GENETIC DIVERSITY, POPULATION STRUCTURE AND INFLUENCE ON LIFE-HISTORY TRAITS OF THE AFRICAN CATFISH, *CLARIAS GARIEPINUS* (BURCHELL 1822), IN KENYA

BY

JAMES BARASA ECHESSA

A THESIS SUBMITTED IN PARTIAL FULFILLMENT OF THE REQUIREMENTS FOR THE AWARD OF THE DEGREE OF DOCTOR OF PHILOSOPHY IN FISHERIES AND AQUATIC SCIENCES (AQUACULTURE), UNIVERSITY OF ELDORET, KENYA

OCTOBER, 2018

DECLARATION PAGE

Declaration by the candidate

This thesis is my original work and has not been presented for a degree in any other University. No part of this thesis may be reproduced without prior written permission from the author and/or University of Eldoret.

Barasa James Echessa

………………………………………….   …………………………………..

NRM/DPHIL/FIS/08/2009   **Date**

Declaration by Supervisors

This thesis has been submitted for examination with our approval as University supervisors.

………………………………………….   …………………………………..
 Prof. Romulus Abila   **Date**
 Maasai Mara University, Narok, Kenya

………………………………………….   …………………………………..
 Prof. Otto George Dangasuk   **Date**
 University of Eldoret, Eldoret, Kenya

………………………………………….   …………………………………..
 Prof. Boaz Kaunda-Arara   **Date**
 University of Eldoret, Eldoret, Kenya

DEDICATION

This piece of work is dedicated to my children: Mary-Magdalene, Jude-Thaddeaus, Mary-Immaculate, Sarah and John-Baptiste. That it may be a source of inspiration in their growth and future endeavors.

ABSTRACT

The African catfish, *Clarias gariepinus* (Burchell 1822) is an important species in fisheries and aquaculture in Africa. In Kenya, farmers use seeds of unknown genetic characteristics. Sourcing of brood stock for propagation at hatcheries is not controlled, with inter-basin transfer of brood stock being common. This study used 427 base pairs (bp) of mitochondrial D-loop sequence markers to determine genetic variation and population structure in 5 natural (Lakes Victoria (LVG), Kanyaboli (LKG), Turkana (LTA), Baringo (LBA) and Jipe (LJP)) and 5 farmed populations (Sangoro Aquaculture Center (SAN), Sagana Aquaculture Centre (SAG), University of Eldoret Fish Farm (UoE), Kibos Fish Farm (KIB), and Wakhungu Fish Farm (WKU)) of *C. gariepinus* collected across Kenya. Similarly, 6 microsatellite DNA markers were used to determine genetic variation in 8 populations (LVG, LKG, LTA, LBA, SAN, SAG, UoE and KIB). The 5 natural populations had higher numbers of haplotypes compared to the 5 farmed populations. Haplotype diversity values were generally consistent with haplotype numbers, with populations of higher haplotypes recording higher haplotype diversity. 88.2% of haplotypes in the 10 populations was private, with LJP showing the highest number at 12, while WKU had the least with 1. All except LJP and LTA populations shared haplotypes, and KIB had the highest number of shared haplotypes at 8. The 68 haplotypes identified in the 10 populations clustered into 5 groups: LVG LJP, LTA, LBA and SAG, both in the Maximum likelihood tree, and in the haplotype network. A total of 31 of 45 pair wise comparisons of the population differentiation index (F_{ST}) values were significantly different (p≤0.05). Microsatellite analysis showed farmed populations of higher number of alleles than natural populations, but higher observed and expected heterozygosity were recorded in the natural populations. The number of private alleles was generally uniform in the populations, although KIB and LVG had higher values. For microsatellites DNA analysis, a total of 15 out of 28 pair wise comparisons of the population differentiation index (F_{ST}) values were significantly different (p≤0.05), with most of the variation attributed to individual samples (96.72%). All populations were in Hardy-Weinberg equilibrium, since none had significant values for exact tests of H-W at all loci. The 8 populations grouped into 4 genetic clusters (LVG, LTA, LBA and SAG) in structure analysis, with all farmed populations grouping into the Lake Victoria population, and 3 grouping into LBA. Mean relative fecundity for the three populations was 81.9±6.0, 50.8±5.6 and 53.0±5.1 eggs/g body weight for lakes Victoria, Baringo and Kanyaboli respectively, with relative fecundity being higher in Lake Victoria than Lakes Baringo and Kanyaboli, which had similar values. Size at first maturity was higher in LBA than LVG and LKG, while a higher size at maturity was recorded in LVG compared to LKG. Therefore fecundity of fish seems to correlate with Hetereozygosity, while size at first maturity seems to be influenced more strongly by environmental factors than genetic characteristics of *C. gariepinus*. Water quality parameters were similar among the three sites (Lakes Victoria, Baringo and Kanyaboli) for nutrients (Total phosphorus and total nitrogen), while the physico-chemical parameters varied significantly (p≤0.05) among sites and months of sampling. The findings suggest that LVG, LTA, LBA, LJP and SAG are genetically distinct populations, which can potentially be exploited for aquaculture. Natural populations had higher genetic variation than farmed populations, possibly due to inbreeding depression from domestication of farmed species. Farmers may increase seed production by using populations of *C. gariepinus* of higher genetic diversity.

TABLE OF CONTENTS

LIST OF TABLES

LIST OF FIGURES

LIST OF APPENDICES

ABBREVIATIONS, ACRONYMS AND SYMBOLS

BecA-ILRI-Hub   Biosciences eastern and central Africa-International Livestock

BMU   Beach Management Unit

BP   Before present

Bp   Base pair

D-loop   Displacement loop region of mitochondrial DNA

DNA   De-Oxyribonucleic Acid

FAO   Food And Agriculture Organization Of The United Nations

gDNA   genomic Deoxyribonucleic Acid

GSI   Gonadosomatic Index

HFC   Heterozygosity fitness correlations

ILRI   International Livestock Research Institute

Kb   Kilo base

L_{m50}   Size at first maturity

mtDNA   mitochondrial Deoxyribonucleic Acid

NFFEPP   National Fish Farming Enterprise Productivity Program

ng/µl   Nanograms per microlitre

PCR   Polymerase Chain Reaction

pmoles/µl   Picamoles per microlitre

RFLP   Random Fragment Length Polymorphism

Rpm   rounds per minute

UV   Ultra-Violet light

µl   microlitres

ACKNOWLEDGEMENT

CHAPTER ONE
INTRODUCTION

1.1. Background information

Conservation of genetic diversity of a species is an important goal of conservation biology. This importance stems from the application of genetic diversity to identify distinct units of a species that require proper management (Lesica & Allendorf, 1995). In natural ecosystems, genetic diversity influences persistence of a species in the habitat. More importantly, genetic diversity is a determinant of fitness traits of a species or population (Knaepkens et al., 2002; Blanck & Lamouroux, 2007), although the association of genetic diversity and fitness traits is both species and trait specific (Knaepkens et al., 2002). Indeed, the theory of life history traits predicts that life history tactics adapted by a species or population is a function of the environment and genetic characteristics (Stearns, 1976). Because of this importance, therefore, genetic diversity is applied in aquaculture to identify populations suitable for use as brood stock not only to improve conservation of threatened fish species, but also increase food fish production, and livelihoods for farmers.

One such species to which information on genetic diversity may be applied to address challenges that constrain its artificial propagation and production on farms is the African catfish, *Clarias gariepinus* (Burchell 1822). The species is a sturdy fish, grows fast and can reach table size of 1 kg in 6- 8 months (Hecht & Britz, 1988), and has high fecundity (Hogendoorn, 1977; Owiti & Dadzie, 1989). The fish breeds during the rainy season, where it swims in floods to spawn in inundated areas. The species feeds on a wide range of food materials and inhabits lakes, rivers and swamps (Bruton, 1988), where it plays an important ecological role as a predator (Corbet, 1961). Similarly, *C. gariepinus* has an extra-ordinary ability to breathe atmospheric oxygen due to the presence of a supra-branchial organ (Bruton, 1988), attributes that

make it an excellent species for aquaculture for improved food production and livelihoods especially in the rural areas in Africa. However, poor survival of juveniles in culture facilities constrain profitable culture enterprises of the species (Hecht, 1985; Hecht & Appelbaum, 1988; Sulem et al., 2006), by limiting quantities of seeds available for expanded aquaculture and the numbers that actually grow to maturity in culture facilities. Despite several strategies being applied to address this problem (Macharia et al., 2005; Rasowo et al., 2007; Rasowo et al., 2008; Nyina-Wamwiza et al., 2010; Chepkurui-Boit et al., 2011; Magondu et al., 2011; Musa et al., 2012), high mortality of fingerlings still persists, with rates of upto 99.8% loss being reported (Hogendoorn, 1980). Recently, it has been suggested that poor quality brood stock of mixed ancestry could be contributing to poor survival of *C. gariepinus* fry at hatcheries (Barasa et al., 2014). Kenya has a natural diversity of *C. gariepinus* populations, some of which are unique reservoirs of genetic diversity (Barasa et al., 2014; 2016; 2017), which could be exploited in genetic improvement programmes for higher food fish production. Similarly, information on genetic diversity could be applied in monitoring of natural stocks to avoid threats such as stock mixtures (Barasa et al., 2016; 2017), overfishing (Aloo, 2003) and predation from exotic fish species (Gourdswaard & Witte, 1997) that lower quality of brood stock through population bottlenecks.

While genetic diversity has been reported to correlate with fitness in some fish species and populations (David & Jarne 1997; Knaepkens et al., 2002; Pojular et al., 2006; Blanck & Lamouroux, 2007), lack of correlations is reported in other species and traits (Scott & Koehn, 1990). These studies illustrate the complexities in heterozygosity fitness correlations (HFC) (David, 1998), because environmental factors also influence differences in fitness traits among populations of a species

(Nicola & Almodovar, 2002). There is a dearth of information on HFC (relationship between genetic diversity and fitness traits) in tropical fish species, and it is unclear if this correlation exists in *C. gariepinus* as well. If so, then it may be expected that farmers would improve survival of fry at hatcheries by using brood stock from populations of higher genetic diversity. Similarly, if *C. gariepinus* populations exhibit differential fecundity, and if these differences correlate with genetic diversity, then farmers would gain by using brood stock of higher fecundity. This may be through higher numbers of fry obtained from a bigger batch of eggs spawned by a female, and also through higher survival of such fry. This study therefore aimed to determine genetic diversity, population genetic structure and relationship with life history traits (fecundity and size at first maturity) of selected natural and farmed populations of *C. gariepinus* in Kenya.

1.2. Justification of the study

Despite the importance of *C. gariepinus* in aquaculture in tropical areas, ranking second only to *O. niloticus* as a preferred fin fish aquaculture species in many African countries including Kenya, average annual production of the species in the country is low. According to FAO (2009), a total of 302 tonnes of *C. gariepinus* was produced in Kenya in 2006. This rose to 3,525 and 3,868 tonnes in 2011 and 2012 respectively (State Department of Fisheries, 2011; 2012), following the public funded National Fish Farming Enterprise Productivity Program (NFFEPP), implemented country-wide. Underlying this low annual production of farmed catfish is low survival of fry (Sulem et al., 2006), which occasions a shortage of quality seeds for expanded aquaculture enterprises. While high growth rates of fingerlings stocked in ponds or tanks are reported (Chepkirui-Boit et al., 2011; Ani-Sabwa et al., 2014), high mortality of fingerlings of 32.5 to 99.8% of the fingerlings stocked also occurs

(Kelleher & Vincke 1976; Hogendoorn, 1980). This leads to disillusionment among farmers, and has stifled the expansion of *Clarias* aquaculture industry, because farmers often abandon catfish production enterprises.

Poor survival of *C. gariepinus* fry is attributed to poor quality diets for fry (Nyina-Wamwiza et al., 2010; Chepkirui-Boit et al., 2011; Musa et al., 2012), presence of predators in fry nursery systems (Sulem et al., 2006), cannibalism among siblings in fry nursery systems (Hecht & Appelbaum, 1988; Sulem et al., 2006; Nyina-Wamwiza et al., 2010), presence of parasites and pathogens in egg incubation and fry nursery systems (Post, 1987; Rasowo et al., 2007; Magondu et al., 2011), and the use of poor quality brood stock of mixed ancestry (Barasa et al., 2014). These problems may therefore be compounded in scenarios where no genetic guidelines are applied in the management of natural stocks of *C. gariepinus*, sourcing of brood stock for propagation at hatcheries and general husbandry practices in both fry nursery and grow-out systems for the species at fish farms.

Information on genetic diversity and population genetic structure is now being applied in identifying fitness traits in fish species and populations (Danzmann et al., 1988; David, 1998; Knaepkens et al., 2002; Blanck & Lamouroux, 2007; Vehvilainen et al., 2012), to determine the purity of fish brood stock for propagation (Barasa et al., 2014; 2016; 2017), to develop a genetic improvement programme for fish species targeting commercially important production phenotypes (Eknath et al., 1993; Miller & Kapuscinski, 2003), and to identify natural populations in need of conservation because of induced population bottlenecks (Barasa et al., 2017), such as drought and overfishing (Barasa et al., 2017). While the correlation between genetic diversity and fitness has been established in some fish species (Zouros, 1987; Danzmann et al., 1988; Thelen & Allendorf, 2001; Knaepkens et al., 2002; Blanck & Lamouroux,

2007; Vehvilainen et al., 2012), no such correlation has been found in some aquatic animals (Scott & Koehn, 1990), and plants (Savolainen & Hedrick, 1995). However, a null result between heterozygosity fitness correlations in some taxa may not necessarily mean total absence of the correlations. This is because the correlation is also influenced by environmental factors (Stearns, 1976), such as age of the organism (David & Jarne, 1997), presence of stress factors (Danzmann et al., 1988), magnitude of the stress (Audo & Diehl, 1995), and the sample size of the species or population being analyzed (David, 1998). It is unclear if a similar relationship exists in *C. gariepinus*. If so, then *C. gariepinus* farmers using brood stock sourced from populations of higher genetic diversity may gain from a possible faster growth rate, higher survival and fecundity. A correlation between fecundity of the species and survival of the young has been established in Arctic charr, *Salvelinus alpinus* (Wallace & Aasjord, 1984), and trout, *Salvelinus fontinalis* (Liskauskas & Ferguson, 1990). It is expected that farmers using *C. gariepinus* populations of higher fecundity may gain from higher survival of fry at hatcheries. This would translate into higher fry from a bigger batch of eggs spawned, and possible higher survival of resultant fry. This would increase seed availability for expanded aquaculture and use as live bait for catching *L. niloticus* in Lake Victoria, thereby increasing food security, livelihoods for farmers, and conservation of natural populations. Similarly, a natural population of the species exhibiting higher fecundity may be expected to persist in the environment, since higher fitness reduces the risk of extinction in fishes (Feiner et al., 2017). This study investigated genetic diversity and population genetic structure in natural and farmed *C. gariepinus* and the influence of genetic diversity on fecundity and size at first maturity in selected natural populations in Kenya.

1.3. Objectives

1.3.1. General objective

The general objective of this study was to describe the genetic diversity and population genetic structure of *C. gariepinus* from different sites in Kenya, and their influence on fecundity outputs of the species.

1.3.2. Specific objectives

The specific objectives of the study were:

1. To determine genetic diversity of *C. gariepinus* from selected farms and lakes in Kenya.

2. To determine the population genetic structure of *C. gariepinus* from selected farms and lakes in Kenya.

3. To determine fecundity and size at first maturity of *C. gariepinus* from Lakes Victoria, Baringo and Kanyaboli of Kenya.

4. To determine the influence of genetic diversity on fecundity and size at first maturity of *C. gariepinus* from Lakes Victoria, Baringo and Kanyaboli of Kenya.

1.4 Hypotheses

The study is guided by the following statistical hypotheses:

H*o* Natural and farmed populations of *C. gariepinus* from Kenya are similar in genetic diversity.

H*o* Natural and farmed populations of *C. gareipinus* from Kenya are similar in population genetic structure.

H*o* Lakes Victoria, Baringo and Kanyaboli populations of *C. gariepinus* have similar fecundity and size at first maturity.

H*o* Lakes Victoria, Baringo and Kanyaboli populations of *C. gariepinus* have similar fecundity and size at first maturity.

