired fins in *C. gariepinus* population in Asejire Lake

Inbreeding affects reproductive success (Slate *et al*., 2000) and survival (Keller *et al*,. 2001). However, it could be utilized in aquaculture via selective breeding (Tave, 1995) but excess of inbreeding results in excessive homozygosity and sometimes failure in meiosis. This is often referred to as inbreeding depression. Too much homozygosity

can be detrimental to individuals or a population's survival traits and fitness; highly homozygous species has severe reproductive problems and this is linked to bilateral asymmetry-unbalanced meristic counts on the right and left halves of the body in fishes (Dunham, 2004).

The result of the assessment of inbreeding tendencies and morphologic values of paired fins revealed that the numerical differences in the left and right side values were not enough to establish inbreeding situation. Values from both sides of the body could be used in establishing bilateral asymmetry in fish and this is useful in tracing inbreeding depression (Dunham, 2004). However, none of the assessed phenotypes revealed bilateral asymmetry. However, the differences although insignificant, suggest the possibility of inbreeding effects in the future. Heterogeneity in some phenotype was also observed in most of the phenotypes and in all subgroups of size and pectoral spine, with pectoral fins attributes (PECSL and PECFL) being the most varied. This indicates that, despite delineation using either size or pectoral spine variant groups, heterogeneity with respect to pectoral fin, especially spine length, still existed. This development could be confirming the catchment relevance of the heterogeneity. This could be as a result of differences in habitat use by individuals of the subgroups owing to their location-based differences with respect to biotic and abiotic conditions.

Kessler *et al*. (1995) assert that four benthic darter species have differences in habitat use in streams at high flow. This difference was found to correspond to differences in morphology. Two of the four species had robust bodies and large pectoral fins, which allowed them to withstand currents on smaller, smoother substrata. Earlier in this study, water flow condition as a result of dam gate-valve opening have been noted as having influence on *C. gariepinus* phenotypes in Asejire reservoir. The present observation corroborates Wainwright and Richard (1995) and Santos *et al.* (2011), who claim that community patterns of food and habitat use as well as dam construction influences morphological traits of species.

CHAPTER SIX

CONCLUSION AND RECOMMENDATIONS

6.1 Conclusion

The results from this study have shown that the genetic structure of *Clarias gariepinus* population in Asejire Lake is being influenced by both environmental and genetic factors. A summary of the conclusions are presented thus:

Tendencies of climatic change effect were observed from the obtained data from the catchments neighborhoods, indicating that climatic change effects could as well be influencing Asejire fisheries.

Assessment of the catchment condition revealed degraded watershed, catchment fragmentation, loss of 8.5 % of the total catchment area, hydrologic area reduction as a result of siltation and loss of flora diversity as potential threat to fish abundance and diversity in the catchment. Also, tendencies of metallic contamination, sometimes spatial fluctuating and limiting nutrients which emanated from industrial activities at Asejire Lake were also identified. Apart from watershed degradation, which was caused by uncontrolled anthropogenic activities, frequency of opening of the dam's gate (dam management techniques) was observed to be central to most of the catchment-based threat factors

Catch structure agreed with Omoike (2004) with respect to declining diversity but greater catch was obtained in this study, which was linked with sampling technique. *Clarias gariepinus* reflected declining status in this study, just as reported in Omoike (2004), while fish abundance and diversity varied significantly ($p<0.05$) across strata.

Variants of *C. gariepinus* based on possession of anteriorly serrated pectoral spine were discovered during phenotypic characterization in this study. Population genetic studies revealed heterogeneous phenotypes of which pectoral spine attributes (PESES) and pectoral spine length (PECSL) were the most varied meristic and morphometric attributes and these were linked with genetic and environmental factors, respectively. Heterogeneous pectoral spine phenotypic value was linked with adaptation to dam gate manipulation, while PESES was linked with presence of morphs.

Sex was not significant as discriminant factor for the population. However, size and possession of anteriorly serrated pectoral spines (PESES) were significant. Based on canonical classification analysis, possession of anteriorly serrated pectoral spines (PESES) was a comparatively stronger discriminant factor when compared with size

effect (allometric growth) in the studied population. Possession of anteriorly serrated pectoral spines (PESES) variants were considered as sympatric morphs of the studied *C. gariepinus* population.

Electrophoresis/biochemical analysis confirmed the genetic and biochemical differences between the morphs of the possession of anteriorly serrated pectoral spines (PESES) and markers for their genetic differentiation were discovered. One of the morphs (variants) was suspected to have potential for nutritional and medical importance.

Genetic variability of DNA fragments of the population confirmed the usefulness of RAPD markers in the DNA testing for the populations. Genetic variability test revealed the suitability of the population as brood stock and for stock improvement, as within and between subgroup genetic heterogeneity was observed in the population. Phenotypic traits assessment for signs of inbreeding depression corroborated the genetic heterogeneity results as phenotypic indices were not observed.

In summary, apart from climatic factor that is somehow global, dam gate-valve opening and watershed land use are major intrinsic physical conditions that have to be monitored in ensuring sustainability of genetic resources in Asejire reservoir environment. Utilization and identification of *C. gariepinus* in the catchment would require recognition of the observed genetic variants.

6.2 Recommendations

Based on the above conclusion, it is important to take holistic approach in management of both the environmental and genetic components of Asejire Lake for sustenance of the benefits of wild fisheries resources. The following recommendations could however be useful in achieving this objective.

The Nigeria government should create awareness in order to change people's orientation on biological and socio-economic importance of dammed river courses. Developing strategies on reducing human population increases at watersheds. Management of increased anthropogenic activities at the watersheds should be considered as a matter of priority by stakeholders. This will be useful in preservation of the physical and biological conditions of Asejire Lake. It is also recommended that proactive methods of reducing socio-economic challenges of rural and peri-urban people should be put in place by local and national governments, as this will go a long way in future plan for conserving the fisheries.

When the use of gate-valve design for lake water management is unavoidable, strict monitoring of frequency of opening of the dam's gate-valve by the dam's management should be instituted. Regulations on watershed forest protection have to be strictly enforced for the catchment.

Fluctuation of some nutrient concentration could be a major reason why some migratory species, like *Chrysichthys sp.* and *Macrobrachium sp.*, were dominant in the catchment. *Macrobrachium* species has economic and export potentials. The identified site for the *Macrobrachium* species could therefore be a useful site for their biology and cage culture if utilized. Further studies on the biology (reproduction and survival) of these species in Asejire Lake are also recommended.

Going by the observations on the genetic structure of *C. gariepinus* in the catchment, Government should start to develop specialized hatcheries where pure strains of economically important but declining fisheries can be mass produced, preserved and improved. Development of Cryopreservation facilities at such centered would also be helpful in quality maintenance of indigenous fishery resources as well as conservation of threatened species.

The observed trend of consistent decline in wild fisheries, of which the studied location is a good example, points to the need for the government to embark on re-stocking programmes for the declining stocks as well as encourage research into breeding and conservation of the observed decimating indigenous species.

Lack of adequate combined data on environmental condition alongside the genetic structure has not allowed better holistic management of wild fish resources. It is, therefore, recommended that a combination of geographic mapping as well as fish population and genetic structure of all Nigeria water bodies be taken as priority.

The potential of the discovered variants of the *C. gariepinus* must be extended to the end users while further research on their potential has to be carried out. The detected genetic markers are potential tools for marker-assisted selection and sub-species identification. This should be encouraged, especially for *C. gariepinus*-based research endeavours. The markers are also tools for genetic improvement.

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Appendix 1

Coordinates of surveyed sites during preliminary survey of Asejire Lake's Catchment (November, 2009)

S/N	Longitude.	Latitude	HEIGHT	REMARK
1.	31N0625356	0813897	4	
2.	31N0625386	0813874	3	end
3.	31N0625324	0813889	6	Oswcos
4.	31N0625281	0813901	5	
5.	31N0625206	0813915	5	
6.	31N0625203	0813917	5	dam
7.	31N0625121	0813951	5	dam
8.	31N0625114	0813940	5	
9.	31N0625048	0813959	5	
10.	31N0625030	0813960	4	Weir pump
11.	31N0625027	0813960	4	’’
12.	31N0625031	0813975	5	’’
13.	31N0625024	0813981	5	’’
14.	31N0624971	0812988	3	
15.	31N0624945	0814119	4	Cocacola plt.
16.	31N0624947	0814124	4	’’
17.	31N0624924	0814120	5	’’
18.	31N0624881	0814144	4	’’ LS
19.	31N0625015	0814231	3	NBL Pump
20.	31N0625012	0814226	3	’’
21.	31N0624895	0814703	3	’’
22.	31N0624969	0815026	4	poor vegetation & bamboo
23.	31N0625044	0815108	4	’’
24.	31N0625050	0815175	3	papa asala ent.
25.	31N0625036	0815181	4	’’
26.	31N0625061	0815235	4	’’
27.	31N0624870	0815249	3	’’
28.	31N0624869	0815280	3	’’
29.	31N0624878	0815330	3	’’

30.	31N0625056	0815313	3	’’
31.	31N0625066	0815303	3	’’
32.	31N0625091	0815296	4	’’
33.	31N0625377	0813881	4	Osun end
34.	31N0624961	0813973	4	Oyo end
35.	31N0625813	0817651	2	Koloko junc.
36.	31N0625872	0818393	4	Confluence breeding site
37.	31N0626079	0818138	4	’’
38.	31N0626132	0818137	4	Agora junc
39.	31N0626317	0818175	4	Agora junc. rock.
40.	31N0626338	0818202	3	Agora end
41.	31N0626674	0818422	5	’’ LS
42.	31N0626699	0818441	4	’’ ‘’
43.	31N0626862	0818519	3	’’muddy & weedy end
44.	31N0626839	0818663	3	’’
45.	31N0626774	0819139	4	’’
46.	31N0626827	0819290	4	’’
47.	31N0626902	0819274	5	’’end of visible end
48.	31N0626215	0817756	4	rocky
49.	31N0625850	0815729	4	Ikire ent.
50.	31N0626609	0815515	-	‘’ rock outcrust
51.	31N0626639	0815512	-	‘’ ‘’
52.	31N0626933	0815406	4	’’ muddy end
53.	31N0626963	0815340	4	’’ ‘’
54.	31N0626692	0815416	3	’’ LS brd site
55.	31N0625890	0815373	4	Ikr ent.
56.	31N0625231	0815906	3	ASALA(ME)
57.	31N0625203	0816168	4	’’ M mid
58.	31N0624835	0816242	5	’’ ‘’ ‘’
59.	31N0624511	0816151	3	’’ ‘’ end1
60.	31N0624491	0816164	4	’’ cassava pt.
61.	31N0624519	0816253	4	’’ end center
62.	31N0624445	0816407	4	’’ ‘’ 2
63.	31N0624456	0816409	3	’’ ‘’ 2*

64.	31N0624619	0816344	3	’’ cassava pt
65.	31N0625220	0816337	4	’’
66.	31N0625308	0816319	3	’’ ME2
67.	31N0625373	0816389	3	entry
68.	31N0625723	0817743	3	koloko junc.1
69.	31N0625679	0817811	2	’’ ‘’ 2
70.	31N0625622	0818281	3	’’ ‘’ 3
71.	31N0625618	0818298	4	’’ ‘’ 4 end
72.	31N0626141	0818145	3	Agora junc. 1
73.	31N0626172	0818127	2	’’ ‘’ 2
74.	31N0626301	0818133	2	’’ ‘’ 3
75.	31N0626325	0818146	3	’’ ‘’ 4
76.	31N0625852	0815726	3	Ikr junc.1
77.	31N0625849	0815691	3	’’ ‘’ 2
78.	31N0626933	0815406	4	’’ end1
79.	31N0626929	0815342	3	’’ ‘’ 2
80.	31N0626770	0815408	3	’’ mid 1
81.	31N0626794	0815482	3	’’ ‘’ 2
82.	31N0626012	0815485	4	ikr junc. 1
83.	31N0626015	0815439	3	’’ ‘’ 2
84.	31N0625397	0813928	3	LS
85.	31N0625443	0813953	3	Cassava pt.
86.	31N0625524	0814259	3	Ikoyi branc.
87.	31N0625677	0814311	3	’’ rock
88.	31N0625816	0814248	3	’’ brdsite+dd eggs
89.	31N0625828	0814271	3	’’ ‘’ ‘’
90.	31N0625854	0814259	3	’’ end
91.	31N0625854	0814277	3	’’‘’,brdsite,ddfs,wd
92.	31N0625597	0814490	2	Ikoyi branc.2
93.	31N0625624	0814760	3	Ikr mi.
94.	31N0625774	0815017	3	’’ ent.1
95.	31N0625843	0815173	2	’’ ‘’ 2
96.	31N0625976	0815054	3	’’ end1
97.	31N0625983	0815075	3	’’ ‘’ 2