CHAPTER TWO

LITERATURE REVIEW

2.1. The Clariidae: Evolution and adaptive radiation

Clariid catfishes are endemic to Africa, a continent that is naturally rich in biodiversity. The sheer wealth of ichthyofaunal biodiversity is for instance evident in the fact that of the 58 species of the genus *Clarias*, 33 occur in Africa while 25 in Asia (Na-Nakorn & Brummett, 2009). This high abundance of species in clariidae not only reflects its importance in natural ecosystems, but even more importantly, the diversity of the genus and therefore its evolutionary ability. The family clariidae, of the order siluriformes, of Africa comprises three genera: *Clarias*, *Bathyclarias* and *Gymnallabes*. *Heterobranchus* is a non-*Clarias* clariid. The Asian stocks of clariidae comprise primarily the genus *Clarias*. Clariid catfishes evolved in the Pliocene epoch (upper tertiary period) about 7-10 million years ago (Sudarto, 2007). At that time, clariid catfishes, like most other aquatic fauna, resided in rivers and streams, the only aquatic habitats then (Nagl et al., 2000). Therefore catfishes became adapted to riverine ecosystems.

The family Clariidae is paraphyletic, consisting of several genera: *Clarias*, *Bathyclarias*, *Dinotopterus*, *Clariallabes*, *Xenoclarias*, and *Heterobranchus* (Eccles, 1992), distributed in various streams, rivers and lakes. The occurrence of these genera varies in different places. For instance, Tanzania has all the 6 genera, with *Dinotopterus* being endemic to Lake Tanganyika (Skelton, 1993; Mwita & Ngwengulila, 2008). *Bathyclarias* is endemic to L. Malawi (Skelton, 1993).

During the Miocene period (23-5 million years ago), major vicariance events like volcanicity, shifting of tectonic plates due to seismic activity, in addition to gradual

palaeoclimatic changes gave rise to an array of habitats through rifting, elevations and depressions (Cane & Molnar, 2001). Elevations formed mountains, rapids and plateaus; while rifting and depressions created lakes, wetlands and valleys. These activities also affected the existing channels and rivers and drainage basins, with some changing direction of flow, size of basins and the accompanying discharge, in addition to separating drainage basins that were once connected (Beadle 1974; Giddelo et al., 2002). This emergence of new habitats had profound impacts on the existing riverine catfishes. Most of the catfishes were dispersed to the new environments (Giddelo et al., 2002). Populations of catfish that once exchanged genes were separated, influencing the distribution of genetic variation. Since the new habitats were separated from each other, populations of catfish inhabiting and adapting to new environments consequently became distinct, a classical case of adaptive radiation, similar to the rise of cichlid species flocks of the Great Lakes of Africa (Greenwood, 1974; Salzburger & Meyer, 2004). Adaptive radiation could therefore be an explanation for the high diversity in clariidae. Genetic diversity in *C. gariepinus*, for instance, is reported to be relatively high compared to other species (Galbusera, 1997; Barasa et al., 2017).

Continous palaeoclimatic changes to the aquatic habitats influenced the adaptive radiation of clariidae. Lake Victoria for instance is reported to have dried out completely 17,500 years before present (BP) and flooded 12,500 years BP (Fryer, 2001; Johnson et al., 1996), with significant implications on the adaptive ability of the resident catfish and other ichthyo-fauna. Such changes to the environment led to the evolution of adaptive mechanisms in catfish to ensure its survival, and could explain the possession of an array of important features by catfish such as the suprabranchial breathing organ. *C. gariepinus* survives well in habitats of low oxygen and disperses

easily due to adaptation to air-breathing, tolerates extreme desiccation, swims well and moves over land (Skelton, 1994). The species is also omnivorous and generally highly resistant to stress (Na-Nakorn & Brummett, 2009), attributes that have made the species commercially important at the global level.

Molecular studies on *C. gariepinus* have shown cladistic differentiation based on different habitats. In their study phylogeography and genetic diversity of 16 populations of *C. gariepinus* from East Africa using the random fragment length polymorphism (RFLP) analysis, Giddelo et al., (2002) showed four groups based on a clear population structure. These included: Lake Vukoni (Lower Tana River), the eastern rift (Upper Tana River, Oloibortoto River and Lake Baringo), the western rift including the Tanzanian shield (Pangani River and Lake Jipe, Lake Edward, Luiche River, Rusizi River and Nyabugogo River) and Lake Mtera.

Phylogenetic work by Agnese and Teugels (2005), suggests that fish fauna of the family clariidae originated in Asia about 40 to 50 million years ago, moved to the Arabian plate 30 million years ago where they stayed up to around 18 million years ago, moved back to Asia before colonizing the African continent 15 million years ago. The origin of the ancestral stock of the clariidae, and this migration all took place after the split of the Pangaea into the Asian and African continents. The split occurred 160 million years ago, long before the emergence of clariidae, whose genetic divergence (12.4%) and the oldest siluriform fossils known from the upper cretaceae about 100 million years old show the ancestral stock was much younger than 160 million years. This, coupled with molecular, parasitological and palaeontological evidence suggests that clariids originated from Asia 40 to 50 million years ago before colonizing the African continent 15 million years ago.

2.2. Aquaculture of *Clarias gariepinus*

In Africa, the genus *Clarias* is endemic and has 33 species. The subgenus *Clarias* has only two species, *C. gariepinus* (Burchell, 1822) and *C. anguillaris* (Linnaeus, 1758), of which *C. gariepinus* is the main farmed species (Na-Nakorn & Brummett, 2009). *Clarias anguillaris* is restricted to West Africa, while *C. gariepinus* has a Pan-African distribution, with a natural range from the Nile to Orange River (Daget et al., 1984) , and extending to the tip of North Africa and Middle East through human influence (Cambray, 2003). Because of its resilience and high adaptability, with a rare ability to walk on land when receding waters suddenly leave it stranded (Cambray, 2003), *C. gariepinus* has been translocated to 35 countries across the world where it plays an important role in commercial aquaculture production (FishBase, 2007). In a number of Asian countries, *C. gariepinus* is imported and crossed with the native Asian catfish, *C. macrocephalus*, for a hybrid favoured for its faster growth and higher resistance to diseases. In Thailand, for instance, a total of 7,000 metric tonnes of *C. gariepinus* was produced in 2001 (FishBase, 2003), while 90% of the total *Clarias* production is of hybrid catfish (*C. macroephalus* females * *C. gariepinus* males), an average of 50,000 metric tonnes annually (Na-Nakorn et al., 2004). In Malaysia, a large percentage of the 14, 693 metric tonnes of farmed *Clarias* produced in 2004 was *C. gariepinus* (Nazia et al., 2010).

In Kenya, *C. gariepinus* is second only to Nile tilapia, *O. niloticus* as a preferred fin fish aquaculture species in Kenya. It is commonly grown in earthen ponds, in polyculture with *O. niloticus* to predate against juvenile tilapias spawned, in order to avoid overpopulation of the production unit (de Graaf et al., 1996). In 2006, a total of 30 countries in Africa, Europe and Asia (Table 1) were reported to produce at least 100 tonnes of catfish each from aquaculture (FAO, 2009). This production amounted

to 300,000 tonnes valued at US$400 million, nearly 60% of total global production of clariid catfishes (FAO, 2009). In Africa, however, the full aquaculture potential of *C. gariepinus* has not been realized, mainly due to the lack of adequate and high quality fry for stocking purposes (Sulem et al., 2006; Rasowo et al., 2008), although rising feed costs curtailed the expansion of catfish aquaculture in Southern Africa (Cambray, 2003).

Apart from stocking in ponds for grow-out as food fish, catfish fingerlings are also used as live bait for the Nile perch *L. niloticus* long line hook fishery in L. Victoria (Ngugi et al. 2005; Chitamwebwa et al., 2009). As a result, recent studies have focused on the improvement of fry production (de Graaf et al., 1995; Macharia et al., 2005; Rasowo et al., 2007; Ani-Sabwa et al., 2014), larval nutrition (Ngugi et al., 2005; Chepkirui-Boit et al., 2011) and testing the conditions suitable for growth of fingerlings (Ozorio et al., 2001). Notwithstanding this serious effort to increase availability of catfish fry to feed the Nile perch long line fishery, less than 2% of live bait used to catch Nile perch in L. Victoria are catfish fry (Mkumbo & Mlaponi, 2007; Chitamwebwa et al., 2009), with the rest being haplochromines, *Rastrineobola argeantae* and *Labeo*. This illustrates the magnitude of limited supply of catfish fry in the Lake Victoria basin. Propagation of catfish at hatcheries for supply as live bait to *L. niloticus* fishermen has been recommended and encouraged (Kaufman & Ochumba, 1993; Mkumbo & Mlaponi, 2007; Chitamwebwa et al., 2009), as a way of reducing reliance on collection of live bait from natural sources, which increases pressure on indigenous threatened species like haplochromines, *R. argentae* and *Labeo*, whose methods of artificial propagation are not yet in place, and their recovery in L. Victoria after decimation by *L. niloticus* predation is hampered (Mkumbo &

Mlaponi, 2007). Also, *C. gariepinus* fingerlings survive longer on hooks, without mortality, and so those that do not catch Nile perch in any day are still re-used.

Table 2. 1: Countries producing at least 100 tonnes of cultured clariid catfish in 2006.

Country	Quantity (Tonnes)
South Africa	100
Cameroon	110
Italy	115
Romania	118
Togo	200
Belgium	250
Mali	300
Kenya	302
Brazil	362
Poland	380
Cambodia	800
Syria	1,030
Hungary	1,724
Philippines	2,376
Netherlands	4,500
Malasyia	18,486
Uganda	20,941
Nigeria	51,916
Indonesia	77,332
Thailand	146,000
Total	**337, 342**

(Source: FAO, 2009).

Propagation of adequate catfish fingerlings from hatcheries is necessary because collection of bait from the natural aquatic habitats is season-dependent, environmentally unfriendly and potentially introduces microbes into *L. niloticus* value chains. On the other hand, although induced breeding techniques in catfish have been

perfected, adequately described and are routinely practiced in many hatcheries, shortage of seeds still persists in Africa (Sulem et al., 2006; Rasowo et al., 2007) due to a variety of reasons including parasitization of catfish eggs by aquatic fungi and bacteria (Rasowo et al., 2007). It is reported that hatch rates of *Clarias* eggs in many hatcheries in Africa vary from 8-70%, depending on the degree of sophistication in the particular hatchery (de Graaf et al., 1995; Macharia et al., 2005), the high fecundity of the species notwithstanding. From these studies, it is apparent that a lot of focus has been directed to addressing problems encountered in the juvenile stages of catfish, while the improvement of catfish in grow-out systems to meet the increasing demand for food fish is neglected. This could in part explain the low annual tonnage of farmed *C. gariepinus* from Africa. There is however renewed interest in reversing this situation through testing production systems with a view of widening the range of production systems (Imorou et al., 2007; Rasowo et al., 2008), improving the efficiency of resource use by catfish farmers (Emokaro & Ekunwe 2009) and testing the suitability of diets in grow out units for catfish (Amisah et al., 2009). These efforts to increase the production of *C. gariepinus* from farms would be enhanced by the use of carefully genetically selected stocks of the species.

Kenya has a natural diversity of populations of *C. gariepinus* in inland lakes, their associated water bodies and drainage basins (Barasa et al., 2017). It is unclear which of these harbors higher growth ability, so that selection for faster growth can be narrowed down to this population to boost production from grow-out systems. The genetic purity and characteristics of cultured stocks of the species widely used on fish farms and hatcheries country wide has never been ascertained. It is possible that these stocks have undergone inbreeding and their ability to grow hampered. Fine scale molecular genetic studies of local populations of *C. gariepinus* would be useful in

selective breeding programs. Ascertaining genetic diversity of populations of the species is also an important first step towards developing specific *C. gariepinus* strains through genetic improvement, for higher production, a process that has been applied to various terrestrial animal and plant species and some aquatic species (Lind et al., 2012). Similarly, genetic diversity is a crucial indicator of population persistence against fluctuating environmental factors, conservation worth and potential for commercial exploitation of the fish resource (Lind et al., 2012).
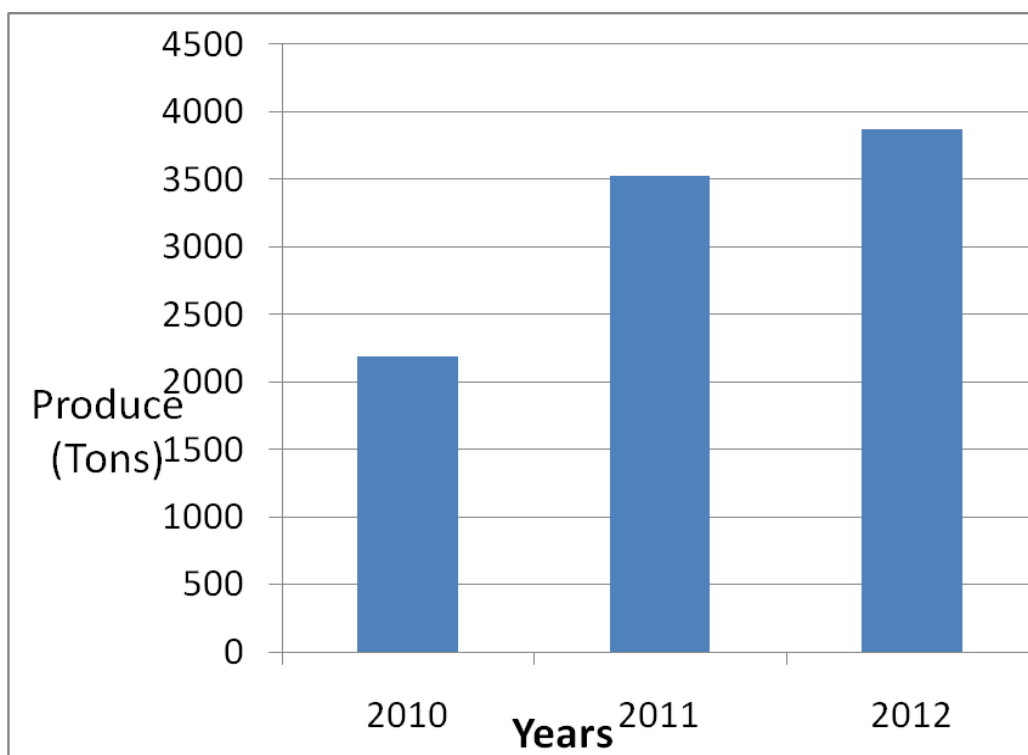
Figure 2.1: Annual production of farmed *Clarias gariepinus* in Kenya between 2010 and 2012. Source: Kenya Fisheries statistical Bulletins (2010; 2011; 2012).

2.2. Population Genetic studies on Clariidae

2.2.1. Mitochondrial and Microsatellite DNA Markers

Over the last two decades molecular markers have increasingly been used to measure genetic diversity in natural and aquaculture stocks of fish, generating more useful and reliable information than phenotypic markers that were used in classical genetics.

Phenotypic markers such as body dimensions, size and pigmentation are weak measures of genetic diversity in fish stocks, because these markers are environmentally influenced, polygenically inherited and have low heritabilities (Smith & Chesser, 1981). Allozyme, microsatellite DNA and mitochondrial DNA are some of the molecular markers commonly used.

Mitochondrial DNA (mtDNA) has several advantages over nuclear DNA and therefore has been increasingly used in molecular genetic studies including population genetic studies. Apart from its very simple structure, devoid of complex introns which otherwise interrupt genes but do not code for any amino acids, mtDNA is abundant, usually 500-1,000 copies per cell as one linkage group compared to only two copies of nuclear DNA. The mtDNA is maternally inherited, since mitochondria are located in the cytoplasm and only the egg contributes cytoplasm to the zygote. Such maternally derived molecules do not recombine genetically in progeny. Therefore, unlike nuclear DNA which gets reconstituted in each generation during meiosis, the only alterations to mtDNA are accidental changes caused by mutations, copying errors or other accidents. Therefore mtDNA preserves information about ancestry. In addition, the D-loop region of mtDNA has a high rate of evolutionary change, and therefore mtDNA has become a useful marker in studying evolutionary trends in species or populations. In clariid catfishes, mtDNA has been applied to infer phylogeny (Agnese & Teugels 2001; 2005; Mwita & Nkwengulila 2008), taxonomy (Agnese & Teugels 2005; Mwita & Nkwengulila, 2008), and also genetic structure and biogeography (Giddelo et al., 2002).
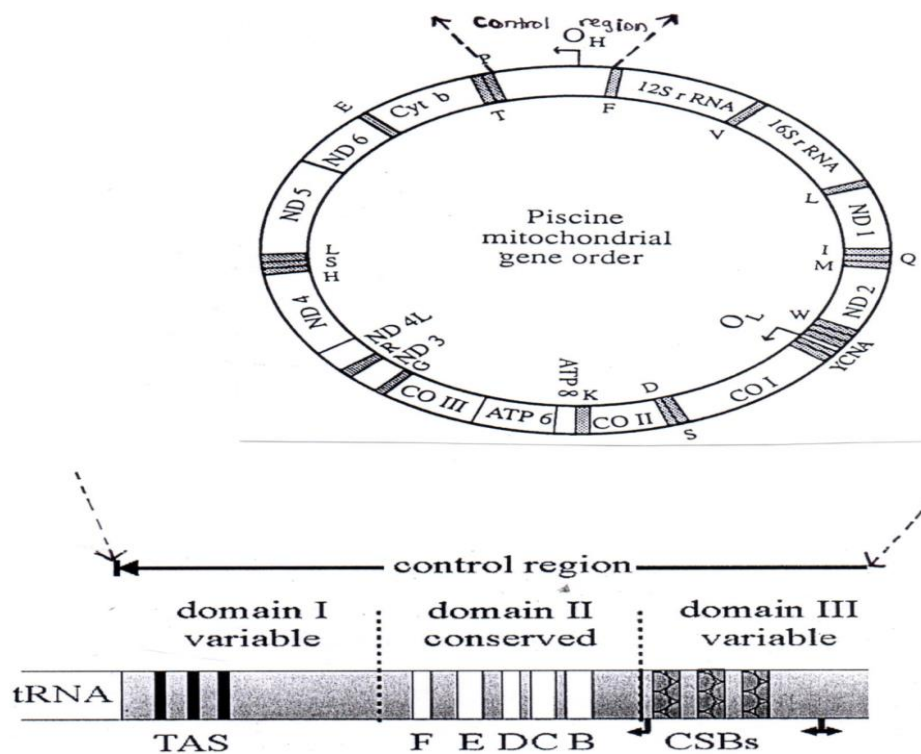
Figure 2.2: Structure of Piscine mitochondrial DNA. The conserved domain preserves ancestral history, while the variable domains capture changes in DNA due to evolutionary processes. Source: Meyer, A. (1993).

Microsatellites have become important molecular markers because of its abundance in genomes, even distribution, small locus size facilitating PCR-based genotyping, co-dominant nature of Mendelian inheritance, and high polymorphism. High polymorphism makes microsatellite DNA markers useful in studies of parentage analysis, quantitative genetics and population genetics (Tautz, 1989). In their study of genetic variability in *C. gariepinus* populations from Lake Victoria, Kenya, Galbusera et al., (1996) used 10 primer sets of microsatellite DNA to show high amounts of allelic polymorphism, with the number of alleles per locus ranging from 5 to 14, and heterozygosity ranging from 43 to 89% for the 38 samples analyzed. The number of alleles conformed to the Hardy-Weinberg equilibrium for most of the markers. Apart

from this study, which focused on using microsatellite DNA primers to study populations of *C. gariepinus*, Galbusera, (1997) studied genetic variation in two more populations of catfish from Kenya. These were populations from Tana River and Riakanau Dam; which were compared with populations of *C. gariepinus* from Cameroon, Syria, Egypt and Senegal. Therefore, only three populations of *C. gariepinus* from Kenya have been studied. It is unclear what the genetic structure and distinctness of the diversity of *C. gariepinus* resources, both wild and cultured, would be. Due to their versatility, microsatellite markers have also been used in cichlids to show genetic diversity and population structure (Abila et al., 2004; Hassanien & Gilbey, 2005), and also levels of inbreeding and gene flow (Hassanien & Gilbey, 2005).

2.2.2. Recent population genetic studies on Clarias.

The general goals of population genetic studies are to characterize the extent of genetic variation within a species and account for this variation. During the last two decades, a large amount of genotype and allele frequency data have been obtained from many fish species, mainly through protein and DNA based molecular genetic techniques. These studies have shown that most species are subdivided into distinct units that differ genetically from each other (Chakroborty & Leimar, 1987). Genetic differences between subpopulations will evolve over time if there is little or no gene flow between them (Chakroborty & Leimar 1987); so that restriction on gene flow may lead to genetic subdivision.

Total genetic variation in a species is a sum of between-population genetic variation and within-population genetic variation. Gene flow among sub-populations is a characteristic attribute of population genetic studies. *Clarias gariepinus*, being

highly predatory and omnivorous, is reported to pose a threat to native fish populations (Lal et al., 2003; Na-Nakorn et al., 2004; Senanan et al., 2004). Hybrids of catfish, popular in farming systems in Thailand and Malaysia, often escape to the wild and backcross with native *Clarias macrocephalus* (Lal et al., 2003; Nazia et al., 2010). Gene flow from escaped hybrids causes introgression in native stocks of *C. macrocephalus*, leading to poor performance in aquaculture systems. Using allozymic analysis to study genetic variation in Indian and Thailand stocks of *Clarias*, Lal et al., (2003) showed that *C. gariepinus* stocks in India were not pure, since allele frequencies departed from the Hardy Weinberg equilibrium. Since *C. gariepinus* is not found in Asia naturally, the authors attributed the presence of different gene pools in Indian stocks to mixing of stocks introduced from different farms and hatcheries, with some of the stocks having suffered drift. *Clarias gariepinus* from India was however shown to be different from populations from Thailand (Lal et al., 2003).

In their study on genetic impacts of hybrid catfish on native catfish populations in Central Thailand, Senanan et al., (2004) used allozymes and mitochondrial DNA to show introgression of *C. gariepinus* alleles into female *C. macrocephalus*. Thai farmers use *C. gariepinus* males to interbreed with *C. macrocephalus* females to obtain a hybrid that is popularly grown on farms every season for higher resistance to diseases and faster growth. Escaped hybrids, however, backcross with their mothers (*C. macrocephalus*) in the wild, so that as farmers collect *C. macrocephalus* during the next season, they do not collect pure but *C. macrocephalus* females introgressed with *C. gariepinus* alleles (Senanan et al., 2004). However, the levels of introgression were found to be low, so that *C. macrocephalus* female gene pools were not swamped with *C. gariepinus* alleles

flowing via escaped hybrids. The authors attributed the low levels of genetic introgression to limited gene flow from hybrids to *C. macrocephalus* due to relatively low number of escaped hybrids, depressed fitness of F1 and advanced generation hybrids and presence of reproductive barriers preventing extensive interbreeding between escaped hybrids and wild *C. macrocephalus*. Several studies have reported reduced fitness in F1 hybrids and later generation hybrids of fish from interbreeding between two genetically distinct groups, due to loss of abilities to adapt to local environments or a disruption of co-adapted gene complexes (Hallerman 2003; Miller et al., 2004). Reproductive barriers, which may be biological (e.g. low survival, low fertility, distinct reproductive timing and behaviour) or physical (e.g. preferences for distinct habitats and resources), limit interbreeding in fish (Happen & Taylor, 2001).

Clarias macrocephalus (Gunther 1864), the main clariid species in Asia, has received a lot of attention (Senanan et al., 2004; Na-Nakorn et al., 2004), due to its commercial importance. These studies have also been prompted by the threats to genetic distinctness of the native *C. macrocephalus* posed by aquaculture of the exotic *C. gariepinus* (Na-Nakorn et al., 2004). A need has therefore arisen to elucidate the population structure of *C. macrocephalus* in order to understand its effective population size and thus the adaptation capacity of the species to cope with changing environment. More recent studies using markers of greater resolution have shown genetic variations in various populations of *C. macrocephalus* in Asia (Na-Nakorn et al., 2004; Senanan et al., 2004), and *C. gariepinus* (Roodt-Wilding et al., 2010; Ojiambo, 2015; Barasa et al., 2014; 2016; 2017).

Population structuring in *C. macrocephalus* from Thailand has been reported by Na-Nakorn et al., (2004), who studied 26 populations from different geographical

locations and found two genetically distinct populations, one from the southern provinces including a population from the east, and one from Chaophraya and Mekong River Basin. Distinct genetic differentiation and population genetic structuring in the African catfish, *C. gariepinus*, has been reported by various studies undertaken on the species from different localities on the continent (Teugels et al., 1992; Galbusera et al., 1996; Giddelo et al., 2002; Ojiambo, 2015; Barasa et al., 2014; 2016; 2017). Overall, these studies demonstrate that the family Clariidae harbours high genetic diversity and therefore has high evolutionary potential.

Due to the high diversity in the family Clariidae, taxonomy of the various groups of fauna found in the family is still largely unresolved (Teugels et al., 1992; Mwita & Nkwengulila 2008). In the early ages, morphological and osteological features of the fish fauna were used to address questions of systematics (Teugels et al., 1992). However this 'classical' taxonomical approach was not always reliable, leading to mis-identification of some fish groups. These problems have now been overcome through molecular genetic techniques, and so molecular studies have been applied to not only accurately identify fish species and populations (Teugels et al., 1992; Lal et al., 2003; Senanan et al., 2004; Agnese & Teugels 2005), but also elucidate both evolutionary trends (Giddelo et al., 2002; Agnese & Teugels 2005) and phylogenetic origins (Agnese & Teugels 2001; 2005; Mwita & Nkwengulila 2008; Barasa et al., 2017) in the family clariidae. The study of genetic diversity in Kenyan populations of *C. gariepinus* would therefore be necessary to provide useful information to guide aquaculture and conservation programs.

2.2.3. Fecundity and size at first maturity in *Clarias*

2.2.3.1 Fecundity

Fecundity is the number of mature ova in the ovary of the female, just before spawning (Bagenal & Tesc, 1978). Fecundity, growth and survival are important phenotypic traits in both fisheries and aquaculture because they constitute fitness traits of any fish species. They are especially important in aquaculture since they determine the choice of a species for aquaculture enterprises (Pillay, 1993), and also impact on the profitability of the enterprise. In Fisheries, the three phenotypes (fecundity, growth and survival) are applied in fisheries management, because they determine the viability and persistence of a fish species, especially in habitats that are impacted by fragmentation, pollution and overfishing. For instance, in studying fecundity of fish species, the Gonadosomatic index (GSI) and size at first maturity (L_{m50}) are usually determined, and applied to identify the breeding season of a species, when spawning activity is most intense. Knowledge of the breeding season of a species is then used to effect closed seasons for a fishery (Smith & Walker, 2004; Njiru et al., 2006), and prohibiting fishing in identified breeding grounds for a prolonged time span for a species with asynchronous spawning (Smith & Walker, 2004). Similarly, where overfishing is a serious problem, a fish species will attain sexual maturity earlier, grow at a faster rate, and spawn more frequently, to compensate for the high fishing mortality (Vila-Gispert & Moreno-Amich, 2002; Blanck & Lamouroux, 2007; Souza et al., 2015).

Table 2.2. Spatial and size-related variation in fecundity of *Clarias gariepinus* in Africa.

Population	Body size (cm)	Fecundity	Mean fecundity	Reference
Lake Victoria-Kenya	48-87	7,966 -229,648	78,152	Owiti and Dadzie, 1989
Lake Victoria-Uganda	50 - 75	32,000-48,000		Greenwood, 1957
Lake McIlwaine-Zimbabwe	45 - 61	19,422 – 71,510		Munro, 1965
Lake McIlwaine-Zimbabwe	30 -70	4069 – 71,935		Clay, 1979
Lake Kariba-Zimbabwe	55	80,000		Bowmaker, 1973
Lake Chamo - Ethiopia		5,000 – 1,240, 000	337, 700	Dadebo et al., 2011
Lake Awassa		8,800 – 650, 000		Dadebo, 2000

Clariid catfishes naturally exhibit high fecundity. The Asian catfish, *Clarias batrachus*, of average length of 32 cm recorded a fecundity of 11,612 eggs in Bangladesh (Mookerjee & Mazumdar, 1950). In the study of maturity and fecundity in *C. gariepinus* of Lake Victoria, Kenya, Owiti & Dadzie, (1989) reported a mean fecundity of 78,152 eggs, with a range of 7,966 to 229,648 for fish size ranging from 48 to 87 cm total length (Table 2.2). On the Ugandan side of the lake, the species is reported to have a fecundity of 32,000 to 48,000 eggs in fish of size ranging 50 to 75 cm (Greenwood, 1957). In Lake McIlwaine of Zimbabwe, Munro, (1965) reported fecundity of *C. gariepinus* as 19,422, 54,428 and 71,510 eggs for fish of length 45cm, 50 cm and 61cm, respectively (Table 2.2). In the same lake, a similar investigation later reported fecundities of 4,069, 22,991 and 71,935 eggs for fish samples of 30 cm, 50 cm and 70 cm respectively (Clay, 1979), while the population in Lake Kariba, Zimbabwe, had 80,000 eggs for fish of 55 cm (Bowmaker, 1973) (Table 2.2). These results demonstrate that fecundity as a life-

history (lifetime pattern of reproduction and development) trait in *C. gariepinus* varies with the size of the fish, with bigger fish exhibiting higher fecundity than smaller fish. It also varies with a locality, where *C. gariepinus* of 50 cm length in Lake McIlwaine produces 22,000 eggs, while fish of almost comparable size (55 cm) in Lake Kariba in the same country has a much higher fecundity of 80,000 eggs. Similar variations have been reported in *C. gariepinus* populations in Ethiopia: a mean fecundity of 337,700 eggs (range of 5,000 to 1,240,000 eggs) in the Lake Chamo fish samples (Dadebo et al., 2011), and a somewhat lower fecundity ranging from 8,800 to 650,000 eggs in the Lake Awassa fish samples (Dadebo, 2000) (Table 2.2).

While differences in fecundity of *C. gariepinus* populations may be due to environmental differences, it may also be genetic. The influence of environmental factors on life-history traits has been demonstrated in several fish species, including brown trout (*S. trutta*) (Lockard, 1975; Nicola & Almodovar, 2002), Vendace (*Coregonus albula*) (Karjalainen et al., 2016) and Yellow perch, *Perca flavescens* (Feiner et al., 2017). According to Stearns & Crandall (1984), the evolution of life-history traits is constrained by trade-offs between the traits, their compatibility with other traits, the amount of genetic variation in the population and phylogenetic inertia. Therefore, while intraspecific variation in fecundity may be attributed to differences in food availability, conductivity, acidity or any other environmental variable in the habitat, it may also be due to genetic variation in the populations of the fish species (Karjalainen et al., 2016; Feiner et al., 2017). Therefore, a population of *C. gariepinus*, for instance, may exhibit a lower fecundity because of a lower genetic variation relative to another population of higher fecundity and higher genetic variation. The population of lower fecundity would show lower

viability and persistence in the habitat as opposed to the one of higher fecundity. Similarly, *C. gariepinus* of lower fecundity would be a less desirable candidate for use in aquaculture enterprises. While lower fecundity of the population may not directly help to infer survival of the individuals of *C. gariepinus*, the use of brood stock of the population in artificial propagation would be a disadvantage in the fewer eggs (and hatchlings) expected. There is a dearth of information on whether fecundity as a life-history strategy correlates with genetic variation of the fish population, especially in species like *C. gariepinus* that are economically important in the tropics. Therefore this study aimed to determine if genetic variation correlates with fecundity as a life-history trait in *C. gariepinus*.

2.2.3.3. Size at first maturity

This is the size of fish at which half the number of individuals in the population or species attains sexual maturity. It represents an important parameter in fish stock management and exploitation. Size and age at maturity influence population model estimates of sustainable harvest rates (Clark, 1991; Heino, 1998; Hard et al., 2008), and are used also in predicting the risk of overexploitation of stocks (Reynolds et al., 2005). It is important in monitoring of stocks to determine if enough juveniles in an exploited stock of fish mature and spawn (Ault et al., 1998; Jennings et al., 1998). The number of fish reaching maturity and contributing to the gene pool from which gametes are sampled for the next generation is a fitness trait for the fish population (Karna & Panda, 2011), as it influences persistence of the species (Heino, 1998; Hard et al., 2008), especially in a changing environment.

As a fitness trait, a higher L_m50 (size at maturity) would contribute to higher recruitment in the fishery, since fecundity correlates with size of fish. In

aquaculture, a higher L_m50 is desirable so that a suitable size for market is still obtained from breeding fish. If the size at first maturity is low, then spawners will not grow to reach a good size for market, since energy is allocated to reproduction at the expense of somatic growth (Quince et al., 2008). Fish in populations under high predation pressure or fishing pressure mature earlier (Vrtilek & Reichard 2016), and this reduces the asymptotic body size, since energy is reallocated from growth to reproduction (Kozlowski, 1992; Heino & Kaitala, 1999; Quince et al., 2008). Higher fishing pressure removes the bigger fish from the fishery, and induces changes that lead to precocious parents, maturing earlier (Gross, 1996; Locham et al., 2016), and this also reduces fecundity (Hamon et al., 2000; Hamon & Foote, 2005). Furthermore, since sexual maturation influences physiological and behavioural changes in a fish, size at first maturity is important in inferring information on fish growth, maximum size and longevity of the fish (Froese & Binohlan, 2000). Various methods are used to estimate size at first maturity (L_m50): linear interpolation, probit analysis, fitting of a logistic curve, or estimation from a plot of percent mature fish samples over length (Binohlan, 1998).

Table 2.3: Scale of sexual maturity stages used in the classification of *Clarias gariepinus*. Adopted from Hopson, 1972 and Lungayia, 1989.