98.	31N0624998	0815208	4	papa(agr.,hill,ston)
99.	31N0624867	0815263	4	’’ ‘’ ‘’
100.	31N0624934	0815221	15	’’ sandbed,brd.
101.	31N0625814	0815044	3	Ikr Mi. ent.1
102.	31N0625976	0815054	3	’’ ‘’ end 1 mud
103.	31N0625983	0815075	3	’’ ‘’ ‘’ 2
104.	31N0625890	0815112	2	’’ ‘’ ent 2
105.	31N0625829	0815243	3	bamboo beside ikr
106.	31N0625809	0815253	2	’’ ‘’ ‘’
107.	31N0625714	0815259	2	HD
108.	31N0625442	0815276	2	HD
109.	31N0625039	0815158	4	EXT. BRD SITE
110.	31N0625032	0815102	6	’’ ‘’ ‘’’
111.	31N0624858	0814753	6	Brd site Exp.
112.	31N0624881	0814680	5	‘’
113.	31N0625654	0815233	2	Ikr.MTbranc
114.	31N0625977	0815569	2	Ikr.Tbranc
115.	31N062 6010	0815550	2	Iky.LS
116.	31N0626586	0815538	2	Ikr.LS
117.	31N0626007	0817374	2	Tekun area
118.	31N0626101	0817783	2	Orobo vil
119.	31N0626092	0817696	2	’’
120.	31N0626591	0818539	2	Agbora(LS)
121.	31N0626625	0818561	2	’’
122.	31N0626660	0818564	2	’’
123.	31N0626712	0818616	2	’’
124.	31N0626438	0818619	2	’’
125.	31N0624955	0818172	2	Faleti(LS)
126.	31N0624946	0818157	2	’’
127.	31N0624958	0818122	2	’’
128.	31N0625185	0817908	2	Egbeta(LS)
129.	$07^0$21’53.9	$004^0$07’49.7	2	B/D(LS)
130.	$07^0$21’43.9	$004^0$08’00.7	2	A/D(LS)
131.	$07^0$21’46.3	$004^0$08’00.4	2	DAM

132.	$07^0$21’ 36.1	$004^0$07’32.1	2	SFMKT
133.	$07^0$21’12.5	$004^0$07’28.3	2	LafunRK(LS)
134.	$07^0$24’20.8	$004^0$07’09.2	2	Olokuta(LS)
135.	$07^0$24’17.2	$004^0$07’08.5	2	‘’
136.	$07^0$24’20.5	$004^0$07’03.0	2	’’
137.	$07^0$24’30.4	$004^0$07’05.0	2	Koloko(LS)
138.	$07^0$24’31.0	$004^0$06’58.5	2	‘’
139.	$07^0$24’31.0	$004^0$06’59.5	2	‘’ Vil. Entry.
140.	$07^0$21’48.7	$004^0$07’55.0	2	Weir pump.
141.	$07^0$21’45.3	$004^0$08’07.1	2	Peter(LS)
142.	$07^0$21’45.3	$004^0$08’07.1	2	‘’
143.	$07^0$21’ 47.1	$004^0$08’08.0	2	Isobo(LS)
144	$07^0$21’ 48.3	$004^0$08’09.3	2	Oswc (LS)

Appendix 2

Sampled Sites and their Identity (January, 2010-December, 2011)

Location	Latitude	Longitude
Main Dam Course		
1 (dam shore)	7.36305	4.13531
2 (dam limnetic)	7.36294	4.13449
3 (dam profundal)	7.36305	4.13355
4 (profundal)	7.3633	4.13266
5 (dam limnetic)	7.3634	4.13208
6 (dam shore)	7.36373	4.13144
7(mid shore)	7.37289	4.13871
8 (mid limnetic)	7.37158	4.13702
9 (mid profundal)	7.3721	4.13702
10 (mid profundal)	7.37287	4.13389
11 (mid limnetic)	7.37326	4.13278
12 (mid shore)	7.37381	4.13191
13(upper)	7.3849	4.14027
14 (upper)	7.38509	4.13935
15 (upper)	7.38536	4.13844
16 (upper)	7.38577	4.1368
17(upper)	7.38593	4.13598
18 (upper)	7.38612	4.13513
Tributaries		
19 (IKMI-entry)	7.37319	4.13916
20 (IKMI-end 1)	7.37329	4.14086
21(IKMI-end2)	7.37355	4.14084
22 (IKMI-entry2)	7.37398	4.13981
23(IKMA-entry)	7.37682	4.14144
24(IKMA-mid)	7.37699	4.14596
25(IKMA-end1)	7.37552	4.14995
26(IKMA-end2)	7.37619	4.15015
27(IKMA-mid 2)	7.37775	4.14653

28(IKMA-entry 2)	7.37866	4.14138
29(ASMA-entry1)	7.38497	4.13389
30(ASMA-mid1)	7.38516	4.12994
31(ASMA-end1)	7.38573	4.12688
32(ASMA-end2)	7.38326	4.12766
33(ASMA-mid 2)	7.38359	4.12997
34(ASMA-entry 2)	7.38287	4.13224
35(ASMI-entry1)	7.37556	4.13231
36(ASMI-end1)	7.3758	4.13051
37(ASMI-end2)	7.37494	4.13059
38(ASMI-entry2)	7.37472	4.13175

- Dam= Impounded Zone of the Dam, Mid= Middle of Dam (post- tributary zone), Upper= Pre-tributary Zone , IKMI=Ikire Minor Arm , IKMA= Ikire Major Arm, ASMA= Asala Major Arm , ASMI= Asala Minor Arm.

Appendix 3

Descriptive Statistics of Spatial Values of water quality parameters of Asejire Lake (January, 2010-December, 2011)

Temperature (^{o}C)

	Wet Season				Dry Season			
Site.	Min.	Max.	Mean	S.D.	Min.	Max.	Mean	S.D.
1	26.50	31.00	29.17	2.36	27.40	31.00	29.47	1.86
2	26.50	30.00	28.83	2.02	27.40	30.50	29.30	1.66
3	26.50	31.00	29.17	2.36	27.40	31.50	30.13	2.37
4	27.00	30.50	29.17	1.89	26.10	30.00	28.53	2.12
5	27.00	31.50	29.67	2.36	26.20	31.80	29.50	2.93
6	27.00	31.00	29.50	2.18	26.10	30.00	28.70	2.26
7	26.00	30.00	28.33	2.08	25.00	32.00	29.33	3.79
8	26.00	30.00	28.33	2.08	25.00	31.00	28.67	3.21
9	26.50	30.10	28.80	1.99	25.50	31.50	29.00	3.12
10	26.80	30.00	28.77	1.72	25.40	30.50	28.63	2.81
11	25.00*	30.00	27.50	2.50	24.30	31.80	28.97	4.07
12	25.00*	32.00*	28.17	3.55	24.30	30.00	28.10	3.29
13	25.00*	31.00	27.67	3.06	24.30	33.00*	29.77	4.76
14	25.00*	31.00	27.67	3.06	24.40	32.00	29.13	4.13
15	25.00*	31.00	27.67	3.06	24.30	31.00	28.43	3.61
16	25.00*	31.00	27.83	3.01	24.30	31.00	28.43	3.61
17	25.00*	32.00*	28.33	3.51	24.30	32.50	29.43	4.47
18	25.50	31.00	28.17	2.75	24.50	31.00	28.67	3.61
19	25.00	30.00	27.67	2.52	24.30	30.00	27.77	3.04
20	27.00	31.00	29.33	2.08	26.10	29.90	28.23	1.94
21	26.60	31.00	29.20	2.31	25.50	32.00	29.50	3.50
22	26.50	31.00	29.17	2.36	25.40	28.80	27.40	1.78
23	26.60	32.00*	29.53	2.73	25.50	31.00	28.83	2.93
24	26.50	31.00	29.16	2.36	25.50	30.00	28.33	2.47
25	25.00*	31.00	27.07	3.06	25.30	32.00	29.27	3.52
26	27.00	31.00	29.67	2.31	26.00	31.00	29.00	2.65

27	25.00*	30.00	27.67	2.52	26.00	32.00	29.50	3.12
28	25.00*	31.00	27.67	3.06	24.10	31.00	28.37	3.73
29	25.00*	30.00	27.67	2.52	24.10	32.00	29.03	4.30
30	25.00*	31.00	27.67	3.06	24.00*	33.00*	29.57	4.86
31	25.60	30.00	28.20	2.31	24.70	30.00	27.93	2.84
32	25.00*	30.00	27.67	2.52	24.00*	31.50	28.70	4.10
33	25.00*	30.00	27.67	2.52	24.00*	32.00	29.00	4.36
34	25.00*	30.00	27.67	2.52	24.00*	30.00	27.67	3.22
35	25.00*	30.00	27.67	2.52	24.00*	31.00	28.50	3.91
36	25.00*	30.00	27.67	2.52	24.00*	31.00	28.50	3.91
37	25.00*	30.00	27.67	2.52	24.00*	32.00	29.00	4.36
38	25.00*	30.00	27.67	2.52	24.00*	31.00	28.33	3.79

*sites having either the minimum or maximum value

Appendix 3b

Descriptive Statistics of Spatial Values of Dissolved Oxygen (mg/l) in Asejire Lake during the Sampling Periods (January, 2010-December, 2011)

	Wet Season				Dry Season			
Site.	Min.	Max.	Mean	S.D	Min.	Max.	Mean	S.D.
1	4.30	6.20	5.27	0.95	5.10	9.00	7.20	1.97
2	5.70	6.50	6.20	0.44	3.60	9.50	6.87	3.00
3	3.90	5.00	4.63	0.64	3.50	9.20	6.67	2.90
4	3.50*	6.50	4.63	1.63	3.20	9.50	6.73	3.22
5	4.10	5.00	4.67	0.49	4.20	9.00	6.83	2.44
6	3.80	6.20	5.00	1.20	4.40	9.30	7.10	2.49
7	4.80	6.10	5.37	0.67	5.10	8.80	6.90	1.85
8	5.50	7.20	6.23	0.87	5.00	8.50	6.73	1.75
9	6.70	7.00	6.83	0.15	3.90	9.60	7.07	2.90
10	6.70	7.40	6.96	0.38	5.50	8.10	6.67	1.32
11	5.30	6.40	6.03	0.64	5.20	9.20	7.17	2.00
12	4.80	5.00	4.93	0.12	5.90	7.40	6.50	0.79
13	5.40	6.80	6.17	0.71	6.10	7.60	6.70	0.79
14	6.30	7.50	7.00	0.63	6.40	8.00	6.93	0.92
15	6.50	7.60	7.03	0.55	4.80	8.00	6.40	1.60
16	5.10	8.00	6.83	1.53	6.10	8.60	7.17	1.29
17	6.30	6.80	6.63	0.29	6.20	8.30	7.00	1.14
18	5.20	6.30	5.73	0.55	5.00	6.20	5.60	0.60
19	6.50	7.70	6.93	0.67	5.10	6.20	5.63	0.55
20	6.70	7.40	7.13	0.38	6.00	7.10	6.53	0.55
21	5.40	7.60	6.77	1.19	4.60	9.20	6.97	2.30
22	6.30	8.10*	7.17	0.90	6.40	10.00*	7.97	1.84
23	6.40	7.30	6.90	0.46	5.00	8.10	6.50	1.55
24	7.20	7.90	7.60	0.36	4.20	8.10	6.23	1.96
25	5.30	7.40	6.23	1.07	1.80	9.10	5.97	3.76
26	6.20	7.50	6.73	0.68	0.90*	7.20	4.97	3.53
27	5.30	7.00	6.37	0.93	3.70	4.90	4.23	0.61

28	5.30	6.70	5.83	0.76	4.90	7.20	6.03	1.15
29	5.20	7.50	6.07	1.25	6.20	7.60	6.80	0.72
30	5.20	7.00	6.13	0.90	7.40	9.80	8.27	1.33
31	6.30	6.80	6.47	0.29	4.80	7.80	6.27	1.50
32	5.20	7.00	6.33	0.99	6.30	7.90	7.23	0.83
33	5.10	5.50	5.27	0.21	5.30	7.30	6.23	1.01
34	5.50	6.30	5.83	0.42	5.10	7.70	6.43	1.30
35	6.10	7.20	6.50	0.61	5.70	7.90	6.80	1.10
36	6.00	6.10	6.03	0.06	5.40	7.60	6.47	1.10
37	6.20	6.50	6.37	0.15	5.70	7.30	6.37	0.83
38	5.90	6.70	6.27	0.40	5.30	7.30	6.20	1.01