Maturity stage	Description	Males	Females
I	Immature	Gonads are a pair of thin threadlike transparent sacs running along the dorsal wall of the body cavity	Sexes indistinquishable macroscopically
II	Developing	Testes are semi-transparent, flattened and firm. Serrations begin to form at one of the edges.	Ovaries are clear reddish, smooth, transparent and light. No thickening. Small ova begin to form and can hardly be seen from outside
III	Maturing, ripening	Testes begin to turn whitish, widen and thicken. No milt exudes when cut or squeezed. Serrations are more prominent.	Ovary is opaque and reddish-brown. Small ova are visible in a transparent matrix of follicular cells. Increases in size.
IV	Mature	Serrations become clear lobes as the testes thicken and enlarge in size. Testes become whitish, and release a small amount of milt when pressed.	Ovary becomes yellowish, fully swollen with translucent yellow ova. Pre-ova has larger volume than the matrix.
V	Running or spawning	Testes are cream and soft. Lobes are fully developed. Readily produces milt when lobes are cut and squeezed.	Ovary is yellow, very soft and swollen. Greenish yellow ova are visible through the superficial membrane. Ova are tightly packed. Little follicular matrix has formed.
VI	Spent	Testes are flat and large, with thin lobes. Milt extrudes when lobes are cut and squeezed.	Ovary is yellow, large and compact. Ova extrude from vent when abdomen is pressed.

In *C. gariepinus*, Dadebo et al., (2011) used the percentages of mature fish (P) of the length classes (L) as described by Echeverria (1987), to determine L_m50, and reported length at first maturity of the species in Lake Chamo, Ethiopia as 58 cm for females and 52 cm for males. On the other hand, Wudneh, (1998) reported L_m50 of

male and female *C. gariepinus* of Lake Tana, Ethiopia as 36 cm and 30.5 cm total

length respectively (Table 2.4). In Lake Awassa of the Ethiopian Rift, *C. gariepinus*

males matured at 33 cm while females matured at 34 cm total length (Dadebo,

2000). Similarly, Yalcin et al., (2001) reported a size at first maturity of 25.05 cm

and 24.70 cm total length of females and males, respectively, of *C. gariepinus* in

**Table 2.4. Spatial variation in size at first maturity of *Clarias gariepinus*
populations.**

Population	Sex of fish	Size at first maturity	Reference
Lake Chamo- Ethiopia	F	58	Dadebo et al., (2011)
	M	52	
Lake Tana- Ethiopia	F	30.5	Wudneh, 1998
	M	36	
Lake Awassa- Ethiopia	F	34	Dadebo, 2000
	M	33	
River Asi- Turkey	F	25.05	Yalcin et al., (2001)
	M	24.70	
Lake Victoria- Kenya	M	41-45	Owiti and Dadzie, 1989
	F	41-45	

`River Asi, Turkey. In the study of maturity and fecundity of *C. gariepinus* of Lake

Victoria, Kenya, Owiti & Dadzie, (1989) reported a size at first maturity of 41-45

cm for both sexes (Table 2.4). These differences in L_m50 in populations of *C.*

gariepinus represent the variability in fitness of the species that could arise in

populations within different localities in a country or in different localities of

different countries or regions. Such inter-population differences in L_m50 could be

attributed to environmental (food resources and water quality (Souza et al., 2015)),

the degree of fishing mortality (Wootton, 1998; Dadebo et al., 2011), and physiological or genetic differences.

Genetic influences on fitness traits such as L_m50 could result from differences in population sizes, where a smaller population would suffer loss in fitness due to inbreeding, bottlenecks or genetic drift that diminishes genetic variability and the evolutionary potential of the species. However, for populations whose sizes are comparably large, and therefore panmictic, genetic influences on fitness would result if levels of genetic diversity are different. There is a dearth of information on genetic influences on fitness traits in fish species, and since correlations of genetic variation and fitness in fish are often species and trait-specific (Knaepkens, et al., 2002), the correlations warrant investigation, especially for tropical species like *C. gariepinus*. Size at first maturity has been investigated in many fish species, both marine (Hutchings & Jones, 1998; Agembe, 2012; McBride et al., 2013; Tampubolon et al., 2014) and fresh water (He & Stewart, 2001; Njiru et al., 2006; Blanck & Lamouroux, 2007; Joanna et al., 2011; Maithya et al., 2012), which reflects its importance in the management of fisheries resources globally. In most of these studies, size at first maturity is presented as a parameter which influences fitness traits of growth, survival and fecundity or reproductive effort (Blanck & Lamourou, 2007; Souza et al., 2015).

When a fish acquires sexual maturity, a substantial energy budget is invested into reproduction, by developing gametes and the actual reproduction events or reproduction in future (Quince et al., 2008; Sibly et al., 2013; Souza et al., 2015). This conversion of energy into reproductive effort limits amount of energy available for somatic growth and survival which are necessary for future reproduction of the species (Link & Burnnett, 2001; Souza et al., 2015). Therefore, in normal

physiological activities of a fish species, the allocation of energy for reproduction is a trade-off with growth, survival and body condition (condition factor) (Souza et al., 2015), which are key fitness traits in fisheries and aquaculture. Studies report that fitness traits or life-history strategies are influenced by demographic, physiological and genetic factors (Vila-Gispert & Moreno-Avich, 2002; Blanck & Lamouroux, 2007), which consequently determine energy and biomass allocation in particular fish species (Vila-Gispert & Moreno-Avich, 2002; Blanck & Lamouroux, 2007; Souza et al., 2015).

If size at first maturity of a fish species is a function of genetic factors for instance, phenotypic variation would be observed in populations of the species of different genetic characteristics. Therefore one population would present fish that sexually mature earlier or at a smaller size, while in another population, fish would mature latter or at a bigger size. The consequences of these phenotypic manifestations would be reduced viability and persistence by a population of smaller size at first maturity, and a higher viability in one of bigger size at maturity. Although these correlations are rarely tested in aquaculture, a species with a smaller size at maturity may present poor growth rates, survival and food conversion rates in aquaculture units, since a substantial amount of energy is invested in reproduction. The best example of this is *O. niloticus*, whose size at first maturity appears to be a function of the environment. In the wild, the species reaches sexual maturity at 2-3 years old at a size of 30 to 40 cm (Moreau et al., 1986; Kolding, 1993; Njiru et al., 2006), but in aquaculture units, *O. niloticus* reaches sexual maturity at 2 to 3 months old, when they are just about 12 cm long and weight of 20g (Bolivar et al., 1993; Egna & Boyd, 1997).

CHAPTER THREE

MATERIALS AND METHODS

3.1. Study sites

Samples of *C. gariepinus* were collected from a total of 10 sites across Kenya, which included 5 lakes (Victoria, Kanyaboli, Turkana, Jipe and Baringo) and 5 public fish farms, (Sangoro Aquaculture Center, Sagana Aquaculture Center, University of Eldoret Fish Farm, Kibos Fish Farm, and Wakhungu Fish Farm) (Figure 3.1). Samples from all the 10 sites were used in the mitochondrial DNA analysis (Table 3.1), while samples from only 8 sites (Lakes Victoria, Kanyaboli, Turkana and Baringo, and four fish farms: Sangoro Aquaculture Center, Sagana Aquaculture Center, University of Eldoret Fish Farm and Kibos Fish Farm) of the 10 sites were used in the microsatellite DNA analysis (Table 3.2).

3.1.1. Lake Victoria

This is the largest freshwater lake in Africa, and the second largest in the world (LVBC, 2011), with a drainage basin of 180,000 km^2. The lake is a transboundary resource, with a total surface area of 69,000 km^2, shared between Kenya, Uganda and Tanzania, and lies at latitudes 2.5° and 1.5°N and longitudes 32° and 35°E. Sampling for *C. gariepinus* was done on the Kenyan portion of the lake, at Kobala beach which lies at 34°38′E and latitudes 0°21′S, Chuowe area of Kendu Bay in Homa Bay County.

3.1.2 Lake Turkana

It is an endorrheic lake drained mainly the Omo River from Ethiopia, and the seasonal Turkwell River from the Kerio Valley. It lies at 3° 37' N 36° 0' E, within the eastern arm of the Rift Valley. It is the world's largest desert lake, with a surface area of 68,680 km^2 at an altitude of 360 m above sea level. Fish samples of *C. gariepinus* were collected from beaches of the Ferguson Gulf, which is highly fertile, because of high total alkalinity, located at Kalokol township of Lodwar, Turkana County.
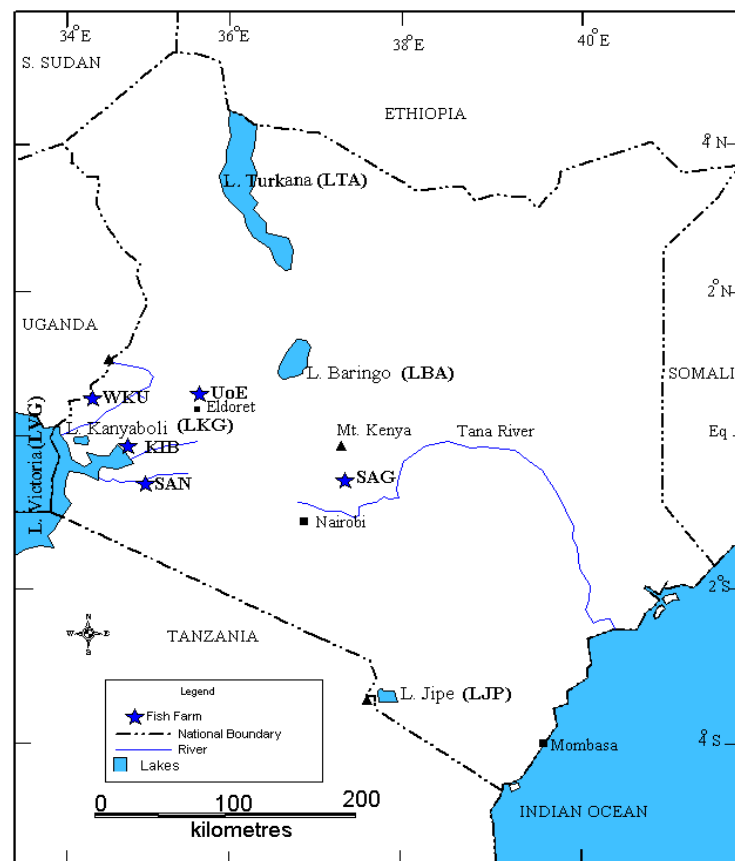
Figure 3.1: Map of Kenya with the location of 10 sampling sites for samples of *C. gariepinus*. Natural populations were collected from 5 lakes: Lakes Victoria (LVG), Kanyaboli (LKG), Turkana (LTA), Baringo (LBA) and Jipe (LJP), represented on the map in light blue colour. Farmed populations were collected from 5 fish farms: Sagana Aquaculture Center (SAG), Sangoro Aquaculture Center (SAN), University of Eldoret Fish Farm (UoE), Kibos Fish Farm (KIB) and Wakhungu Fish Farm (WKU), represented by a star in deep blue colour. Sampling for fecundity was done on fish samples from Lakes Victoria (LVG), Baringo (LBA) and Kanyaboli (LKG). Source: Author, 2017.

3.1.3. Lake Kanyaboli

It is a satellite of Lake Victoria, located in the extensive Yala swamp in Siaya County. It has a surface area of 10.5 Km^2, a maximum depth of 4.5 m and is fringed by dense papyrus vegetation (Plate 1), bordered on the north by River Nzoia and to the south by River Yala. The massive papyrus (*Cyperus papyrus* and the sedge *Echinocloa*) swamp separates the lake from L. Victoria and apparently prevents any exchange of fish between the two lakes. It lies at latitudes 00°04′30″N, and longitudes 34°09′36″E, and at altitude of 1140 m above sea level.

Plate 3.1: Dense papyrus fringe around Lake Kanyaboli at Kadenge beach, one of the sampling sites for *Clarias gariepinus* for studies on both genetic analyses and fecundity. Water at the fore forms the channel from the landing beach to the lake. Source, Author, 2012.

Table 3. 1: Sampling sites, coordinates, sample sizes, weights and lengths and sequence accession numbers of *Clarias gariepinus* samples from 10 sites in Kenya sequenced from the mtDNA D-loop control region gene. Samples from 8 (LVG, LKG, LTA, LBA, SAN, SAG, UoE and KIB) of these sites were also genotyped with 6 microsatellite DNA loci.

Site	Population Code	Coordinates	Sample size	Range in weight (g)	Range in length (cm)	GenBank sequence Accession numbers
Lake Victoria	LVG	34°38′E, 0°21′S	24	47.3-510	15.2-56	KC594181-KC594205
Lake Kanyaboli	LKG	00°04′30″N, 34°09′36″E	28	141-850	28.7-49.5	KC594206-KC594232
Lake Turkana	LTA	3° 37' N 36° 0' E	28	82-3,010	25-74	KJ814254-KJ814281
Lake Baringo	LBA	0° 38' N 36° 05' E	24	120-3,004	26-77.5	KJ814282-KJ814305
Lake Jipe	LJP	3° 35' S 37° 45'	32	138-702	18-48.5	KJ814306-KJ8143037
Sangoro Aquaculture Centre	SAN	0° 30' N 0° 45' N	29	140-1,855.1	28.5-71.9	KJ814338-KJ814367
Sagana Aquaculture Centre	SAG	0° 39' S 37° 12'E	23	168-2,424	34-76	KJ814368-KJ814390
University of Eldoret Fish Farm	UoE	0° 57' N 35° 30' E	29	320-1,227	29.6-55	KJ814391-KJ814419
Kibos Fish Farm (LBDA)	KIB	0°04'S 4°48'E	30	360-1,740	36-60	KJ722140-KJ722165
Wakhungu Fish Farm	WKU	0° 30' N 0° 00'E	29	180-900	25-47.6	KJ814420-KJ814444

3.1.4 Lake Baringo

It has a surface area of 130 km^2 located at 0° 38' N 36° 05' E and altitude of 970 m above sea level. It is drained by several rivers, including Ol Arabel, Mukutan, Endao and Chemeron which are seasonal, and Molo, and Perkerra which are perennial. The Lake loses water through underground seepage (Onyando et al., 2005), which together with surface evaporation because of high temperatures, help to maintain the waters fresh.

3.1.5 Lake Jipe

Lake Jipe, with a surface area of 30 km^2 lies at an altitude of 705 m above sea level, and at 3° 35' S 37° 45' E. It straddles both Kenya and Tanzanian borders, being situated to the south east of Kilimanjaro in Taita Taveta County and in the southern Kilimanjaro region of Manga district, Tanzania. The Lake is fed by River Lumi, and outflow is via the Pangani River in Tanzania. It is colonized by mainly *O. niloticus* and *C. gariepinus*.

3.1.6 Sagana Aquaculture Center

Located at Sagana township of Kirinyaga county 106 km north of Nairobi, Sagana Aquaculture Center lies at 0° 39' S 37° 12' E and altitude of 1,231 m above sea level. The Center was started in 1948 by the British colonial Government to support aquaculture development in the country, and has 109 operational earthen ponds, of which 72 are for research and the rest for fish production. The Center also has a hatchery unit for propagation and nursery of *O. niloticus*, *C. gariepinus* and *C.*

auratus. Water supply is harnessed from the neighboring Ragati River, and flows naturally by gravity.

3.1.7 Sangoro Aquaculture Center

It is situated at 0° 30' N 0° 45' N in the lower plains of Nyakach along the Sondu Miriu River at Nyakwere. It produces mainly *O. niloticus*, *C. gariepinus* and *C. auratus*. It has a total of 40 ponds covered with pond liners and a hatchery for propagation, nursery and rearing of the fish.

3.1.8 University of Eldoret (UoE) Fish Farm

It is located at the University of Eldoret, developed by the Department of Fisheries and Aquatic Sciences in 2003, for teaching, research and fish production. It lies at 0° 57' N 35° 30' E, and altitude of 2,180 m above level on a flat land along the Eldoret-Ziwa-Kitale road. Its water supply is from a reservoir created by the surrounding extensive Marura swamp. It has a total of 42 earthen ponds of different sizes, and a modern hatchery for propagation and nursery rearing of *C. gariepinus* and *O. niloticus* and *C. auratus*.

3.1.9 Kibos Fish Farm

Owned by the Lake Basin Development Authority (LBDA), Kibos Fish Farm lies at 0°04'S 4°48'E, on the outskirts of Kisumu city. It has a total of 13 ponds, and an outdoor hatchery, where artificial propagation of *C. gariepinus* is done. The farm also grows *O. niloticus* in earthen ponds.

Plate 3.2: One of the earthen ponds at Kibos Fish Farm used to rear *Clarias gariepinus*. Source: Author, 2012.

3.1.10 Wakhungu Fish Farm

It is located at 0° 30' N 0° 00' E in Busia County, and has a total of 15 ponds, in which *C. gariepinus*, *O. niloticus* and *C. auratus* are reared. It has a modern hatchery for propagation and nursery of *C. gariepinus*.

3.2. Collection of fin clips

During field work, fin clips were collected from samples of *C. gariepinus* for use in the laboratory as the source of DNA. For natural populations, fish samples were taken from fishermen's landings, while for fish farms, samples were taken from the rearing ponds. Sampling exercise was done between January to April 2012 for all the sites, except for Lake Jipe, where sampling was done in February 2014. Sample sizes ranged from 23 to 32 (Table 3.1). At each sampling site, samples of catfish were obtained and approximately 25 mg piece of fin tissue clipped off using a clean pair of scissors. The fin clip was preserved in 95% ethanol in a sterile cryovial (eppendorf) tube (1.5 ml). Each tube was clearly labeled with the specimen number, and taken to the laboratory for molecular analysis.

3.3. DNA extraction

From each fin tissue, DNA was extracted using the Invitrogen Purelink genomic DNA extraction kit using the Manufacturer's protocol, as used in Barasa et al., (2014; 2016; 2017). DNA extraction from fin clips of the African catfish was done using the protocol by the Invitrogen PureLink genomic DNA mini kit. 25 mg of fin tissue was placed in a clean vial and 180 μl of genomic digestion buffer added. Then 20 μl of proteinase K enzyme was added to the vial and incubated at 55°C for 2 hours with vortexing every 30 minutes. RNase enzyme was added, vortexed and incubated at room temperature. On a cold or rainy day, incubation was done at 37°C for 20 minutes to allow for complete enzyme action. The sample was centrifuged for 3 minutes at 14,000 rpm to remove any impurities. 200 μl of Genomic lysis or binding buffer was added to sample, and then 200 μl of absolute alcohol added, vortexed for homogenization.

The lysate was transferred to a spin column and centrifuged for 1 minute at 14,000 rpm. The flow throw was discarded, spin column transferred to a collection tube, 500 μl of wash buffer 1 added and spinned for 1 minute at 14,000 rpm. The flow through was discarded and spin column transferred to a new collection tube, 500 μl of wash buffer 2 added and spinned for 1 minute at 14,000 rpm. The flow through was discarded and the spin column transferred to a new collection tube. This was spinned again for 11 minute at 14,000 rpm to wash off any excess alcohol, which would otherwise interfere with downstream manifestation of DNA. The spin column was transferred to a clean microcentrifuge tube (1.5 ml) and eluted with 50 μl of Genomic elution buffer. The purity of eluted DNA was checked by nanodrop spectrophotometry (on a nanodrop spectrophotometer 2000), where the yield of DNA was also quantified (ng/μl) (Appendix 1 to 7), and the DNA visualised electrophoresis on 1.6% agarose gel at 100 W for 35 minutes, and viewed under ultraviolet light (uv) (Appendix 10). The DNA was stored in freezer (-20°C) for PCR amplification later. DNA extraction and PCR amplification for D-loop ananlysis were done at the Biosciences eastern and central Africa-International Livestock Research Institute (BecA-ILRI Hub) laboratories in Nairobi, Kenya. For microsatellite DNA analysis, extracted DNA was freeze-dried and freighted to the University of the Free State in South Africa, where PCR amplification and genotyping was done at the Department of Genetics laboratories.

3.4 Primers

Mitochondrial D-loop region primers were used for amplifying the D-loop region. The forward primer was L16473 5′- CTA AAA GCA TCG GTC TTG TAA TCC- 3′ while the reverse primer was H355 5′-CCT GAA ATG AGG AAC CAG ATG- 3′. Both primers were reconstituted by adding low salt TE buffer to the primers for the

stock solution. To the forward primer, 205 µl of buffer was added, to make a stock solution of 100 pmoles/µl. A total of 228.3 µl of TE buffer was added to the reverse primer, to make a stock solution of 100 pmoles/ µl. From each primer, 10 µl was picked and mixed with 90 µl of nuclease free water (NFW), to make a working concentration of 10 pmoles/µl.

3.5 Polymerase Chain Reaction (PCR)

Extracted DNA was PCR amplified in a thermal cycler using a pair of primers (L16473 5′ –CTA AAA GCA TCG GTC TTG TAA TCC-3′ and H355 5′- CCT GAA ATG AGG AGG AAC CAG ATG- 3′ as the forward and reverse primers respectively) for D-loop gene as used by Nazia et al., (2010). The reaction volume was 20µl, containing bioneer premixes, and 18 µl distilled water, 0.5 µl forward primer and 0.5µl reverse primer, and 1µl of template (sample) DNA normalized to 50 ng/µl, i.e. 1 µl of sample to contain 50 ng DNA. This was run in a thermal cycler under the following PCR conditions (Nazia et al., 2010): 5 minutes of initial denaturation at 94°C, and 35 cycles each of 30 seconds at temperature of 94°C, 30 seconds at annealing temperature of 56°C, 1 minute at 72°C, and a final elongation of 10 minutes at 72°C. PCR products were electrophoresed on 1.6% agarose gel stained with 2.5 µl of gelRed, and 3 µl of each sample of PCR product was loaded into wells, at 100W for 35 minutes, and visualized under ultraviolet (UV) light.

3.6 Purification of PCR products for sequencing

PCR products were purified using the sodium acetate-alcohol precipitation method, as described by Uthice & Benzie (2003), which involved pelletization of DNA under low temperatures, which is washed off impurities and recovered in distilled water. To a sample of PCR products (16 µl) were added 1/10 volumes of 3 molar sodium acetate

of pH 4.8, and 2.5 volumes of absolute alcohol (iced). A master-mix of the two was prepared to cover all samples of PCR products. The mixture was spinned (Eppendorf centrifuge 5424R) for 20 minutes at 14,000 rpm at 4ºC, to pelletize the DNA. The supernatant was discarded and pellet washed with 300 μl of 70% ethanol.

The mixture was spinned (Eppendorf centrifuge 5424R) for 15 minutes at 14,000 rpm at 4ºC. The supernatant was discarded, and the pelletised DNA dried briefly on paper towels, and transferred to a hood (Aura 550E, Labcaire) for 20 minutes for complete drying. The DNA was re-suspended in 20 μl distilled water. The purified products were stored at -20ºC for use later (sequencing). However, the quality (purity) and quantity of the products and therefore the success of the purification process was confirmed by taking nanodrop readings (on Nanodrop spectrophotometer 2000) and running samples on 1.6% agarose gel electrophoresis. Before loading the DNA in wells in the agarose gel, 3μl DNA was mixed with 3 μl orange loading dye in a dilution plate, and all mixture (6 μl) loaded in respective wells. The first well on the gel was loaded with 6 μl of 1 kilo-base (kb) ladder to help in determining the size of the PCR product. The samples were electrophoresed at 100 w for 35 minutes, before visualization under UV light (Appendix 11).

3.7 Sequencing

Purified amplicons of the D-loop region were sequenced with the D-loop reverse primer H 355 on an ABI 3730xl Automated sequencer. The BigDye terminator premix sequencing kit (cat. No. 4336911) was used for sequencing reactions, following the manufacturer's protocol. Products of sequence reaction were cleaned by precipitation in absolute alcohol, re-suspended in Hi Di^{TM} Formamide, before running on the sequencer of 50 cm capillary length.

3.8. Microsatellite DNA analysis protocol

Extracted DNA samples of *C. gariepinus* from 8 sites were tested using 6 SSR markers (Table 3.2), of which 4 (Cga1, Cga3, Cga9 and Cga10) were developed by Galbusera et al., (1996), and 2 (Cba2, Cba19) were developed by Yue et al., (2003). For 4 markers (Cga1, Cga9, Cga10 and Cba2), PCR reaction was carried out in 25 µl reaction volume, comprising of 1.25 µl each of forward and reverse primers, 8 µl of distilled water, 12.5 µl of 2x Kapa2G™ Robust HotStart Ready mix, and 2 µl of template DNA sample.

Table 3.2: Microsatellite DNA primers with nucleotides, range of allele size, dye colour and reference for the 6 loci used to genotype samples of *Clarias gariepinus* from 8 sites in Kenya.

Primer	Nucleotides	Size range	Dye colour	Reference
CGA01	5′ GGC TAA AAG AAC CCT GTC TG 3′ 3′ TAC AGC GTC GAT AAG CCA GG 5′	92-104	Green	Galbusera et al., 1996
CGA03	5′ CAC TTC TTA CAT TTG TGC CC 3′ 3′ ACC TGT ATT GAT TTC TTG CC 5′	142-168	Blue	Galbusera et al., 1996
CGA09	5′ CGT CCA CTT CCC CTA GAG CG 3′ 3′ CCA GCT GCA TTA CCA TAC ATG 5′	180-196	Green	Galbusera et al., 1996
CGA10	5′ GCT GTA GCA AAA ATG CAG ATG C 3′ 3′ TCT CCA GAG ATC TAG GCT GTC C 5′	102-138	Green	Galbusera et al., 1996
CBA02	5′ GCC CTG CGA ACA TCT CCA 3′ 3′ TGG CTC CAG CAC TCA CAA 5′	176-190	Yellow	Yue et al., 2003
CBA19	5′ CAG GGC TAA ATT ACC CAT AAT CA 3′ 3′ GGC ATG TGT TAT AAC ATG TGA GG 5′	215-255	Green	Yue et al., 2003

For Cga3, the PCR reaction mix were the same as for above, except 6 µl water and 2 µl mgcl$_2$ were used, while for Cba19, 7 µl water and 1 µl mgcl$_2$ were used. The thermal profile for PCR reaction for Cga1, 3, 9 and 10 was: initial denaturation of 3 minutes at 95°C, 35 cycles of amplification each at 95°C for 15 seconds, 15 seconds at respective annealing temperature for each primer, and 15 seconds at 72°C, with a final elongation step of 10 minutes at 72°C and with 15°C hold.

For Cba2 and 19, thermal profile for PCR was initial denaturation of 3 minutes at 94°C, 35 cycles of amplification of 30 seconds at 94°C, 30 seconds at 56°C and 1 minute at 72°C, with final elongation step of 5 minutes at 72°C and with a 15°C hold.

Samples were co-loaded with primer sets based on the annealing temperatures of the markers and PCR conditions, i. e.

Load 1 Cga03 + Cga10: marker sets had annealing temperature of 60°C, and similar PCR thermal profiles.

Load 2 Cba02 + Cba19: marker sets had annealing temperature of 56°C and their cycle parameters were the same.

Load 3 Cga01 and Cga09: since each marker had different annealing temperatures, they were loaded separately. Success of PCR was confirmed by electrophoresis on 2% agarose gel at 100 W for 35 minutes. 1 µl of diluted PCR product was added to 8.75 µl of Hi-Di Formamide and 0.25 µl of GeneScan-350 ROX size standard and genotyped on the genetic analyzer ABI 3130.

3.9. Determination of life-history parameters in populations of *Clarias gariepinus* from Lakes Victoria, Baringo and Kanyaboli of Kenya.

3.9.1. Fecundity

The study focused on three populations of *C. gariepinus*: Lakes Victoria (LVG), Baringo (LBA) and Kanyaboli (LKG). LVG and LKG represented populations of higher genetic variation, while LBA represented a population of lower genetic variation (Barasa et al., 2017), and following microsatellite DNA analysis in section 4.1.2 and Table 4.2 in the current study. Fish samples were collected monthly for 5 months, from September 2016 to January 2017, from beaches of the three lakes (Appendices 12 to 26). A total of 499, 527 and 354 fish were sampled from Lakes Victoria, Baringo and Kanyaboli respectively. For LVG samples, fish sizes ranged 21 cm and 51.8g to 107 cm and 3,762g (Appendices 12 to 16). Fish samples from LBA ranged in size from 29cm and 136g to 100 cm and 7, 865g (Appenndices 17 to 21), while for LKG sampled fish ranged in size from 21cm and 39g to a length of 82cm and weight of 3,780g (Appendices 22 to 26). For each fish sample, total length was taken (to the nearest 0.1 cm) on a measuring board, and total weight taken (to the nearest 0.1g) on a top loading digital weighing balance (maximum weight 6 kg). The fish was then dissected, the sex recorded after observing the gonads, and gonads removed carefully and weighed on a top loading digital balance for small weights (maximum 600g*0.1). The gonad maturity stage of the fish was recorded after careful visual observation of the gonads, and following Bagenal, (1978) and Lung'ayia, (1989). The maturation scheme was as follows: I- immature, II- immature, III- maturing, IV- mature, V- active, and VI- spent (Table 2.3).

For female fish with eggs (running ripe or maturity stage 5) in the ovary, the removed ovaries (both lobes of ovaries for each fish sample) were placed in small labelled

polythene bags and dissolved in Simpson's solution for estimation of fecundity in the laboratory.

In the laboratory, each of the preserved ovaries was analyzed for fecundity. The sac of the ovary containing the eggs was removed carefully, and the mass of the eggs (both ovaries for each fish sample) weighed again on a digital balance (to the nearest 0.01g). Fecundity was determined using the gravimetric method (Bagenal, 1978). The number of eggs making up 1g for each ovary was counted and recorded. Two more repeats were made on batches of eggs making up 1g for the same sample of ripe ovary, in order to make three replicates, and an average of the three determined, to get an accurate estimate of the total number of eggs making up 1g. The total number of eggs in the ovaries for each fish sample was calculated by multiplying the average number of eggs making up 1g by the total weight of the eggs in both ovaries (Appendices 12 to 26). Relative fecundity of each fish sample was then computed by dividing the total number of eggs by the weight of each female fish from which the eggs were obtained.

3.9.2. Size at first maturity

Size at first maturity for the fish samples was determined according to King, (1995) and recently used by Locham et al., (2014). The proportion of mature fish individuals (fish with gonad maturity stages III-V) (Appendices 27 to 32) was determined for each length class, and the results fitted to a logistic function using least squares regression in Microsoft Excel.

3.9.3. Water quality parameters

During the monthly sampling for fish at each of the three Lakes, water samples were also collected, for analysis of nutrients (total nitrogen and total phosphorus). All water samples were fixed *in situ* with sulphuric acid, and transported to the laboratory for analysis. Physico-chemical parameters (dissolved oxygen, temperature, specific conductivity, Ph and salinity) were taken at each site using a hydro-lab probe. Total phosphorus was analyzed by the ascorbic acid-molybdate method, while the Kjeldahl method was used to analyze for total nitrogen of the water samples.

3.10. Data analyses

3.10.1. Mitochondrial (mtDNA) DNA analysis

Raw sequences were aligned, assembled and trimmed in the CLC Bio Main work bench software. This gave a uniform length for the sequences with base pairs of 346. Duplicate haplotypes were identified using DNAsP (Librado & Rosas, 2009). Genetic diversity within populations was determined as number of distinct haplotypes, haplotype frequencies and nucleotide diversities, using DNAsP and Arlequin (Excoffier et al., 2005). Arlequin was also used to determine genetic differentiation between populations, expressed as F_{ST} (Wright, 1965). A maximum likelihood tree was drawn using MEGA (Tamura, 2007), with 1,000 bootstrap repeats, and *Clarias liocephalus* as the out-group. A minimum spanning Network resolving the relationships between the D-loop haplotypes was drawn using Network 4.56, with a median joining approach (Bandelt et al., 1999), available at http://www.fluxus-engineering.com.

3.10.2. Microsatellite DNA data analysis

Microsatellite DNA data was scored on Gene mapper, and allele frequencies per population (LVG, LKG, LTA, LBA, SAN, SAG, UoE and KIB), allele counts per population and the size of alleles recorded as per Barasa et al., (2017). The mean observed heterozygosity (H_O) and expected heterozygosity (H_E) values for each population were determined in Microsatellite Toolkit (Park 2001), while the mean number of private alleles were computed in Arlequin version 3.5 (Excoffier et al., 2005).

Departures from Hardy-Weinberg equilibrium (HWE) were tested using Arlequin 3.5 based on permutation method (1,000 iterations) to estimate levels of F_{IS} values. Similarly, linkage disequilibrium was tested using a randomization test (a permutation method with 1,000 iterations), in Arlequin, and levels of significance tested by the Chi square method. Analysis of molecular variance (AMOVA) (Excoffier et al., 1992) was determined in GenAlEx 6.502 (Peakall & Smouse, 2012). Using AMOVA, the total variance was partitioned into covariance components attributed to within individuals, among individual and among population differences, with fixation indices computed as F_{CT}, F_{SC} and F_{ST} respectively (Wright, 1965). Similarly, the neighbor joining tree showing the phylogenetic relationship of the alleles of the *C. gariepinus* samples from 8 different sites was generated in GenAlEx 6.502 (Peakall & Smouse, 2012).