*sites having either the minimum or maximum value

Appendix 3c

Descriptive Statistics of Spatial Values of Total Hardness (mg/l) in Asejire Lake during the Sampling Periods (January, 2010-December, 2011)

	Wet Season				Dry Season			
Site.	Min.	Max.	Mean	S.D.	Min.	Max.	Mean	S.D.
1	40.00	56.00	50.00	8.72	52.00	62.00	58.00	5.29
2	42.00	68.00	56.00	13.12	40.00	54.00	48.00	7.21
3	36.00	62.00	49.33	13.01	44.00	60.00	53.33	8.33
4	44.00	54.00	49.33	5.03	44.00	52.00	48.00	4.00
5	42.00	74.00	56.00	16.37	42.00	58.00	51.33	8.33
6	36.00	56.00	45.33	10.07	44.00	60.00	53.33	8.33
7	38.00	48.00	44.00	5.29	44.00	68.00	58.67	12.86
8	32.00	80.00	54.00	4.25	48.00	66.00	58.67	9.45
9	44.00	88.00*	60.00	24.33	40.00	44.00**	42.67	2.31
10	38.00	62.00	51.33	12.22	46.00	52.00	48.67	3.06
11	38.00	58.00	50.67	11.02	34.00	46.00**	41.33	6.43
12	44.00	52.00	48.00	4.00	44.00	62.00	54.00	9.17
13	38.00	54.00	46.00	8.00	24.00*	44.00**	39.33	5.03
14	10.00*	58.00	44.67	14.05	42.00	58.00	50.67	8.08
15	34.00	62.00	46.67	14.19	36.00	56.00	48.67	11.02
16	38.00	56.00	48.00	9.17	44.00	54.00	50.00	5.29
17	42.00	58.00	49.33	8.08	38.00	62.00	52.67	12.86
18	34.00	58.00	46.67	12.06	46.00	72.00	62.00	14.00
19	38.00	62.00	48.67	12.22	34.00	48.00**	42.00	7.21
20	36.00	54.00	47.33	9.87	52.00	62.00	57.33	5.03
21	36.00	56.00	45.33	10.07	38.00	58.00	50.00	10.58
22	40.00	68.00	49.33	16.17	54.00	60.00	56.67	3.06
23	34.00	74.00	50.67	20.82	42.00	72.00	60.67	16.29
24	40.00	68.00	50.67	15.14	44.00	54.00	48.67	5.03
25	38.00	76.00	54.67	19.43	52.00	60.00	56.00	4.00
26	42.00	76.00	56.67	17.47	58.00	70.00	64.00	6.00

27	40.00	64.00	50.67	12.22	44.00	48.00**	45.33	2.31
28	40.00	60.00	48.67	10.26	46.00	56.00	51.33	5.03
29	44.00	72.00	53.33	16.17	44.00	48.00**	46.67	2.31
30	44.00	54.00	48.67	5.03	44.00	76.00	64.00	17.44
31	44.00	56.00	50.67	6.11	42.00	60.00	52.67	9.45
32	44.00	58.00	50.00	7.21	40.00	68.00	57.33	15.14
33	42.00	54.00	47.33	6.11	46.00	94.00*	63.33	26.63
34	44.00	52.00	46.67	4.62	42.00	46.00**	44.67	2.31
35	40.00	50.00	44.67	5.03	38.00	58.00	50.00	10.58
36	38.00	58.00	48.67	10.07	50.00	62.00	56.67	6.11
37	40.00	56.00	46.67	8.33	48.00	74.00	64.00	14.00
38	40.00	58.00	48.00	9.17	48.00	54.00	50.67	3.06

* asteric on minimum values indicates critical limiting value;*asteric on maximum column indicate highest value ** asterics indicates maximum value showed limitation

Appendix 3d

Descriptive Statistics of Spatial Values of Total Alkalinity (mg/l) in Asejire Lake during the Sampling Periods(January, 2010-December, 2011)

	Wet Season				Dry Season			
Site.	Min.	Max.	Mean	S.D.	Min.	Max.	Mean	S.D.
1	60.00	72.00	66.67	6.11	76.00	194.00	116.00	67.56
2	48.00	70.00	60.67	11.37	78.00	182.00	114.00	58.92
3	46.00	72.00	60.67	13.32	78.00	142.00	99.33	36.95
4	64.00	76.00	70.00	6.00	94.00	178.00	123.33	47.39
5	58.00	72.00	64.00	7.21	56.00	162.00	92.00	60.63
6	50.00	68.00	59.33	9.02	60.00	146.00	90.00	48.54
7	12.00*	80.00	55.33	37.65	48.00	184.00	94.67	77.39
8	62.00	100.00*	74.67	21.94	56.00	184.00	100.67	72.23
9	50.00	70.00	62.67	11.02	68.00	158.00	98.67	51.39
10	42.00	68.00	58.00	14.00	70.00	188.00	110.67	67.00
11	50.00	72.00	62.00	11.14	54.00	148.00	86.67	53.15
12	56.00	70.00	63.33	7.02	52.00	166.00	90.67	65.24
13	60.00	64.00	62.00	2.00	62.00	162.00	96.67	56.62
14	60.00	72.00	66.67	6.11	68.00	154.00	99.33	47.51
15	52.00	76.00	62.67	12.22	64.00	160.00	99.33	52.78
16	54.00	70.00	62.67	8.08	72.00	184.00	110.67	63.54
17	58.00	66.00	61.33	4.16	68.00	168.00	102.00	57.17
18	66.00	74.00	70.00	4.00	76.00	152.00	102.67	42.77
19	54.00	66.00	61.33	6.43	74.00	164.00	105.33	50.85
20	46.00	64.00	57.33	9.87	60.00	128.00	83.33	38.70
21	58.00	72.00	64.67	7.02	56.00	164.00	92.67	61.78
22	66.00	80.00	71.33	7.57	76.00	146.00	100.67	39.31
23	54.00	78.00	68.00	12.49	62.00	186.00	104.67	70.47
24	56.00	72.00	66.67	9.23	52.00	136.00	80.67	47.93
25	64.00	88.00	72.00	13.87	66.00	174.00	102.67	61.78
26	60.00	88.00	70.67	15.14	74.00	204.00	118.67	73.93

27	60.00	78.00	68.00	9.17	82.00	196.00	121.33	64.69
28	56.00	76.00	66.67	10.07	80.00	208.00	124.00	72.77
29	54.00	80.00	67.33	13.01	70.00	148.00	96.67	44.47
30	52.00	72.00	63.33	10.26	66.00	180.00	104.67	65.25
31	62.00	68.00	65.33	3.06	52.00	154.00	86.67	58.32
32	54.00	66.00	61.33	6.43	56.00	174.00	96.00	67.56
33	66.00	70.00	69.33	1.15	62.00	178.00	101.33	66.40
34	58.00	66.00	62.67	4.16	76.00	152.00	102.00	43.31
35	60.00	72.00	64.67	6.43	70.00	184.00	108.67	65.25
36	56.00	74.00	63.33	9.45	66.00	142.00	96.00	40.45
37	58.00	66.00	62.67	4.16	64.00	160.00	96.67	54.86
38	60.00	72.00	64.67	6.43	78.00	182.00	114.00	58.92

Appendix 4

Correlation of Water Quality Parameters

Wet seasons correlates of temp and DO

Correlations

		TEMP	DO
TEMP	Pearson Correlation	1	-.093
	Sig. (2-tailed)		.580
	N	38	38
DO	Pearson Correlation	-.093	1
	Sig. (2-tailed)	.580	
	N	38	38

DRY SEASON CORRELATE OF TEMP AND DO

Correlations

		Vadrytemp	VAR00003
Vadrytemp	Pearson Correlation	1	.053
	Sig. (2-tailed)		.751
	N	38	38
VAR00003	Pearson Correlation	.053	1
	Sig. (2-tailed)	.751	
	N	38	38

Wet season correlate of temp and DO at O_YS

Correlations

		VAR00008	VAR00009
VAR00008	Pearson Correlation	1	-.312
	Sig. (2-tailed)		.194
	N	19	19
VAR00009	Pearson Correlation	-.312	1
	Sig. (2-tailed)	.194	
	N	19	19

Key var008/009

Wet season temp and DO correlate on OsS

Correlations

		VAR00005	VAR00006
VAR00005	Pearson Correlation	1	-.121
	Sig. (2-tailed)		.622
	N	19	19
VAR00006	Pearson Correlation	-.121	1
	Sig. (2-tailed)	.622	
	N	19	19

Key=var005/006

Dry season correlate of temp and DO at O_YS

Correlations

		VAR00015	VAR00016
VAR00015	Pearson Correlation	1	.441
	Sig. (2-tailed)		.059
	N	19	19
VAR00016	Pearson Correlation	.441	1
	Sig. (2-tailed)	.059	
	N	19	19

Key var0015/0016

Dry season temp and DO correlate on OsS

Correlations

		VAR00012	VAR00013
VAR00012	Pearson Correlation	1	-.201
	Sig. (2-tailed)		.410
	N	19	19
VAR00013	Pearson Correlation	-.201	1
	Sig. (2-tailed)	.410	
	N	19	19

Key=var0012/0013

Appendix 5

Effects of dams gate opening at Asejire Lake during January, 2010-December, 2011

Exposed underground pipes at Oyo and Osun axis of Asejire dam catchment after Lakes' water was drawn-down

Sections of exposed shore areas after Lakes water was drawn-down


High fish mortality at tributary and around impounded area after water draw-down


Exposed rock outcrop with trapped fresh water prawn. and exposed breeding site at Lake after water was drawn down during 2010-2011sampling period


Sections of exposed shore area

Sections of exposed shore area, damaged set-net and catch after Lakes water withdrawal

Appendix 6a

Fish catch and diversity at strata of Asejire Lake

(January, 2010-December, 2011)

catch by strata	wet season		on OYS		
	OCT/NOV	DEC/JAN	FEB/MAR	TOTAL	%
1	3	30	29	***62***	***8.38***
2	3	18	0	21	2.83
3	1	8	4	13	1.76
10	0	0	0	0	0
11	0	2	0	***2***	***0.27***
12	0	4	2	6	0.81
16	1	0	0	1	0.13
17	4	0	0	**4**	**0.54**
18	2	0	2	4	0.54
29	1	6	0	7	0.94
30	10	2	0	***12***	**1.62**
31	0	4	6	10	**1.35**
32	24	0	11	***35***	***4.73***
33	2	0	***0***	***2***	***0.27***
34	2	1	7	***10***	1.35
35	0	12	0	***12***	1.62
36	0	4	83	**87**	**11.76**
37	0	2	0	***2***	0.27
38	0	59	0	***59***	7.97
	53	152	144	349	47.14

Catch by strata
OSS

	OCT/NOV	DEC/JAN	FEB/MAR	TOTAL	%
4	0	1	3	**4**	**0.54**
5	0	0	0	0	0
6	2	0	62	64	8.65
7	10	0	1	11	1.48
8	1	0	0	***1***	***0.13***
9	0	0	0	0	0
13	23	3	0	26	3.51
14	3	0	0	**3**	**0.4**
15	0	0	1	1	0.13
19	0	3	47	50	6.75
20	17	0	4	21	2.83
21	7	85	0	92	12.43
22	2	2	0	***4***	***0.54***
23	3	19	36	58	7.84
24	15	0	7	22	2.97
25	2	0	4	**6**	**0.81**
26	1	12	0	13	1.75
27	1	1	3	5	***0.67***
28	7	1	2	10	1.35
	94	127	170	391	52.78

catch by strata dry season on OYS

Site	OCT/NOV	DEC/JAN	FEB/MAR	TOTAL	%
1	37	52	8	***97***	***14.87***
2	0	1	5	6	0.92
3	0	0	11	11	1.69
10	0	0	5	5	0.77
11	33	54	39	126	19.32
12	5	6	2	13	1.99
16	9	16	0	***25***	***3.83***
17	1	1	0	2	0.31
18	7	8	3	***18***	***2.76***
29	4	5	8	***17***	2.61
30	14	20	10	***44***	***6.75***
31	4	4	5	***13***	1.99
32	8	14	0	***22***	3.37
33	1	1	8	***10***	***1.53***
34	1	1	1	***3***	0.46
35	3	2	4	***9***	1.38
36	7	12	3	***22***	3.37
37	2	2	0	***4***	0.61
38	7	7	2	***16***	2.45
	143	206	114	463	70.98

catch by strata	dry season		on OSS		
Site	OCT/NOV	DEC/JAN	FEB/MAR	TOTAL	%
4	0	0	3	3	0.46
5	4	6	1	11	1.69
6	9	16	0	25	3.83
7	4	5	0	9	1.38
8	3	3	14	20	3.07
9	0	0	0	0	0
13	2	2	2	***6***	***0.92***
14	3	4	0	7	1.07
15	3	3	4	10	1.53
19	1	1	1	3	0.46
20	3	3	0	***6***	0.92
21	5	9	6	20	3.07
22	8	8	0	***16***	2.45
23	0	0	16	***16***	***2.45***
24	2	3	2	***7***	1.07
25	0	0	3	***3***	0.46
26	0	0	0	***0***	0
27	7	10	1	***18***	2.76
28	3	3	3	***9***	1.38
	57	76	56	189	28.97

Diversity of fish populations from seasons and spatial sites of Asejire Lake (January, 2010-December, 2011)

Diversity comparism of seasons

	Dry	Wet	Boot p(eq)	Perm p(eq)
Taxa S	36	35	0.346	0.164
Individuals	652	740	0	0
Dominance	0.07823	0.06915	0.021	0.019
Shannon H	3.053	2.961	0.047	0.054
Evenness e^H/S	0.5885	0.5519	0.244	0.219
Simpson indx	0.9218	0.9309	0.021	0.019
Menhinick	1.41	1.287	0.128	0.048
Margalef	5.401	5.146	0.132	0.048
Equitability J	0.8521	0.8328	0.15	0.13
Fisher alpha	8.204	7.635	0.132	0.048
Berger-Parker	0.1933	0.1243	0	0

Diversity indices for catch at spatial sites during dry seasons (sites 1-9-A-I)

	A	B	C	D	E	F	G	H	I
Taxa_S (ZERO SPECIES)	3	3	2	1	3	2	2	3	NOT DONE
Individuals	6	4	5	3	3	6	4	3	
Dominance_D	0.3889	0.375	0.68	1	0.3333	0.5	0.5	0.3333	
Shannon_H	1.011	1.04	0.5004	0	1.099	0.6931	0.6931	1.099	
Simpson_1-D	0.6111	0.625	0.32	0	0.6667	0.5	0.5	0.6667	
Evenness_e^H/S		0.9165	0.9428	0.8247	1	1	1	1	1
Menhinick	1.225	1.5	0.8944	0.5774	1.732	0.8165	1	1.732	
Margalef	1.116	1.443	0.6213	0	1.82	0.5581	0.7213	1.82	
Equitability_J	0.9206	0.9464	0.7219		1	1	1	1	
Fisher_alpha	2.388	5.453	1.235	0.5252	0	1.051	1.592	0	
Berger-Parker	0.5	0.5	0.8	1	0.3333	0.5	0.5	0.3333	

Diversity indices for catch at spatial sites during dry seasons (sites 10- 19 J to S)

	J	K	L	M	N	O	P	Q	R	S
Taxa_S	1	3	3	3	2	3	2	2	3	3
Individuals	1	4	7	3	2	5	6	2	5	3
Dominance_D	1	0.375	0.3469	0.3333	0.5	0.36	0.5	0.5	0.36	0.3333
Shannon_H	0	1.04	1.079	1.099	0.6931	1.055	0.6931	0.6931	1.055	1.099
Simpson_1-D	0	0.625	0.6531	0.6667	0.5	0.64	0.5	0.5	0.64	0.6667
Evenness_e^H/S	1	0.9428	0.9806	1	1	0.9572	1	1	0.9572	1
Menhinick		1.5	1.134	1.732	1.414	1.342	0.8165	1.414	1.342	1.732
Margalef		1.443	1.028	1.82	1.443	1.243	0.5581	1.443	1.243	1.82
Equitability_J		0.9464	0.9821	1	1	0.9602	1	1	0.9602	1
Fisher_alpha	0	5.453	1.989	0	0	3.167	1.051	0	3.167	0
Berger-Parker	1	0.5	0.4286	0.3333	0.5	0.4	0.5	0.5	0.4	0.3333

Diversity indices for catch at spatial sites during dry season (sites 20-26-T to Z)

	T	U	V	W	X	Y
Taxa_S	2	2	2	1	3	1
Individuals	4	6	5	7	4	2
Dominance_D	0.5	0.5	0.52	1	0.375	1
Shannon_H	0.6931	0.6931	0.673	0	1.04	0
Simpson_1-D	0.5	0.5	0.48	0	0.625	0
Evenness_e^H/S	1	1	0.9801	1	0.9428	1
Menhinick	1	0.8165	0.8944	0.378	1.5	0.7071
Margalef	0.7213	0.5581	0.6213	0	1.443	0
Equitability_J	1	1	0.971		0.9464	
Fisher_alpha	1.592	1.051	1.235	0.3193	5.453	0.7959
Berger-Parker	0.5	0.5	0.6	1	0.5	1

Diversity indices for catch at spatial sites during dry season (sites 27-38)

Taxa_S	3	3	3	3	3	2	3	3	3	3
2	3									
Individuals	5	4	4	7	9	6	4	3	7	8
2	7									
Dominance_D	0.36	0.375	0.375	0.3878	0.4074	0.5	0.375	0.3333	0.3469	0.3438
0.5	0.3878									
Shannon_H	1.055	1.04	1.04	1.004	0.965	0.6931	1.04	1.099	1.079	1.082
0.6931	1.004									
Simpson_1-D	0.64	0.625	0.625	0.6122	0.5926	0.5	0.625	0.6667	0.6531	0.6563
0.5	0.6122									
Evenness_e^H/S	0.9572	0.9428	0.9428	0.9099	0.8749	1	0.9428	1	0.9806	0.9837
1	0.9099									
Menhinick	1.342	1.5	1.5	1.134	1	0.8165	1.5	1.732	1.134	1.061
1.414	1.134									

Margalef	1.243	1.443	1.443	1.028	0.9102	0.5581	1.443	1.82	1.028	0.9618
1.443	1.028									
Equitability_J	0.9602	0.9464	0.9464	0.9141	0.8783	1	0.9464	1	0.9821	0.9851
1	0.9141									
Fisher_alpha	3.167	5.453	5.453	1.989	1.576	1.051	5.453	0	1.989	1.743
0	1.989									
Berger-Parker	0.4	0.5	0.5	0.4286	0.4444	0.5	0.5	0.3333	0.4286	0.375
0.5	0.4286									

Diversity indices for catch at spatial sites during wet season (sites 1-5)

	A	B	C	D	E
Taxa_S	3	2	3	2	nd
Individuals	7	3	3	3	nd
Dominance_D	0.3469	0.5556	0.3333	0.5556	nd
Shannon_H	1.079	0.6365	1.099	0.6365	nd
Simpson_1-D	0.6531	0.4444	0.6667	0.4444	
Evenness_e^H/S	0.9806	0.9449	1	0.9449	
Menhinick	1.134	1.155	1.732	1.155	
Margalef	1.028	0.9102	1.82	0.9102	
Equitability_J	0.9821	0.9183	1	0.9183	
Fisher_alpha	1.989	2.622	0	2.622	
Berger-Parker	0.4286	0.6667	0.3333	0.6667	

Diversity indices for catch at spatial sites during wet season (sites 6-10)

	F	G	H	I	J
Taxa_S	2	2	1	ND	ND
Individuals	4	5	1		
Dominance_D	0.625	0.68	1		
Shannon_H	0.5623	0.5004	0		
Simpson_1-D	0.375	0.32	0		
Evenness_e^H/S	0.8774	0.8247	1		
Menhinick	1	0.8944			
Margalef	0.7213	0.6213			
Equitability_J	0.8113	0.7219			
Fisher_alpha	1.592	1.235	0		
Berger-Parker	0.75	0.8	1		

Diversity indices for catch at spatial sites during wet season (sites 11-21)

	A	B	C	D	E	F	G	H	I	J	K
Taxa_S	2	2	1	1	1	1	2	2	2	2	2
Individuals	4	3	1	1	1	1	3	6	2	5	3
Dominance_D	0.625	0.5556	1	1	1	1	0.5556	0.5556	0.5	0.52	0.5556
Shannon_H	0.5623	0.6365	0	0	0	0	0.6365	0.6365	0.6931	0.673	0.6365
Simpson_1-D	0.375	0.4444	0	0	0	0	0.4444	0.4444	0.5	0.48	0.4444
Evenness_e^H/	0.8774	0.9449	1	1	1	1	0.9449	0.9449	1	0.9801	0.9449
Menhinick	1	1.155					1.155	0.8165	1.414	0.8944	1.155
Margalef	0.7213	0.9102					0.9102	0.5581	1.443	0.6213	0.9102
Equitability_J	0.8113	0.9183					0.9183	0.9183	1	0.971	0.9183
Fisher_alpha	1.592	2.622	0	0	0	0	2.622	1.051	0	1.235	2.622
Berger-Parker	0.75	0.6667	1	1	1	1	0.6667	0.6667	0.5	0.6	0.6667

Diversity indices for catch at spatial sites during wet season (sites 22-38)

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P
Taxa_S	3	2	2	2	3	3	2	2	2	2	1	3	1	2	1	1
Individuals	5	4	2	2	4	4	3	2	4	2	1	3	2	5	1	2
Dominance_D	0.44	0.5	0.5	0.5	0.375	0.375	0.5556	0.5	0.5	0.5	1	0.3333	1	0.52	1	1
Shannon_H	0.9503	0.6931	0.6931	0.6931	1.04	1.04	0.6365	0.6931	0.6931	0.6931	0	1.099	0	0.673	0	0
Simpson_1-D	0.56	0.5	0.5	0.5	0.625	0.625	0.4444	0.5	0.5	0.5	0	0.6667	0	0.48	0	0
Evenness_e^H/S		0.8621	1	1	1	0.9428	0.9428	0.9449	1	1	1	1	1	1	0.9801	1	1
Menhinick	1.342	1	1.414	1.414	1.5	1.5	1.155	1.414	1	1.414	1.732	0.7071	0.8944		0.7071	

Margalef	1.243	0.7213	1.443	1.443	1.443	1.443	0.9102	1.443	0.7213	1.443
1.820	0	0.6213		0						
Equitability_J	0.865	1	1	1	0.9464	0.9464	0.9183	1	1	1
1		0.971								
Fisher_alpha	3.167	1.592	0	0	5.453	5.453	2.622	0	1.592	0
0	0	0.7959	1.235	0	0.7959					
Berger-Parker	0.6	0.5	0.5	0.5	0.5	0.5	0.6667	0.5	0.5	0.5
1	0.3333	1	0.6	1	1					

Correlation of Seasons and Stratas' Catches

Paired Samples Statistics for wet (VAR00002**) and dry (**VAR00003**)seasons catches**

		Mean	N	Std. Deviation	Std. Error Mean
Pair 1	VAR00002	17.1579	38	24.42144	3.96168
	VAR00003	19.4737	38	25.17800	4.08441

Paired Samples Correlations for wet (VAR00002**) and dry (**VAR00003**) seasons catches**

		N	Correlation	Sig.
Pair 1	VAR00002 & VAR00003	38	.175	.295

2tailed =0.667

Paired Samples Statistics for catches from strata during wet season

		Mean	N	Std. Deviation	Std. Error Mean
Pair 1	Oyswetcatc	18.3684	19	24.64912	5.65490
	Osswetcatc	20.5789	19	26.32345	6.03901

Paired Samples Correlations for catches from strata during wet season

		N	Correlation	Sig.
Pair 1	oyswetcatc & osswetcatc	19	-.193	.428

Sig 2tailed=.810

Paired Samples Statistics for catches from strata during dry season

		Mean	N	Std. Deviation	Std. Error Mean
Pair 1	Oysdrycatc	24.3684	19	32.60063	7.47910
	Ossdrycatc	9.9474	19	7.30657	1.67624