To estimate the number of populations of *C. gariepinus* present in the microsatellite dataset, the program STRUCTURE 2.3.4 (Pritchard et al., 2000; Falush et al., 2007) was used. STRUCTURE uses a model-based full Bayesian, Markov Chain Monte Carlo (MCMC) approach to assign individuals or samples to the most likely clusters

based on the frequencies of alleles of samples, to minimize Hardy Weinberg disequilibrium and gametic phase disequilibrium between loci within groups. Simulations were on putative populations of K from 2 to 7. For each K, the posterior probability was calculated using a model-based assignment. Burn-in was set at 10,000 steps, followed by 100,000 MCMC iterations. Simulations were run ten times for each K to check for convergence of the MCMC. Clustering was performed under the admixture model without prior population information, and with correlated allele frequencies between populations. To determine the most likely number of clusters fitting the dataset, the rate of change in the log probability of data between successive K values was evaluated in Structureharvester (Earl & vonHoldt, 2012), a Python program with a web-based front-end for quickly parsing and summarizing output data from Structure, available at http://taylor0.biology.ucla.edu/structureHarvester.

This was combined with a series of runs of STRUCTURE to identify all the clusters constituting the samples. Membership coefficient of each of the 8 pre-defined populations in each of the identified genetic clusters was determined as an average of outputs of ancestry proportions generated by STRUCTURE 2.3.4, as determined in Barasa et al., (2017).

To determine genetic differentiation between populations of *C. gariepinus*, Arlequin 3.5 (Excoffier et al., 2005) was used to calculate pair-wise estimates of $F_{ST.}$ The Fixation index F, is a widely used measure of genetic differentiation between populations (Wright, 1978), and has a minimum of 0 for no genetic differentiation, and a maximum of 1for a fixation of alternative alleles in the sub-populations.

3.10.3. Analysis of data on fecundity and size at first maturity

Mean values of monthly and overall fecundity, and condition factor were computed in Excel, and analysis of variance across populations computed in MINITAB. Size at first maturity (L_{m50}) was determined from a logistic curve equations:

$$Ln \ (1(1/P1) -1 = S1 - S2 * L$$

$$L_{M50} = S1/S2,$$

Where PL is the probability of maturity at length L, S1 is the intercept, and S2 the slope.

CHAPTER FOUR

RESULTS

4.1. Genetic diversity of *Clarias gariepinus* inferred from mitochondrial D-loop control region and microsatellite DNA markers.

4.1.1. Mitochondrial D-loop control region

The nucleotide diversity (π) for the lake (natural) samples ranged from a low of 0.006 in Lake Kanyaboli (LKG) to a high of 0.037 in Lake Jipe (LJP) (Table 4.1). In samples from fish farms, nucleotide diversity was low in both Sangoro (SAN) and Wakhungu Fish Farm (WKU), at 0.006, but higher in Sagana (SAG) which had a value of 0.067. However, nucleotide diversity for University of Eldoret Fish Farm (UoE) and Kibos Fish Farm (KIB) samples was intermediate at 0.009. The number of haplotypes was 13, 10, 8, 8, 12, 9, 14, 7, 7 and 9 for LVG, LKG, LTA, LBA, LJP, SAN, SAG, WKU, UoE, and KIB populations respectively (Table 4.1). The number of haplotypes was generally higher in natural than farmed samples, except for SAG, which recorded the highest number of haplotypes among samples from the 10 sites.

All samples from the 10 sites except LTA and LJP shared haplotypes (Table 4.1). A total of 8 haplotypes were shared among the samples. This therefore left each of the populations with a number of singletons (private haplotypes), with LJP having the highest at 12 (haplotypes H-18 to 29) (Appendix 8) followed by SAG with 10 (haplotypes H-51 to 60). LTA had 8 (haplotypes H-36 to 43), while LVG and LBA had 7 private haplotypes each (H-44 to 50 and H-10 to 13, 15 to 17 respectively). LKG had 5 (haplotypes H-30 to 32, 34 to 35) while SAN had 4 (H-61 to 64). UoE had 3 (H-65 to 67), while KIB and WKU had a single private haplotype each (H-7 and H-

68 respectively). Therefore, with the exception of SAG, all samples from fish farms had a lower number of singletons than samples from natural sites (Table 4.1).

Similarly, a total of 386 segregating sites defined 68 haplotypes from the 268 samples (sequences), and 88.2% of the haplotypes were private.

Table 4.1. Genetic diversity values for samples of *Clarias gariepinus* from 10 different sites in Kenya inferred from mtDNA D-loop region. Π is the nucleotide diversity and *h* is the haplotype diversity.

Population	LVG	LKG	LTA	LBA	LJP	SAN	SAG	WKU	UoE	KIB
Sample	25	26	28	24	32	30	23	25	29	26
Π	0.009	0.006	0.009	0.006	0.037	0.006	0.067	0.006	0.009	0.009
No of haplotypes	13	10	8	8	12	10	14	7	7	9
H	0.813	0.745	0.791	0.870	0.679	0.766	0.941	0.720	0.732	0.812
Haplotypes shared	6	5	0	1	0	6	4	6	4	8
Singletons	7	5	8	7	12	4	10	1	3	1
Polymorphic sites	21	18	12	16	161	12	112	11	12	11

Therefore, 8 of the haplotypes were shared among the populations. Haplotype 2 was the most frequent (Appendix 8), appearing in 76 individuals of the LVG group.

The diversity of haplotyes was consistent with the number of haplotypes, where populations with a higher number of haplotypes also had a higher diversity of haplotypes. However, LJP which had the third highest number of haplotypes had the lowest haplotype diversity (Table 4.1). Haplotype diversity values ranged from 0.6794 in LJP to 0.9407 in SAG, with most of the farmed samples showing lower

values than samples from natural sites (Table 4.1). The D-loop region in the samples of *C. gariepinus* segregated at a total of 386 polymorphic sites, with LJP having the highest with 161sites, while SAG had 112, LVG and LKG had 21 and 18 sites respectively. LBA had 16, SAN, UoE and LTA 12 sites each, while WKU and KIB had 11 each.

4.1.2. Genetic diversity of samples of *Clarias gariepinus* from 8 sites in Kenya inferred from microsatellite DNA markers genotyped at 6 loci.

The mean number of alleles per locus (Na) was generally higher in farmed than natural *C. gariepinus* populations (Table 4.2). SAN had the highest mean number of alleles per locus (10.83±3.66), while LBA had the lowest mean number of alleles (3.80±0.84). Among the natural populations, LKG had a relatively higher number of alleles (8.17±3.31), while LVG and LTA had an equal number of alleles (8.00±3.52). All the farmed populations except SAG had higher mean number of alleles per locus than natural populations. The mean observed heterozygosity (H_O) was moderate in populations, ranging from 0.47±0.05 in LBA to 0.80±0.04 in SAN. H_O values for LVG, LKG, LTA, SAG, UoE and KIB were 0.79±0.05, 0.72±0.05, 0.74±0.05, 0.55 ±0.05, 0.74±0.04, and 0.70±0.05 respectively. Similarly values for expected heterozygosities (H_E), ranged from 0.58±0.05 in LBA to 0.84±0.05 in LVG, and were slightly higher than H_O values. H_E values for LKG, LTA, SAN, SAG, UoE and KIB were 0.83±0.05, 0.82±0.04, 0.84±0.04, 0.76±0.04, 0.82±0.04 and 0.85±0.04 respectively (Table 4.2).

All the populations had private alleles, with KIB reporting the highest mean number at 5.91±0.67, LVG with 5.86±0.79, LBA with 5.75±0.43, while UoE had 5.61±0.56.

SAG, LTA and SAN had 5.55±0.62, 5.53±1.11and 5.50±0.78 mean number of private

alleles respectively.

Table 4.2: Level of genetic diversity in 160 samples of *Clarias gariepinus* from 8 different sites in Kenya, genotyped with 6 microsatellite DNA loci.N is the sample size at each sampling site, Na is the number of alleles, H_O is the observed heterozygsity, H_E is the expected heterozygosity, while F_{IS} is the coefficient of inbreeding. F_{IS} values in bold are significantly different at p<0.05. Values are given as mean±standard error (S.E).

Population	N	Na	H_O	H_E	No. of private alleles	Coefficient of inbreeding (F_{IS})
LVG	23	8.00±3.52	0.79±0.05	0.84±0.05	5.86±0.79	-0.614
LKG	20	8.17±3.31	0.72±0.05	0.83±0.05	5.47±0.87	**0.112**
LTA	19	8.00±2.68	0.74±0.05	0.82±0.04	5.53±1.11	0.266
LBA	18	3.80±0.84	0.47±0.05	0.58±0.05	5.75±0.43	0.198
SAN	20	10.83±3.66	0.80±0.04	0.84±0.04	5.50±0.78	0.016
SAG	20	7.67±2.73	0.55 ±0.05	0.76±0.04	5.55±0.62	**0.250**
UoE	20	8.83±2.56	0.74±0.04	0.82±0.04	5.61±0.56	**0.095**
KIB	20	9.67±2.88	0.70±0.05	0.85±0.04	5.91±0.67	**0.069**

On the other hand, out of the 8 sites from which *C. gariepinus* was sampled, 4 had significantly different (p<0.05) coefficients of inbreeding (F_{IS}), indicating that the fish were inbred. The inbred samples were LKG, SAG, UoE and KIB, with F_{IS} values ranging from 0.069 to 0.250. F_{IS} values for LVG, LTA, LBA, and SAN ranged from 0.016 to 0.266, and were not significantly different (p>0.05).

Table 4.3: P-values for Hardy Weiberg Equilibrium (HWE) Exact tests for 160 samples of *C. gariepinus* sampled from 8 different sites (4 natural and 4 fish farms) in Kenya. Samples were genotyped with 6 loci. Values in bold are significantly different at p<0.01, and p<0.05.

| Population | Locus | | | | | |
	Cga1	Cga3	Cga9	Cga10	Cba2	Cba19
LVG	0.366	**0.003**	0.411	0.366	0.451	0.015
LKG	0.064	0.116	0.014	0.423	0.317	0.711
LTA	0.058	0.127	0.042	0.029	0.258	0.637
LBA	0.013	0.563	**0.010**	0.348	-	0.651
SAN	0.579	0.246	0.015	0.023	0.821	0.033
SAG	0.026	0.270	0.014	0.015	0.057	0.140
UoE	0.015	0.763	0.016	0.883	0.546	0.474
KIB	0.077	0.954	0.020	0.170	0.166	0.135

4.2. Population genetic structure of *Clarias gariepinus* in Kenya inferred from mtDNA D-loop control region.

4.2.1. Population differentiation indices (F_{ST}) of samples of *Clarias gariepinus* from 10 different sites in Kenya.

There was population differentiation among the10 populations, with significantly different (p<0.05) population differentiation (F_{ST}) indices among 31 out of 45 pair wise comparisons, mainly for LTA, LBA, and LJP with other populations, and LVG compared with samples from the natural populations (Table 4.4). Pair-wise population comparisons without differentiation (i.e. with F_{ST} values not significantly different (P>0.05)) included comparisons of LVG or LKG with samples from farms, and comparisons among farmed samples. F_{ST} values ranged from 0.00007 for LKG-SAN to 0.9620 for LJP-SAG comparisons (Table 4.4).

Table 4.2: Pair wise comparisons of F*ST* values of samples of *Clarias gariepinus* from 10 different sites in Kenya inferred from sequences of mtDNA D-loop control region. Values in bold are significantly different (P<0.05). A total of 31 of 45 pair wise comparisons are significantly different. 1 is LVG, 2 is LKG, 3 is LTA, 4 is LBA, 5 is LJP, 6 is SAN, 7 is SAG, 8 is WKU, 9 is UoE and 10 is KIB.

	1	2	3	4	5	6	7	8	9	10
1	0.000									
2	0.014	0.000								
3	**0.853**	**0.877**	0.000							
4	**0.534**	**0.652**	**0.870**	0.000						
5	**0.957**	**0.959**	**0.959**	**0.958**	0.000					
6	0.011	0.000	**0.883**	**0.660**	**0.962**	0.000				
7	**0.253**	**0.281**	**0.393**	**0.337**	**0.921**	**0.290**	0.000			
8	0.058	0.155	**0.870**	**0.562**	**0.958**	0.163	**0.275**	0.000		
9	0.019	0.092	**0.847**	**0.482**	**0.959**	0.087	**0.253**	0.058	0.000	
10	0.040	0.141	**0.851**	**0.411**	**0.957**	0.153	**0.268**	0.043	**0.069**	0.000

4.2.2. Maximum likelihood tree for phylogenetic relationships among samples of *Clarias gariepinus* from 10 sites in Kenya.

From the Maximum likelihood tree (Figure 4.1), haplotypes of *C. gariepinus* samples grouped into 5 clusters: cluster 1 comprised of the LVG population, which, apart from LVG haplotypes, also included haplotypes from LKG, SAN, KIB, UoE and SAG. The second cluster comprised haplotypes of LJP population, which did not have any shared haplotypes. Cluster 3 comprised LBA and included samples from two farms

(UoE and WKU). Cluster 4 comprised of LTA haplotypes, and included haplotypes

from SAG, while the last cluster was SAG which also carried haplotypes from SAN.
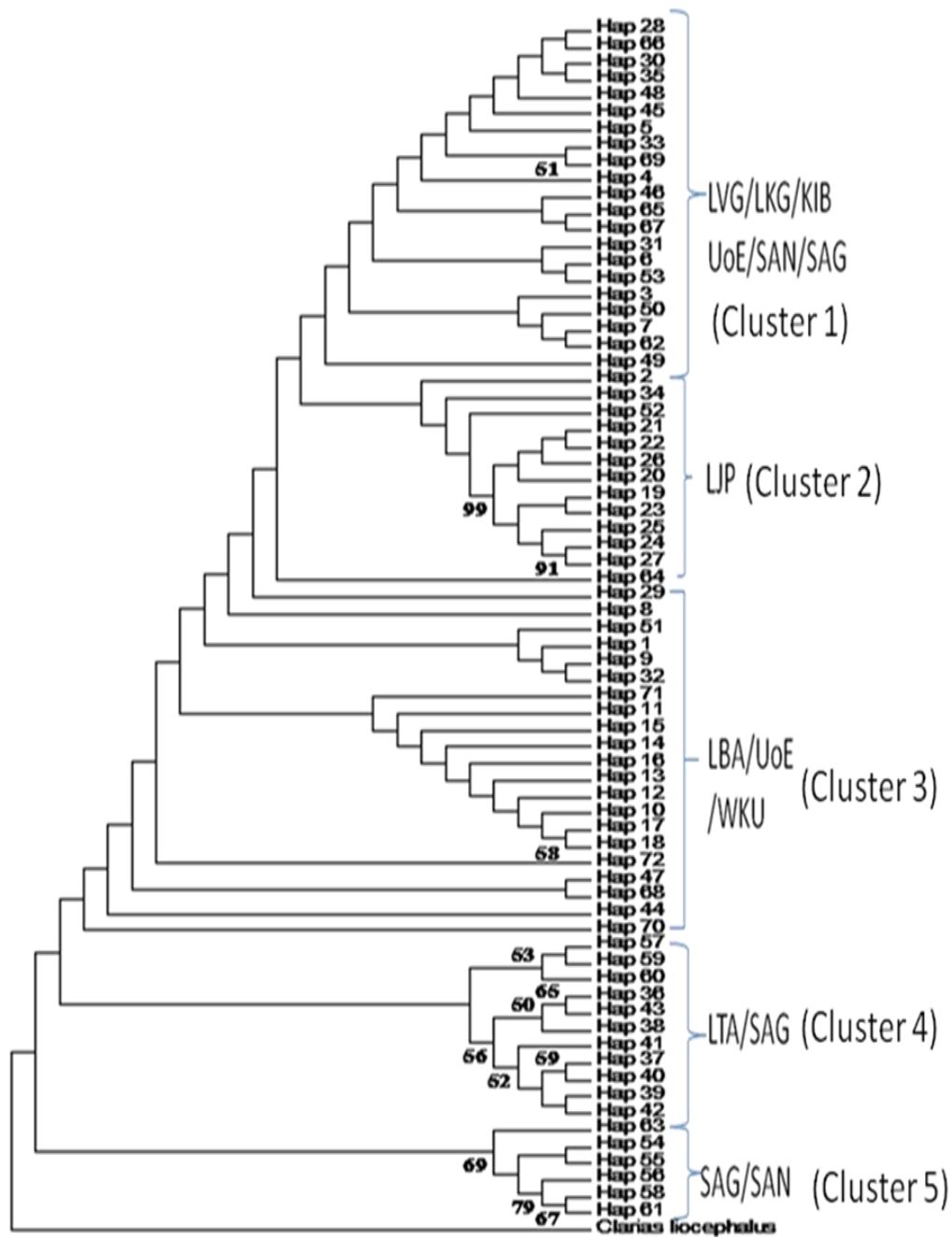
Figure 4.1: Maximum likelihood tree illustrating the clustering of haplotypes for samples of *Clarias gariepinus* from 10 different sites in Kenya inferred from sequences of mtDNA D-loop control region. Haplotypes of the samples grouped into 5 clusters. Numbers on branches are percentage bootstrap values based on 1,000 replicates, and nodes without numbers have confidence levels less than 50%. *Clarias liocephalus* is the out-group. Source: Author, 2014.

4.2.3. Minimum spanning networks for phylogenetic relationships among samples of *Clarias gariepinus* from 10 different sites in Kenya.

The haplotype network for *C. gariepinus* samples showed 5 distinct clusters (Figure 4.2), consistent with the Maximum likelihood tree: the LVG, LBA, LTA LJP and SAG. Cluster 1, the LVG group, comprised LVG haplotypes and haplotypes from LKG and all the farmed populations, while cluster 2 comprised mainly of LBA, with haplotypes of UoE, SAN and SAG. Although some haplotypes of LVG were present in cluster 2, LBA haplotypes were virtually absent in cluster 1. Cluster 3 comprised LTA haplotypes, and did not have any shared haplotype. Cluster 4 had haplotypes of SAG. Similarly, LJP which formed the fifth cluster was distinct from the other clusters, sharing haplotypes with no other populations. Haplotype 2 was the most common, appearing in a total of 76 samples (Appendix 8). Therefore, haplotype 2 could be the ancestral haplotype, from which all the other samples radiated via 1 to 8 mutation steps.
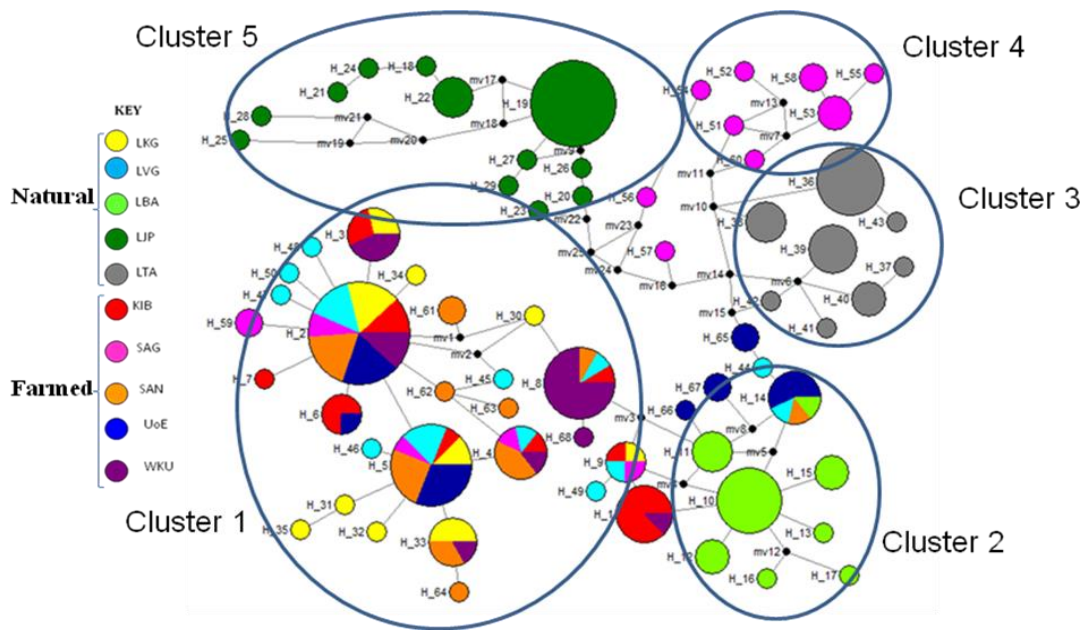
Figure 4.2: Haplotype networks for samples of *Clarias gariepinus* from 10 different sites in Kenya, inferred from sequences of mtDNA D-loop control region. A total of 5 clusters comprising LVG (cluster 1), LBA (cluster 2), LTA (cluster 3), SAG (cluster 4) and LJP (cluster 5) are discerned. Source: Author, 2014.

4.3. Population genetic structure of samples of *Clarias gariepinus* from 8 sites in Kenya inferred from microsatellite DNA markers.

4.3.1. Analysis of molecular variance (AMOVA) of samples of *C. gariepinus*.

The analysis of molecular variance revealed that sub-divisions among populations contributed the lowest to the total observed variation in the samples of *C. gariepinus*, with only 22% variance (Table 4.5). However, the sub-division among populations contributed significantly ($F_{ST}= 0.221$, $p<0.05$) to the genetic structure of the samples. On the other hand, the sub-division among individuals contributed slightly higher to the observed variation with 26%, and this contribution to the genetic structure of the samples was also significant ($F_{SC} = 0.333$, $p<0.05$). The sub-division within

individuals contributed the highest (52%) to observed variation in samples of *C. gariepinus*, with a significantly higher ($F_{CT} = 0.481$, $p<0.05$) contribution to the genetic structure of the samples.

Table 4.3: Analysis of molecular variance among alleles of *C. gariepinus* samples from 8 different sites of Kenya.

Source	d.f	Sum of squares	Variance components	Percentage of variation	Fixation index	p-value
Among populations	3	76.25	0.570	22	$F_{ST} = 0.221$	0.001
Among individuals	76	203.091	0.667	26	$F_{SC} = 0.333$	0.001
Within individuals	80	107.000	1.338	52	$F_{CT} = 0.481$	0.001
Total	159	386.338	2.575	100		

4.3.2. Neighbor joining tree for phylogenetic relationships among samples of *C. gariepinus*.

A total of four genetic clusters were deciphered from alleles of *C. gariepinus* samples from 8 sites in Kenya. These were the Lake Victoria (LVG), Lake Turkana (LTA), Lake Baringo (LBA) and SAG (Sagana Aquaculture center) clusters. The clusters grouped interchangeably in the neighbor joining tree (Fig. 4.3). Farmed samples grouped predominantly in the LVG cluster, although some farmed samples also grouped in the SAG and LTA clusters. Samples of LKG also grouped in the LVG cluster.
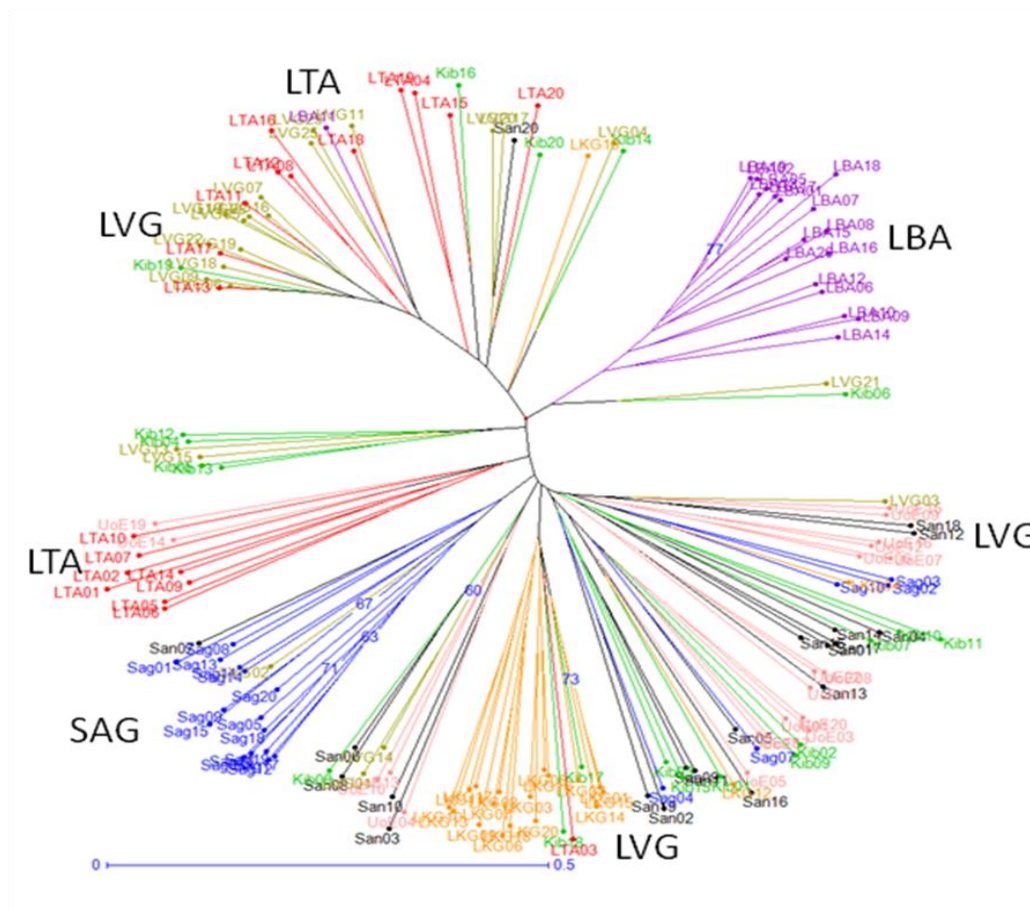
Figure 4.3: Neighbor joining tree of alleles of *C. gariepinus* samples from 8 different sites in Kenya, genotyped at 6 microsatellite loci. 4 genetic clusters are discerned, in which alleles of *C. gariepinus* samples grouped: LVG (Lake Victoria), LBA (Lake Baringo), LTA (Lake Turkana), and SAG (Sagana Aquaculture center). Source: Author, 2017.

4.3.3. Population genetic structure of samples of *C. gariepinus* using STRUCTURE.

Samples were arranged according to the sampling site: LVG, LKG, LTA, LBA, SAN, SAG, UoE and KIB. All samples from the four fish farms (SAN, SAG, UoE and KIB) and LKG from the wild, grouped with LVG. UoE, KIB and SAN also grouped with LBA (Figure 4.4). Four distinct genetic clusters were discerned, identified as LVG, LTA, LBA and SAG.
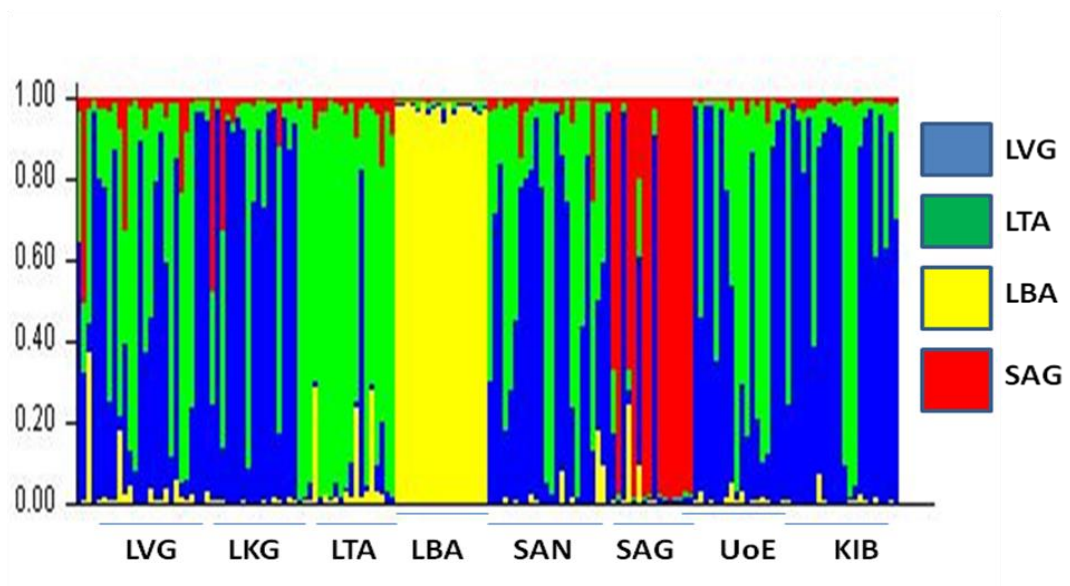
Figure 4.4: Bar plot of the STRUCTURE assignment test for 160 samples of *Clarias gariepinus* **collected from 8 different sites (4 lakes- LVG, LKG, LTA and LBA, and 4 farms-SAN, SAG, UoE and KIB) in Kenya, and genotyped with 6 microsatellite DNA loci. Source: Author, 2016.**

Samples from the LVG and LKG pre-defined population dominated the LVG cluster, with a membership coefficient of 0.4483 and 0.7592 respectively. Similarly, the LBA, LTA and SAG clusters were dominated by samples from the LBA, LTA and SAG pre-defined populations respectively, as evidenced by high respective membership coefficients (Table 4.6).

Table 4.4: Proportion of membership of each pre-defined population in each of the 4 genetic clusters (K=4) inferred in samples of *Clarias gariepinus* from 8 different sites in Kenya genotyped at 6 microsatellite DNA loci. STRUCTURE was run with 10,000 Burn-in period and 100,000 Monte Carlo simulations.

Pre-defined Population	Inferred genetic cluster				Sample size
	LVG/LKG	LBA	SAG	LTA	
LVG	0.4482	0.0400	0.0690	0.4429	23
LKG	0.7592	0.0094	0.0538	0.1776	20
LTA	0.0733	0.0561	0.0466	0.8241	19
LBA	0.0099	0.9748	0.0052	0.0101	18
SAN	0.5385	0.0119	0.0239	0.4257	20
SAG	0.2339	0.0380	0.6219	0.1062	20
UoE	0.5873	0.0131	0.0131	0.3865	20
KIB	0.7092	0.0110	0.0138	0.2660	20

The number of genetic clusters (the actual populations) in the samples from the 8 sites was 4 (K=4), i.e. the number corresponding to the highest peak in the output of the STRUCTUREHARVESTER (Figure 4.5). In the web based program, the most likely number of K that best suits the dataset is inferred at the point where the rate of change in the log of likelihood of prior probability of K ceases to increase, or plateaus off (Earl and vonHoldt, 2012).

From biological information, the first three clusters were identified as LVG, LTA and LBA.
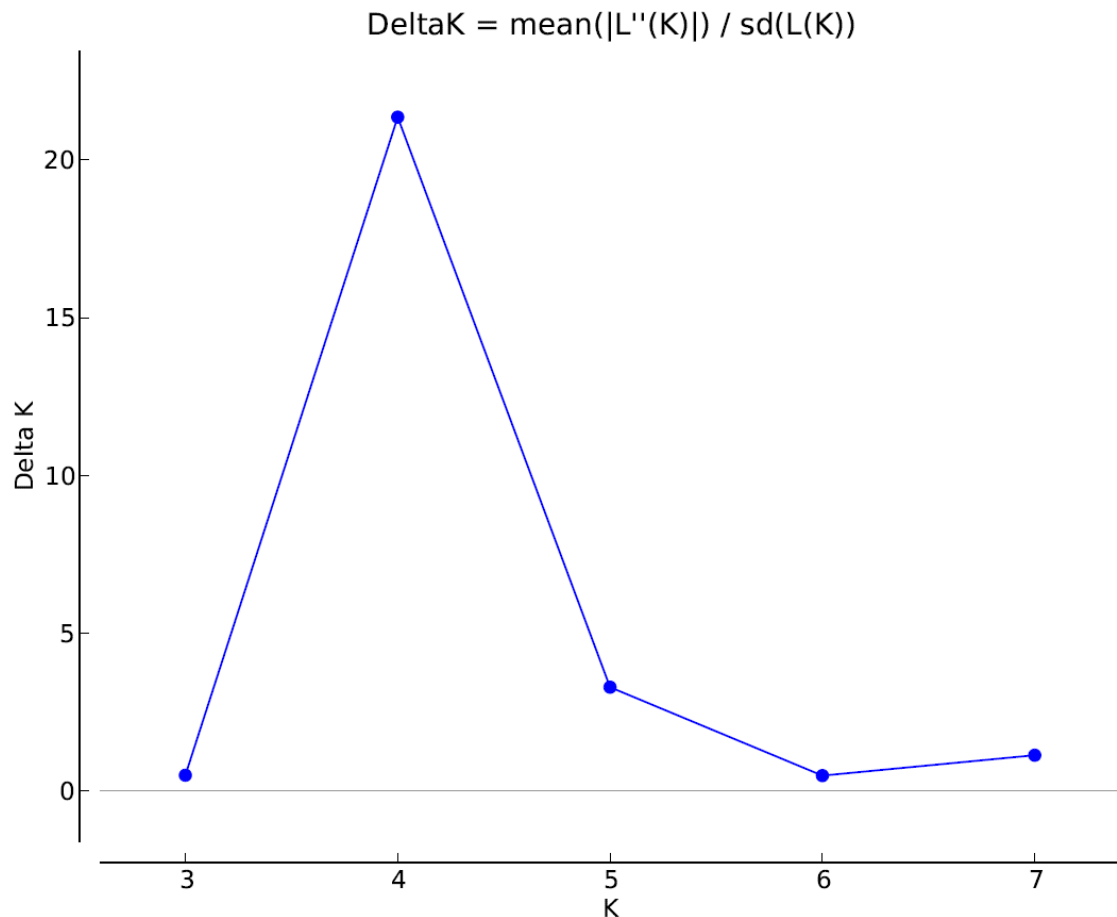
Figure 4.5: The most likely number of populations K for the samples of *Clarias gariepinus*, as implemented in the Evanno method. Samples were drawn from the following sites LVG, LKG, LTA, LBA, SAN, SAG, UoE, and KIB. Source: Author, 2014.