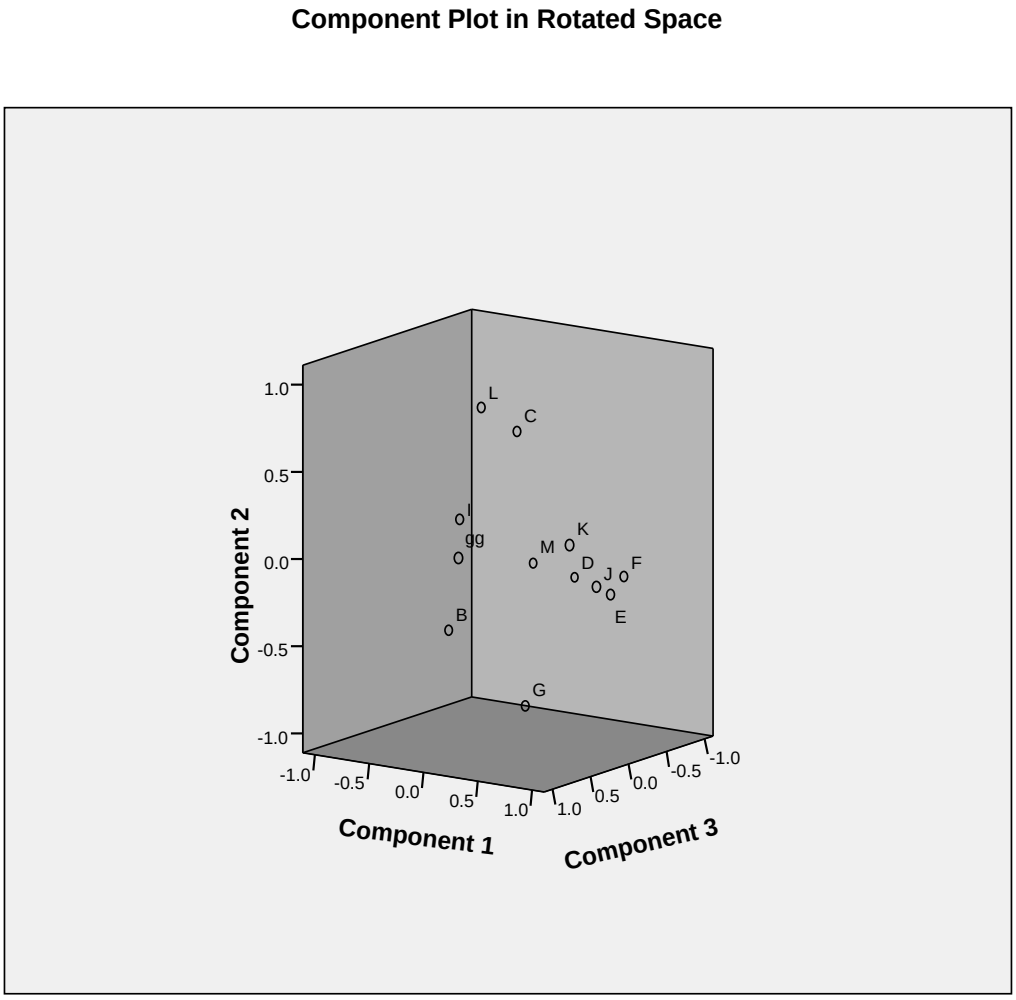
Paired Samples Correlations for catches from strata during dry season

		N	Correlation	Sig.
Pair 1	oysdrycatc & ossdrycatc	19	.067	.786

Sig. 2tailed=.072

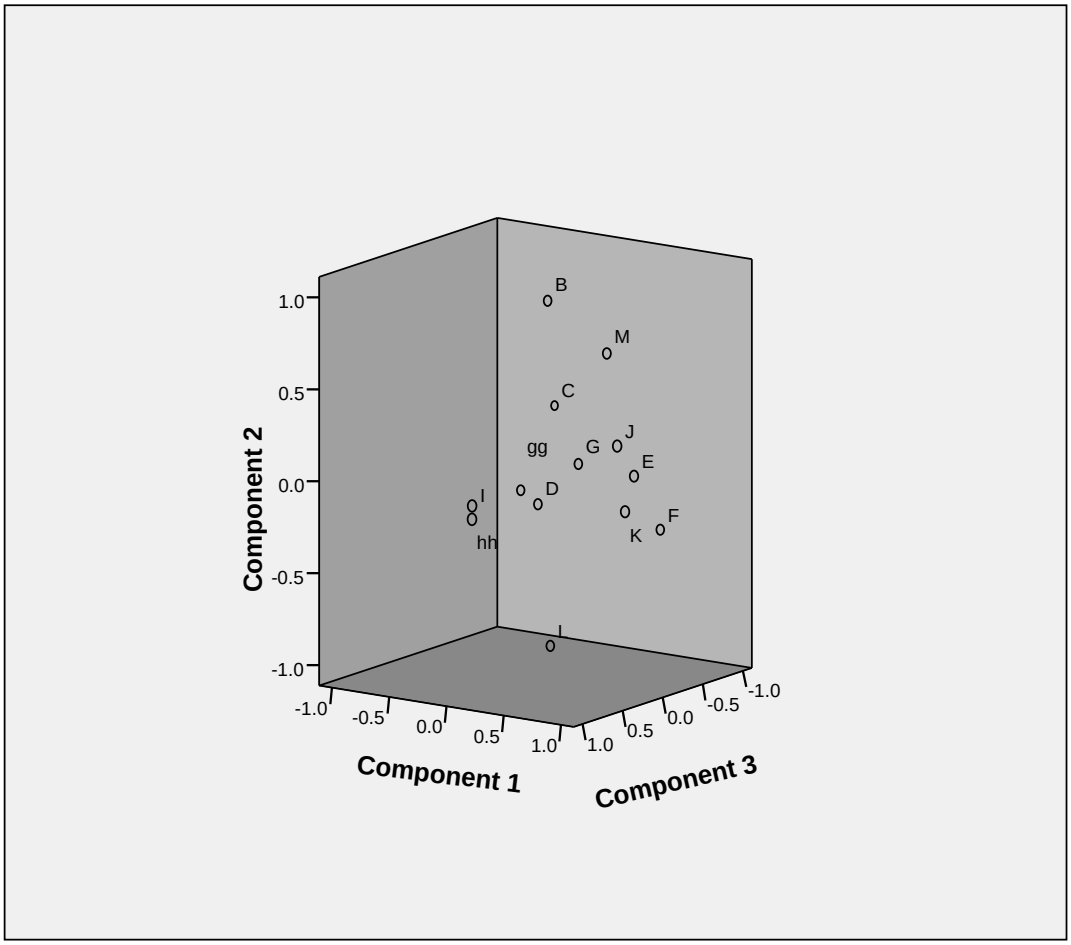
Appendix 7a
Factor analysis of heterogeneous phenotypes of

***C. gariepinus* phenotypes**



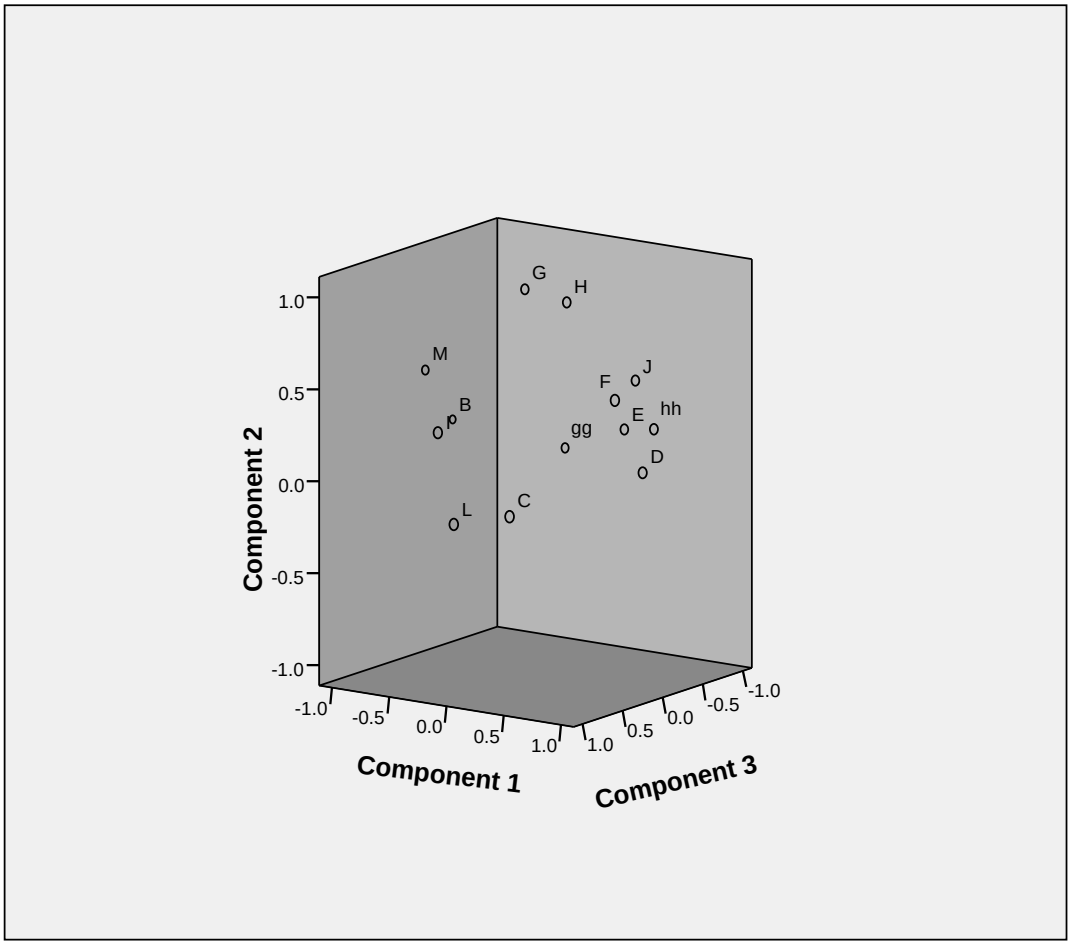
Iterations of multi-modal attributes of *C. gariepinus* population (Total population)

*** G* was represented as gg in box and it indicate the meristic attribute DR (G)* ; other alphabets represents attributes as described in previous Table.**



Iterations of multi-modal attributes of female subgroup of *C. gariepinus*

***asteric indicates meristic attributes; Alphabets represents attributes as described in previous table**



Iterations of multi-modal attributes of male subgroup of *C. gariepinus*

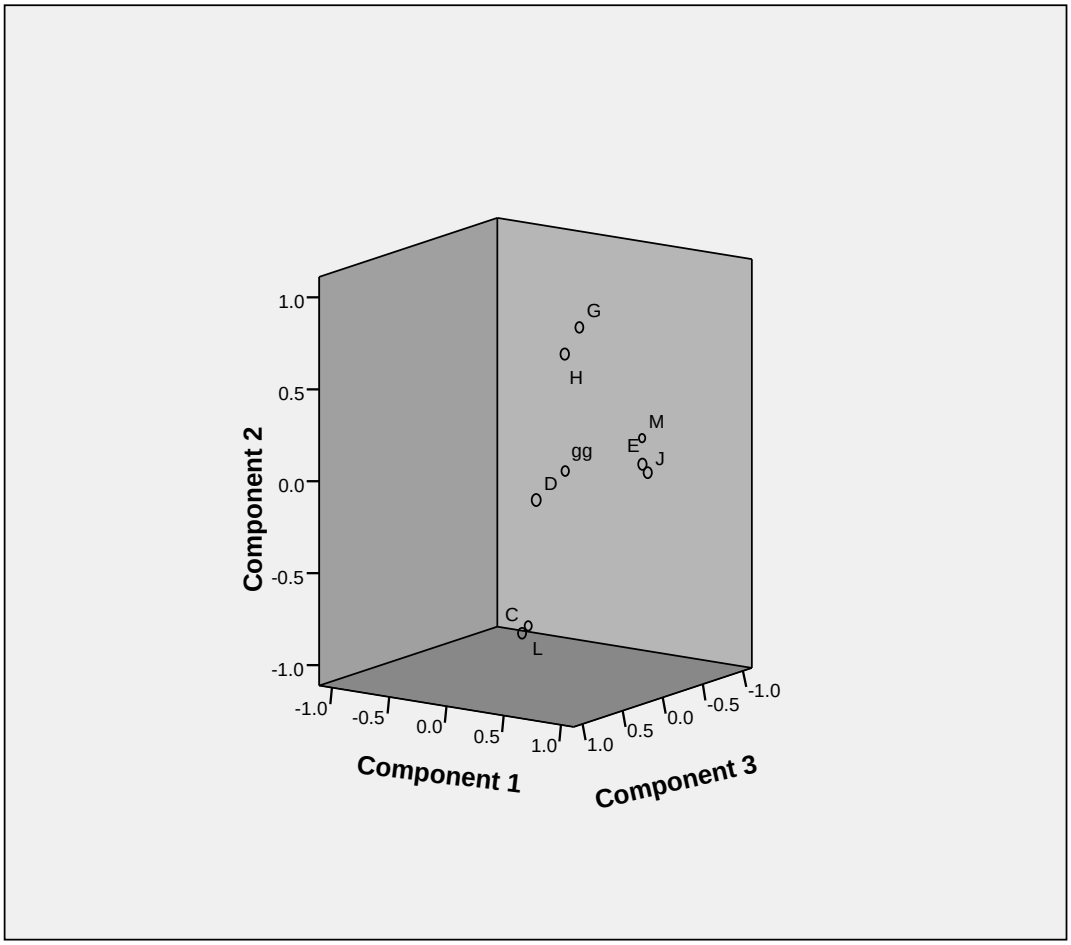


Figure 11: Iteration of multimodal attributes of Size group 2

Appendix 7b

Attribute Preference on Extracted Latent Components in multimodal phenotypes of *C. gariepinus* Population

Component preferred	Preferred attributes	% Number of attribute
1	E,F,G,J, K	41.66
2	C,L	16.67
3.	B,G*	16.67
4	D,I,	16.67
5	M	8.33

***asteric indicates meristic attribute; Alphabets represents attributes as described in previous table**

Attributes Preference on Extracted Components with Reference to multimodal Attributes in Female *C. gariepinus* Population

Component attribute preferred	Preferred attributes	% Number of
1	E, F, G, J, K, M	46.15
2	I, L, H*	23.08
3.	C, D,	15.08
4	B	7.69
5	G*	7.69

***asteric indicates meristic attribute; Alphabets represents attributes as described in previous table**

Attributes Preference on Extracted Components with Reference to multimodal Attributes in Male *C. gariepinus* Population

Component preferred	Preferred attributes	% Number of attribute
1	D, E, F, J, H*	38.46
2	C and L	15.39
3.	B, G, H, I and M	38.46
4.	G*	7.69

Attribute Preference on Extracted Components with Respect to multimodal Attributes in Size Group 2

Component preferred	Preferred attributes	% Number of attribute
1	E ,G, H, J	44.44
2	C, D and L	33.34
3.	M	11.11
4.	G*	11.11

***Meristic attributes**

Appendix 8

Discriminant analysis of phenotypic values

Eigen values

Function	Eigenvalue	% of Variance	Cumulative %	Canonical Correlation
1	10.771(a)	92.9	92.9	.957
2	.821(a)	7.1	100.0	.671

a First 2 canonical discriminant functions were used in the analysis.

Wilks' Lambda

Test of Function(s)	Wilks' Lambda	Chi-square	df	Sig.
1 through 2	.047	24.521	22	.321
2	.549	4.796	10	.904

Standardized Canonical Discriminant Function Coefficients

	Function	
	1	2
Hl	7.777	-.134
Bdmax	-2.677	.939
Bdmin	-4.261	-.254
pecfll	6.293	.842
pecflr	6.370	-1.488
pecsll	6.436	2.900
pecslr	4.110	-.444
Dl	19.203	1.664
pelfl1	3.840	4.436
pelflr	-1.293	-1.783
Afl	7.816	2.488

Structure Matrix

	Function	
	1	2
afl	.146(*)	.116
pecflr	.144(*)	.085
pecslr	-.078(*)	.066
pecfll	.063(*)	.020
pecsll	-.164	.254(*)
bdmin	.052	-.199(*)
bdmax	.068	.188(*)
dl	.026	-.178(*)
pelflr	.094	.126(*)
pelfll	.069	.089(*)
hl	-.041	-.076(*)
cfl(a)	-.011	-.036(*)

Pooled within-groups correlations between discriminating variables and standardized canonical discriminant functions

Variables ordered by absolute size of correlation within function.

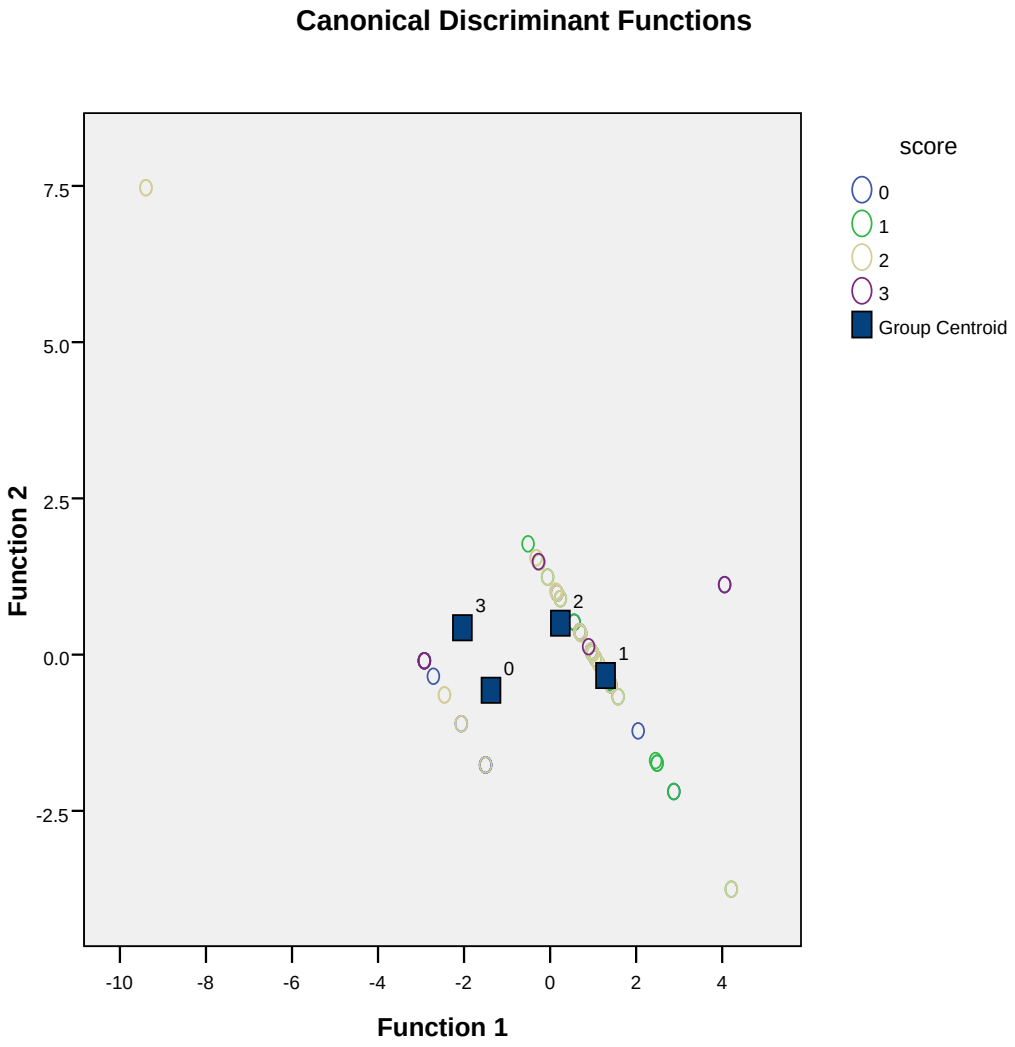
* Largest absolute correlation between each variable and any discriminant function

a This variable not used in the analysis.

Functions at Group Centroids

	Function	
score	1	2
.00	-1.504	1.352
1.00	-6.800	-1.070
2.00	1.962	-.327

canonical discriminant functions evaluated at group means



Plot of the size groups on canonical variation functions

*0= Group 1

1= Group 2

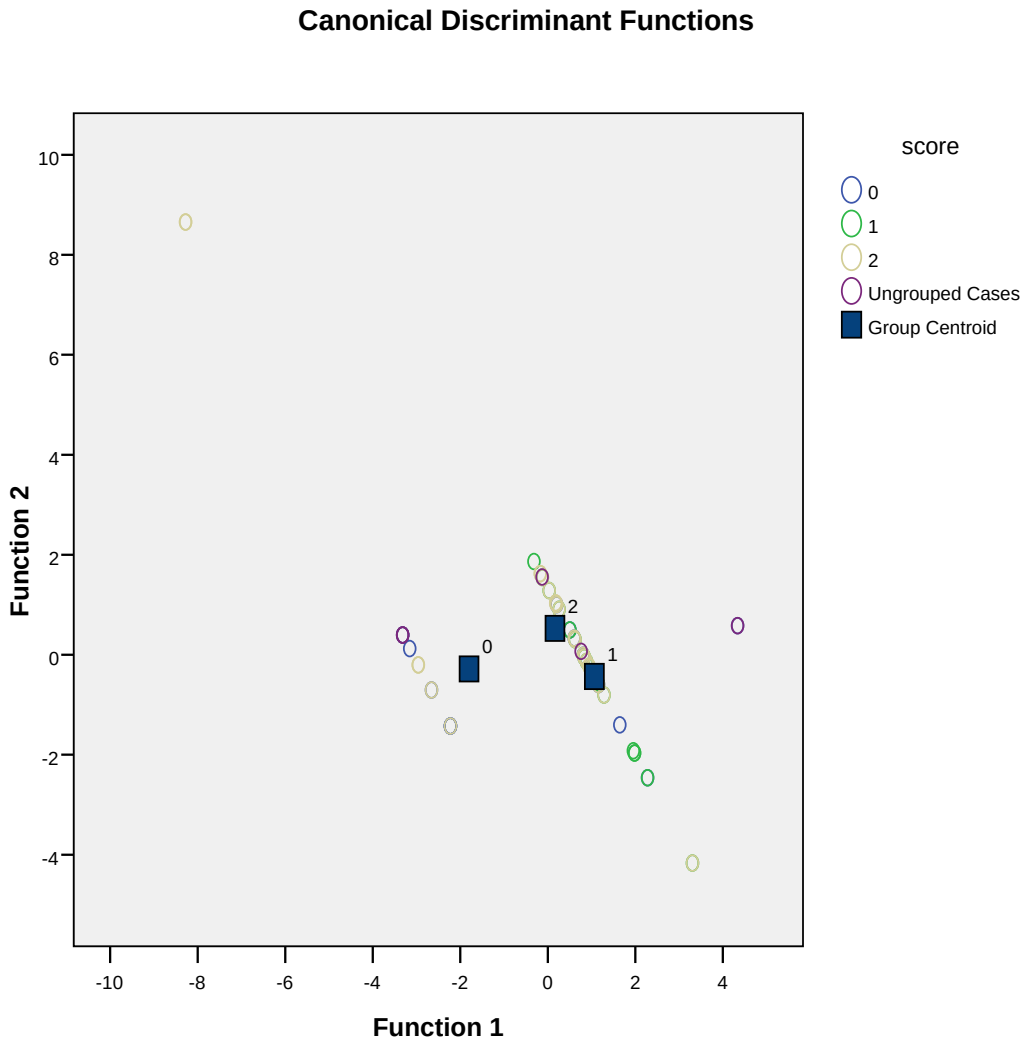
2= Group 3

3= Group 4

Territorial map of *C. gariepinus* size groups plot on discriminate functions.

***asteric on map indicates Groups centroid**

0 indicates group 1, 1= group 2, 2= group 3 and 3= group 4.

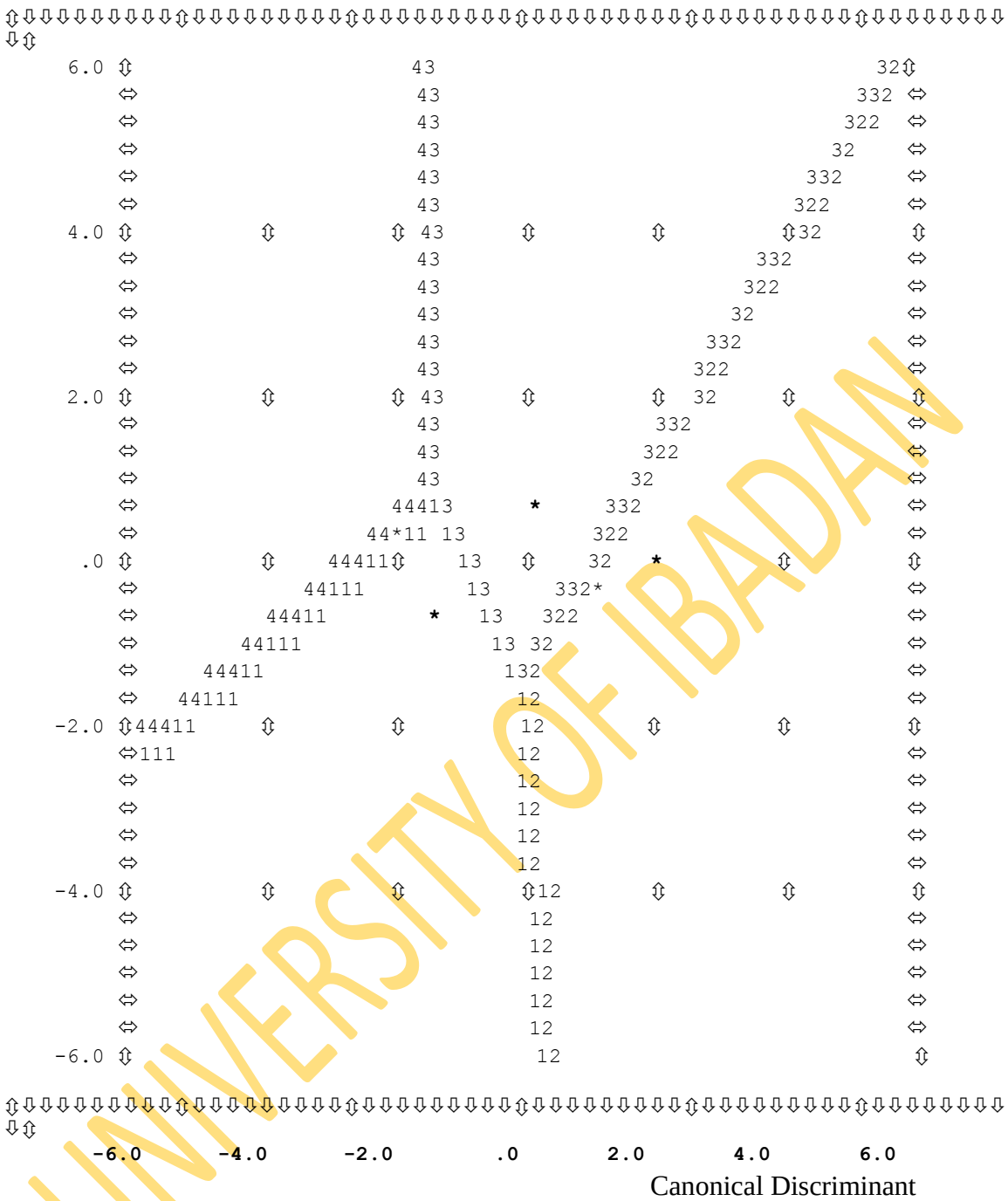


Plot of the values of Pectoral Spine Sub-groups on canonical variation functions before correction for Allometry

***0 indicates S group, 1= P group, while 2= C group**

Function 2

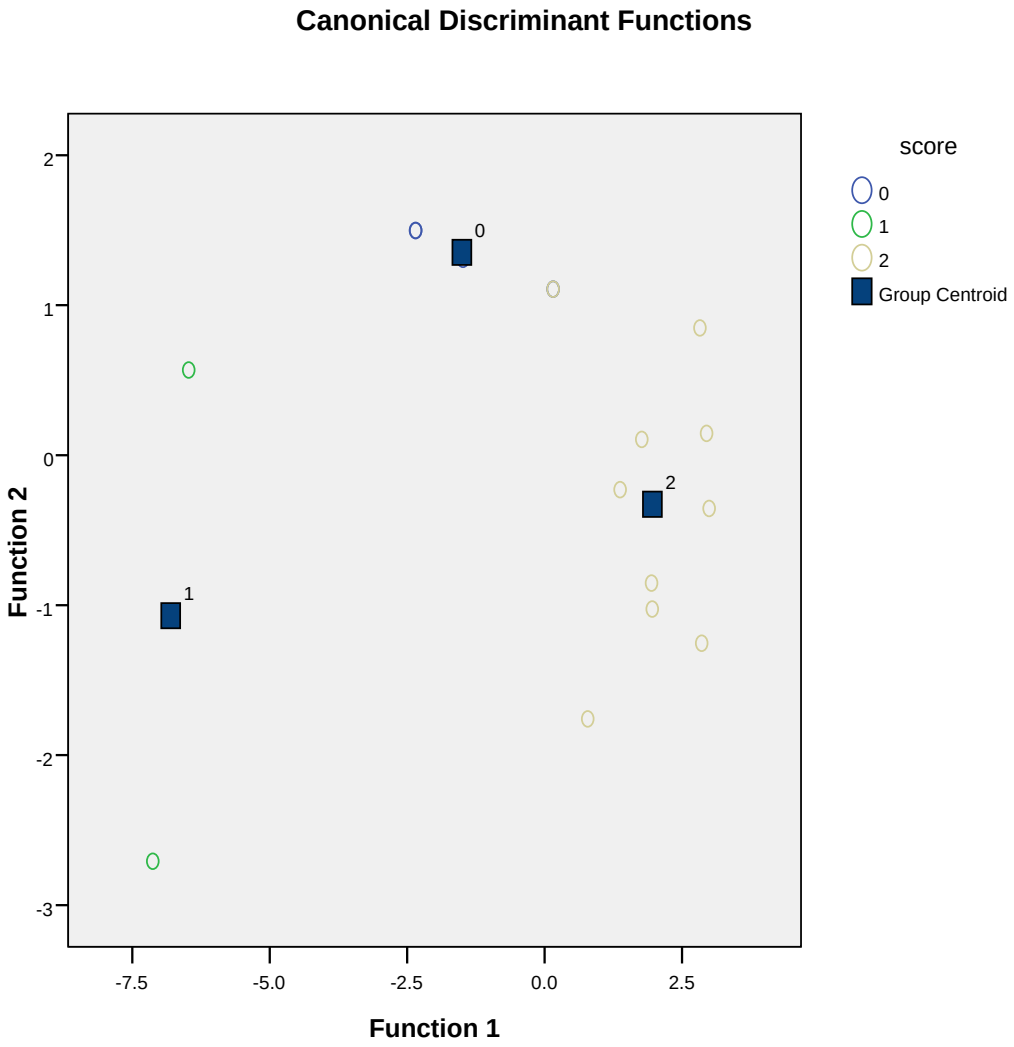
-6.0 -4.0 -2.0 .0 2.0 4.0 6.0



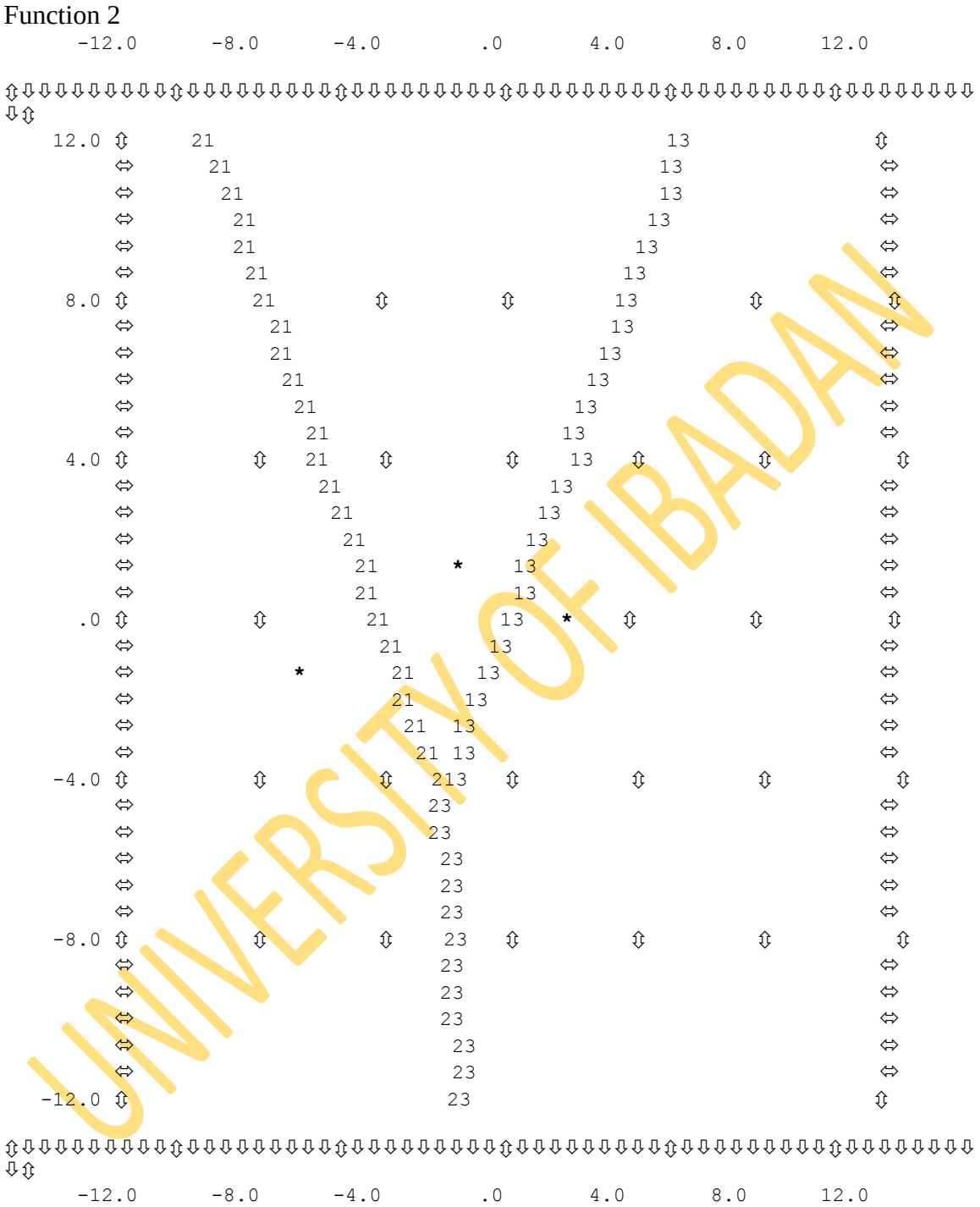
Territorial map of plotted discriminate functions on Pectoral Spine Sub-groups in *C. gariepinus* before correction for Allometry.

* indicates groups centroids

1, 2, 3 and 4 represents the subgroups



Plot of size corrected PESES sub-groups on canonical discriminant functions



Territorial map for size effect corrected PESES groups.

Appendix 9

Information on subgroup of origin of the electrophoretically analyzed individuals.

Sample Number	Score	Subgroup

1	1	c
2	1	c
3	1	c
4	1	c
5	1	c
6	1	c
7	1	c
8	1	c
9	1	c
10	1	c
11	1	c
12	1	c
13	0	s
14	1	c
15	0	s
16	1	c
17	0	s
18	0	s

C-complete anteriorly serrated pectoral spine individual (score-1);S-Smooth anteriorly serrated pectoral spine individuals (Score-0).

Appendix 10

Protein Electrophoresis Band Scores for the DNA analysed Samples

Samples	Band scores											
1	0	1	1	1	1	1	1	1	0	1	0	1
2	0	1	1	1	1	1	1	1	0	1	0	1
3	0	1	1	1	1	1	1	1	0	1	1	1
4	0	1	1	1	1	1	1	1	0	1	1	1
5	0	1	0	1	0	1	1	1	0	1	0	1
6	0	1	0	1	0	1	1	0	0	1	0	1
7	0	1	1	1	1	1	1	0	1	1	1	1
8	0	1	0	1	0	1	0	1	1	1	1	1
9	0	1	0	1	0	0	0	0	1	1	1	1
10	0	1	0	1	0	0	1	0	1	1	1	1
11	0	1	1	1	0	0	1	1	0	1	0	1
12	0	0	1	1	0	1	1	1	0	1	1	1
13	0	0	1	1	0	0	1	1	1	1	0	1
14	0	0	1	1	1	0	0	0	0	1	0	1
15	0	1	0	1	1	0	0	0	0	0	0	1

16	**0**	**1**	**1**	**1**	**0**	**1**	**0**	**1**	**1**	**0**	**1**
	1	**1**									
17	**0**	**1**	**0**	**1**	**1**	**1**	**0**	**0**	**1**	**1**	**0**
	1	**1**									
18	**1**	**1**	**0**	**1**	**1**	**1**	**1**	**0**	**1**	**1**	**0**
	1	**1**									

Appendix 11

Information on subgroup of origin of the RAPD-DNA analyzed individuals.

Sample Number	Score	Subgroup
1	1	C
2	1	C
3	1	C
4	1	C
5	1	C
6	1	C
7	1	C
8	1	C
9	1	C
10	1	C
11	1	C
12	1	C
13	0	S
14	1	C
15	0	S
16	1	C
17	0	S
18	0	S
19	0	S
20	1	C

Group C individuals has complete anteriorly serrated pectoral spine and their score =1 while group S individuals has smooth anteriorly pectoral spine and their score=0.

Appendix 12
Band score for RAPD primers

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	0	0
0	0	0	0	1	0	1	0	1	0	0	0	1	1	1	1	1	1	1	0
1	1	1	1	1	0	1	0	1	0	0	0	1	1	1	1	1	1	0	0
1	1	1	1	1	0	1	0	1	0	0	0	1	1	1	1	0	0	1	0
1	1	1	1	1	0	1	0	1	0	0	0	1	1	1	1	1	0	1	0
1	0	0	1	1	0	1	1	1	0	0	0	1	1	0	1	1	0	1	0
1	0	0	1	1	0	1	1	1	0	0	0	1	1	0	1	1	0	1	0
0	1	0	0	1	0	1	1	0	0	0	0	1	1	0	0	1	1	0	0
0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
0	1	0	0	1	0	0	0	0	0	0	0	0	1	1	1	0	1	1	0
0	1	0	0	1	0	0	1	1	0	0	0	0	1	1	1	0	1	1	0
0	1	0	0	1	0	0	1	1	0	0	0	0	1	1	1	0	1	1	0
0	1	1	0	1	0	0	1	1	0	0	0	1	1	1	1	1	1	1	0
1	0	0	1	1	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0
1	0	1	1	1	0	1	1	1	0	0	0	1	1	1	1	1	1	0	0
1	1	1	0	0	0	1	0	1	1	0	0	0	0	0	0	0	0	0	1
1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1

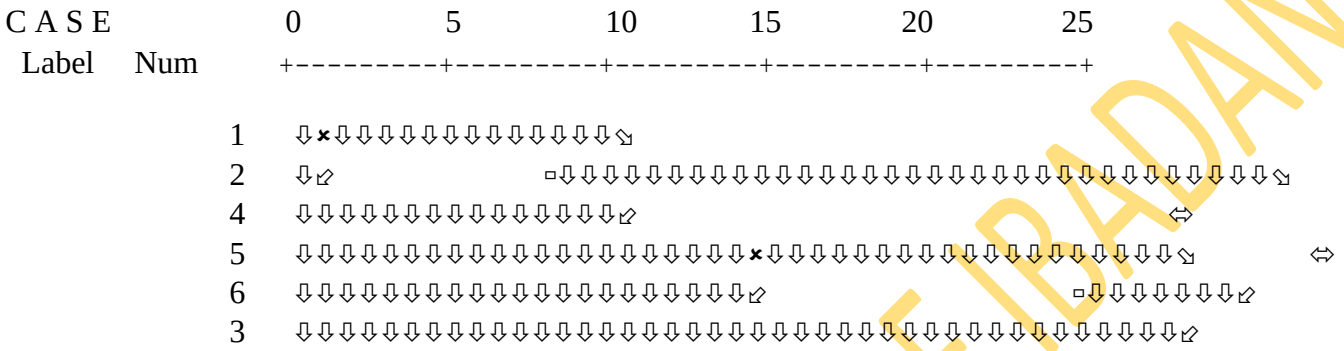
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
1	0	0	1	1	0	0	0	1	1	1	1	0	1	1	0	1	0	1	1
1	0	0	1	1	0	0	0	1	1	1	1	0	1	1	0	1	1	1	1
1	1	1	1	1	0	0	0	1	1	1	1	1	1	1	0	0	1	0	0
1	0	0	1	1	0	0	0	1	1	1	1	0	1	1	0	1	1	1	1
1	0	1	1	0	0	0	0	1	1	1	1	1	0	0	0	1	0	1	1
0	1	1	1	1	0	0	1	1	1	1	1	1	1	0	0	0	1	1	1
0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
0	0	1	1	0	1	0	0	0	0	0	0	0	0	0	1	0	1	0	0
1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1	1	1
1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	0	1	1

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	**17**	18	19	20
1	0	0	0	1	0	0	1	1	0	0	1	1	0	0	0	0	0	0	0
1	0	0	0	1	0	0	1	1	0	0	1	1	1	1	0	1	1	0	0
1	0	0	0	1	0	0	1	1	0	0	1	1	1	1	1	1	1	0	0
1	0	1	1	1	0	0	1	1	0	0	1	1	1	1	1	1	1	0	0
1	0	1	1	1	0	0	1	1	0	0	1	1	1	1	1	1	1	0	0
1	0	0	1	1	0	0	1	1	0	0	1	1	1	1	1	1	0	0	0
1	0	1	1	1	0	0	1	0	0	0	1	1	1	1	1	1	0	0	0
1	1	1	1	1	0	0	1	1	0	0	1	1	1	1	0	1	1	0	0
0	0	0	0	1	0	0	1	0	0	1	1	1	1	1	0	1	1	0	0
1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	**17**	18	19	20
0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	1	1	1	0	0
0	0	0	1	1	0	0	0	1	0	0	0	1	1	0	1	1	1	1	0
1	0	0	1	1	0	0	0	1	0	0	0	1	1	0	1	1	1	1	0
1	0	1	1	1	0	0	0	1	0	0	1	1	1	0	1	1	1	1	0
1	0	0	1	0	0	0	0	1	0	0	0	1	1	1	1	1	1	1	0
0	0	0	0	1	0	0	0	1	0	0	0	1	1	1	1	1	1	0	0
1	0	1	1	1	0	0	1	1	0	0	0	1	1	1	1	1	1	1	0
0	0	0	1	1	0	0	0	1	0	0	0	1	0	1	0	0	0	0	0
0	1	0	0	0	1	1	1	1	1	0	0	0	1	1	1	1	1	1	1
1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	**17**	18	19	20
0	1	1	1	1	1	0	0	0	0	0	0	0	1	1	1	1	**0**	0	0
0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	**0**	0	0
1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
0	0	0	1	1	0	0	1	1	1	1	0	1	1	0	0	0	0	0	0
0	1	0	1	0	0	0	1	0	0	1	1	1	1	0	0	1	**1**	0	1
1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	0	1	1	0	1
0	0	0	1	1	0	0	0	1	0	0	0	0	1	1	1	0	1	1	1
1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
0	0	0	0	0	0	0	0	1	0	0	0	0	1	1	1	0	1	0	0
1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	0
1	1	1	0	1	1	0	0	0	1	0	0	1	1	1	1	1	**1**	0	1
1	1	1	1	1	1	0	0	0	0	0	0	0	1	1	1	0	**1**	1	0

Appendix 12b
Linkage Between the six polymorphic RAPD primers



Dendrogram showing Average Linkage Between the six polymorphic primers with respect to the studied populations

- **1=OPAD-09, 2=OPAE-04, 3=OPAE-09, 4=OPAF-08, 5=OPAE-05, 6=OPAF-07**

Appendix 12C

Classification results for the *C. gariepinus* population's genotypes.

		Predicted Group Membership		Total
	Score	0.00	1.00	
Original Count	0.00	5	0	5
	1.00	0	15	15
%	0.00	100.0	0.0	100.0
	1.00	0.0	100.0	100.0

100.0% of original grouped cases correctly classified.

Appendix 13
Nimet data (2000-2010)
RELATIVE HUMIDITY @ 09 HOURS (%)

STN	YEAR	JAN	FEB	MAR	APR	MAY	JUN	JUL	AUG	SEP	OCT	NOV	DEC
Ibadan	2000	72	46	68	78	79	84	85	88	87	84	77	69
Ibadan	2001	75	61	80	80	82	85	89	91	88	83	79	77
Ibadan	2002	57	70	76	80	81	84	88	88	86	83	78	59
Ibadan	2003	73	80	84	82	80	82	86	88	86	83	82	77
Ibadan	2004	72	71	70	80	82	83	87	88	83	83	79	79
Ibadan	2005	51	76	78	78	82	87	89	86	86	82	77	80
Ibadan	2006	78	63	68	73	81	84	88	89	84	83	78	78
Ibadan	2007	70	78	76	81	81	83	88	88	85	84	79	70
Ibadan	2008	50	63	73	78	80	84	88	87	87	82	73	75
Ibadan	2009	48	55	75	78	80	83	86	85	85	83	76	73
Ibadan	2010	68	73	74	75	82	81	89	84	86	83	74	57

							TMAX						
STN	**YEAR**	**JAN**	**FEB**	**MAR**	**APR**	**MAY**	**JUN**	**JUL**	**AUG**	**SEP**	**OCT**	**NOV**	**DEC**
Ibadan	2000	33.3	34.6	36	33.3	32.2	30.3	28.5	27.7	29.1	30.6	32.8	33.2
Ibadan	2001	33.3	35.5	35.2	32.7	31.9	30.1	28.6	26.8	28.8	31	33.4	33.3
Ibadan	2002	33.5	23.7	35.1	32.5	32.1	30.5	28.9	27.9	29.1	30.5	32.9	33.5
Ibadan	2003	33.4	34.7	35.4	32.6	32.5	31.1	28.1	28.5	29.6	30.8	32.7	33.3
Ibadan	2004	35	35	33	31	38	29	27	30	31	32	33	33.4
Ibadan	2005	34.0	35.4	34.7	34.0	32.0	29.5	28.3	28.1	29.6	30.9	33.2	33.2
Ibadan	2006	33.3	35.2	36.9	33.1	32	31.1	28.1	28.2	29.5	30.8	32.9	32.5
Ibadan	2007	33.5	34.9	34.6	33	31.6	31	29.3	27.7	30.1	30	32.2	32
Ibadan	2008	32.9	36.2	35.5	33.7	31.8	29.9	28	27.2	28.3	30.9	32.1	33.3
Ibadan	2009	33.8	35.5	33.8	33.8	32.4	30.7	28.8	27.8	30.1	31	32.2	32.4
Ibadan	2010	34.5	36.1	35	34.2	32.1	31.1	29.3	28.8	30	31.2	32.3	33.6

						TMIN							
STN	**YEAR**	**JAN**	**FEB**	**MAR**	**APR**	**MAY**	**JUN**	**JUL**	**AUG**	**SEP**	**OCT**	**NOV**	**DEC**
Ibadan	2000	22.8	22.1	24	23.6	23.5	22.6	21.7	21.3	22.2	22.4	23.8	22.5
Ibadan	2001	22.6	23.1	23.8	23.1	23.1	22.5	22.3	21.6	21.7	22.7	23.9	23.7
Ibadan	2002	21.6	29.8	24.4	23.9	23	22.5	22.3	21.8	21.9	22	23.6	22.4
Ibadan	2003	22.6	24.5	24.8	23.5	23.4	22.6	21.5	21.7	21.9	22.5	23.4	22.4
Ibadan	2004	24	25	24	23	22	22	22	22	22	24	24	22.2
Ibadan	2005	21.3	24.7	24.1	24.6	23.5	22.5	22.3	21.3	22.4	22.7	23.9	30.9
Ibadan	2006	23.2	22.9	24.6	23.2	23	23.1	22.2	21.5	21.8	22.2	23.8	23
Ibadan	2007	22.9	24	24.4	23.2	23.3	23	22.5	21.8	22	21.5	23.3	21
Ibadan	2008	20.2	22.9	24.3	23.8	22.3	22.1	22	21.4	21.7	22.1	21.9	22.4
Ibadan	2009	20.9	22.5	22.9	23.5	23.3	22.4	22	21.5	21.8	22.3	22.1	22.2
Ibadan	2010	22.5	24.9	25.2	24.7	23.9	23.8	22.5	22.5	21.8	22.6	23.2	23.5

		RAINFALL (mm)											
STN	**YEAR**	**JAN**	**FEB**	**MAR**	**APR**	**MAY**	**JUN**	**JUL**	**AUG**	**SEP**	**OCT**	**NOV**	**DEC**
Ibadan	2000	30.1	0	95.7	126.1	80.6	116	220.7	232.4	127	215.9	0	0
Ibadan	2001	0	8.4	121.6	142.2	231.2	114.9	257.1	53.2	285.6	72.3	2.1	1.1
Ibadan	2002	0	6.9	57	122.8	184.3	323.8	171.7	247.2	114.5	207.4	79.7	0
Ibadan	2003	25.2	81.6	3.6	184.1	191.3	147.8	156.2	40.9	128.5	132.1	51.7	0
Ibadan	2004	78.7	32.5	92	231.9	183.9	181.2	161.2	156.2	196.3	0.3	0	Trace
Ibadan	2005	0	33.1	101.9	118.2	114.7	212.6	182.9	64	225.7	134.9	4	12.2
Ibadan	2006	19.1	1.5	109.1	79	197.3	164.5	65.2	128.1	312.5	166	17.8	0
Ibadan	2007	0	0.5	36.2	39.5	303.8	173.7	138.3	98.1	231.7	254	6.5	8.3
Ibadan	2008	9.3	0	200.4	158.1	128.9	98.8	63.8	111.8	113.6	182.9	5.8	23.7
Ibadan	2009	1.5	138.1	80.4	203.7	129.9	217.4	205.6		328.5	205.5	17.1	5.2
Ibadan	2010	0.8	18	64.4	88.8	195	76.9	109.5	320.3	311.3	214.7	16.9	0