DeltaK = mean($|L''(K)|$)/sd(L(K)).

The first three of the 4 populations inferred from STRUCTURE are LVG, LTA and LBA (Fig. 4.5). In order to infer the fourth population out of the remaining samples, a series of runs of STRUCTURE were made using samples from 7 sites (i.e. excluding 1 of the five LKG, SAN, SAG, UoE or KIB) during each run (Barasa et al., 2017). For each of the 5 combinations, STRUCTURE HARVESTER analysis returned an output of K=3, except when SAG was included in the run, that K changed to 4 (Figure 4.6).
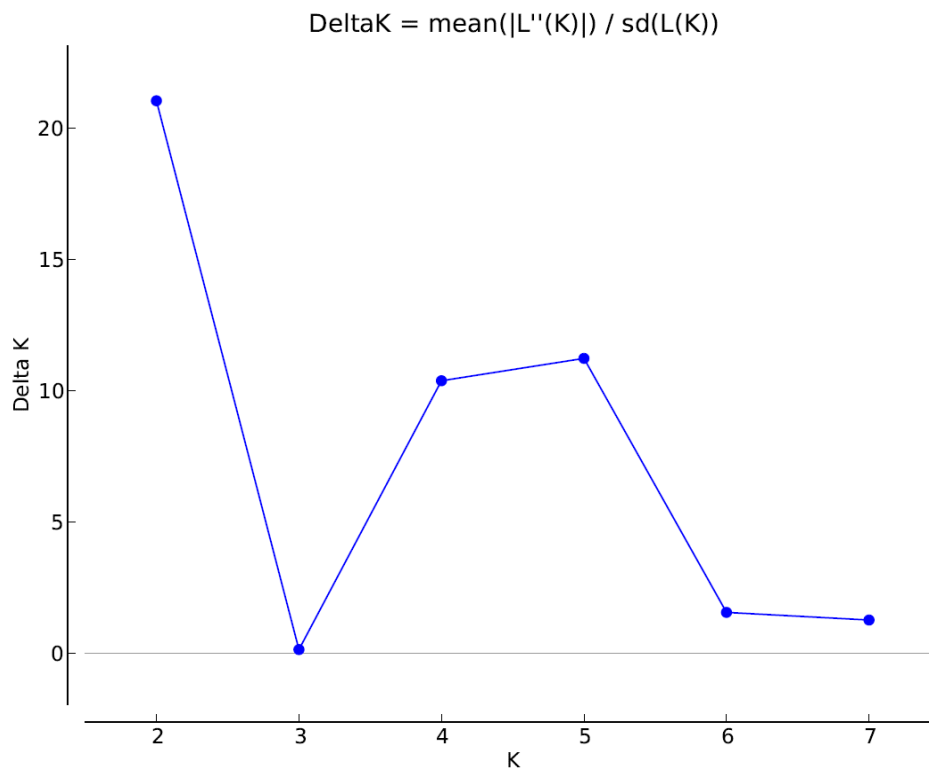
Figure 4.6: Output of STRUCTUREHARVESTER with 4 as the most likely number of populations K, as implemented in the Evanno method. This output was obtained only when SAG (out of the four possible sites of SAN, SAG, UoE, and KIB) was included in the samples included in the run of STRUCTURE. Source: Author, 2014.

4.3.4. Population differentiation indices (F_{ST}) of populations of *Clarias gariepinus* inferred from Microsatellites DNA analysis.

The pattern of population differentiation among samples was similar to that reported in the mtDNA analysis, with significantly different ($p<0.05$) F_{ST} values being reported in 15 out of 28 pair-wise comparisons (Table 4.7). The Significantly different values were reported in comparisons of samples from natural populations. However, comparisons of natural and farmed samples revealed significantly different ($p<0.05$) F_{ST} values only in comparisons of LTA and farmed samples, and also LBA with farmed samples (Table 4.7).

Table 4.5: Estimates of pairwise F_{ST} values, for 160 samples of *Clarias gariepinus* collected from 8 sites (LVG, LKG, LTA, LBA, SAN, SAG, UoE and KIB) in Kenya and genotyped at 6 microsatellite loci. Values in bold are significantly different (p<0.05). A total of 15 out of 28 pair wise comparisons are significantly different. LJP and WKU were not included in genotyping.

	LVG	LKG	LTA	LBA	SAN	SAG	UoE	KIB
LVG	0.000							
LKG	0.247	0.000						
LTA	**0.071**	0.172	0.000					
LBA	**0.000**	**0.018**	**0.243**	0.000				
SAN	0.187	0.089	0.189	**0.253**	0.000			
SAG	0.227	0.159	**0.163**	**0.253**	**0.077**	0.000		
UoE	0.206	0.112	**0.152**	**0.267**	**0.033**	**0.092**	0.000	
KIB	0.115	0.083	**0.095**	**0.210**	0.029	0.088	**0.040**	0.000

4.4. Life-history parameters and genetic diversity of three populations (Lakes Victoria, Kanyaboli and Baringo) of *Clarias gariepinus* of Kenya.

4.4.1. Relative Fecundity

The mean monthly relative fecundity among the three natural populations of *C. gariepinus* was significantly different (p<0.05) in the months of October (F=5.559, p=0.009) and December (F=8.869, p=0.0009) 2016, but not significantly different (p>0.05) in the months of September (F=0.177, p=0.839), November (F=1.707, p=0.196) and January (F=2.862, p=0.072) (Table 4.8). In both October and December, relative fecundity was significantly higher in LVG than LBA and LKG, but not significantly different (p>0.05) among LBA and LKG. The overall mean relative fecundity was significantly different among the three populations (F=9.593,

p=0.0001), with the relative fecundity of LVG being higher than LBA and LKG (p<0.05), but similar among LBA and LKG (p>0.05).

Table 4.6: Mean monthly relative fecundity (±S.E) of LVG, LBA and LKG populations of *Clarias gariepinus*, with respective p-values, sampled for 5 months from September 2016 to January 2017. Values with similar superscripts in a row are statistically similar.

Month	LVG	LBA	LKG	ANOVA F	P-value
September	62.3 ± 12.1^a	76.7 ± 27.9^a	78.8 ± 13.5^a	0.177	0.839
October	79.1 ± 6.5^a	42.8 ± 7.3^b	56.3 ± 9.8^b	5.559	0.009
November	96.0 ± 15.4^a	67.3 ± 9.5^b	65.5 ± 11.9^b	1.707	0.196
December	95.2 ± 13.7^a	38.4 ± 5.2^b	52.3 ± 11.2^b	8.869	0.0009
January	66.4 ± 12.6^a	39.9 ± 6.6^b	33.4 ± 8.4^b	2.862	0.072
Overall means	81.9 ± 6.0^a	50.8 ± 5.6^b	53.0 ± 5.1^b	9.593	0.0001

4.4.2. Size at first maturity (L_{m50})

In the Lake Victoria population, *C. gariepinus* females reached sexual maturity at a total length of 55.0 cm, while males matured at 57.0 cm total length (Fig. 4.7).
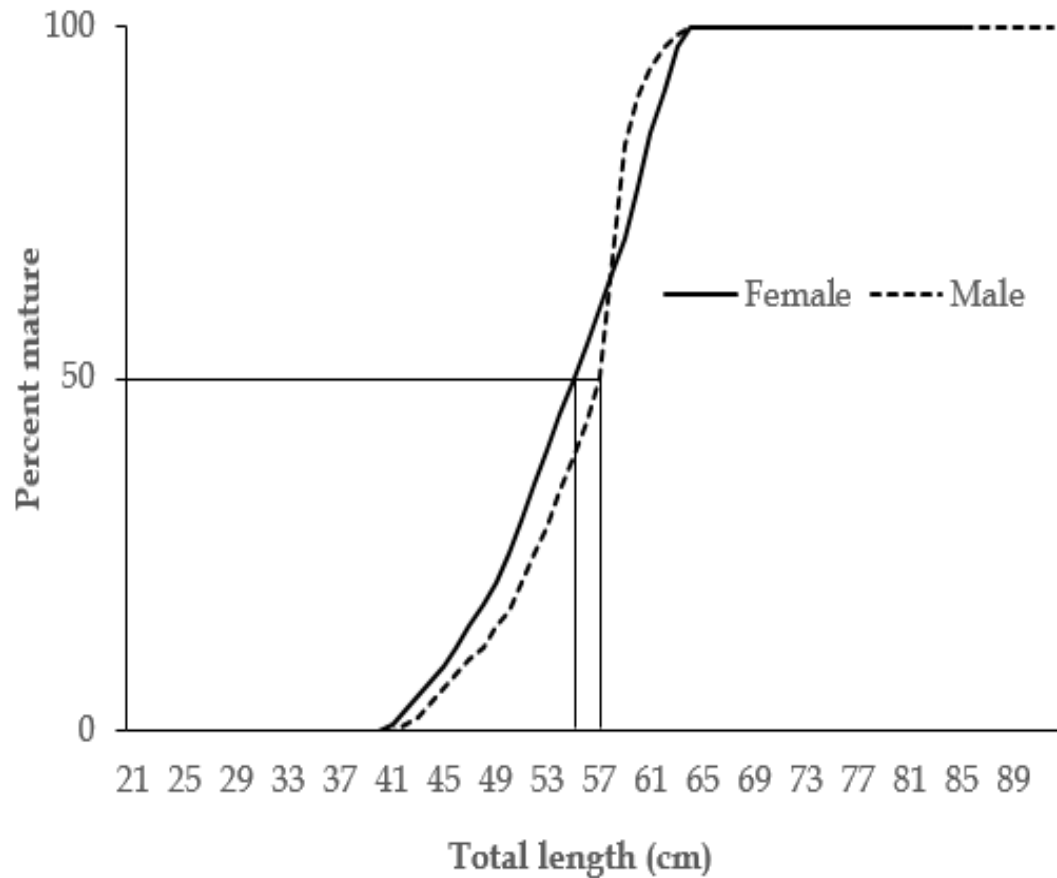
Figure 4.7: Size at first maturity of *Clarias gariepinus* population of Lake Victoria (LVG). Data is based on 499 fish samples collected over 5 months (September 2016 to January 2017).

In LBA population, females matured at a total length of 57.0 cm, while males matured later at 60.0 cm total length (Fig. 4.8).
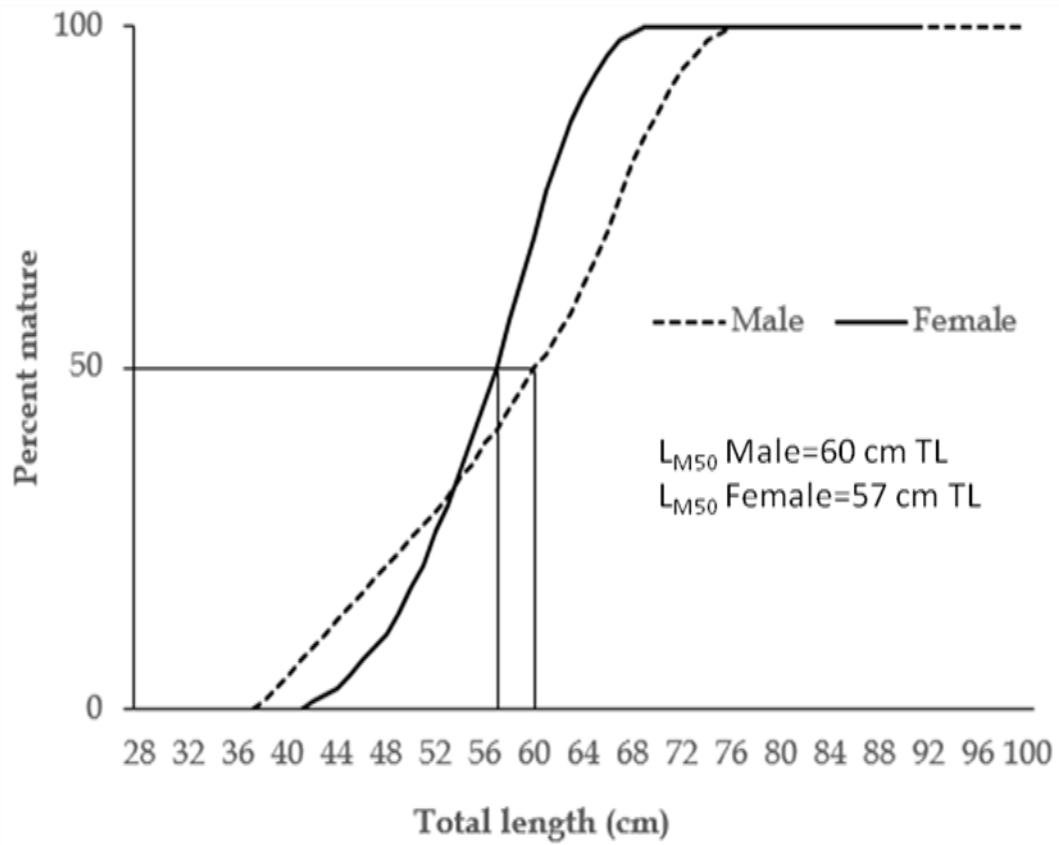
Figure 4.8: Size at first maturity of *Clarias gariepinus* population of Lake Baringo (LBA). Data is based on 527 fish samples collected over 5 months (September 2016 to January 2017).

In LKG, males matured at a total length of 51 cm, while females matured earlier at 48 cm total length (Fig. 4.9).
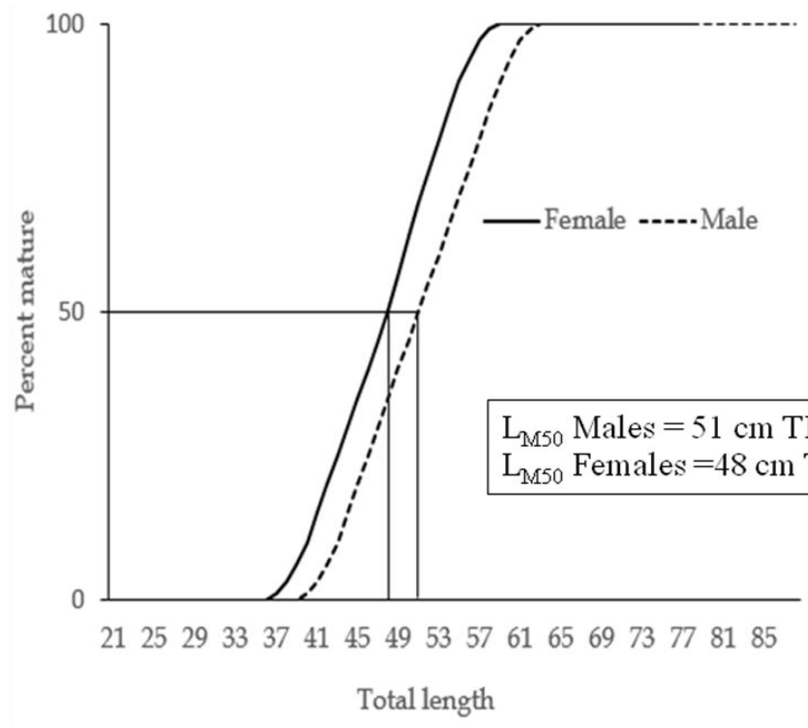
Figure 4. 9: Size at first maturity of *Clarias gariepinus* population of Lake Kanyaboli (LKG). Data is based on 354 fish samples collected over 5 months (September 2016 to January 2017). Total length is in cm.

4.4.3. Water quality parameters

There was no significant difference (p>0.05) in the overall mean values of nutrients among the three lakes during the study period (Table 4.9). Total phosphorus was similar among the study sites (F=1.24, p=0.218), while total nitrogen was also similar among the lakes (F=2.4, p=0.133).

Table 4.7: Overall mean values of nutrients (total phosphorus and total nitrogen) of Lakes Victoria, Baringo and Kanyaboli over the study period of September 2016 to January 2017.

Nutrients	Sampling Sites (Populations)			Anova	
	LVG	LBA	LKG	F	P
Total phosphorus (mg/L)	0.085±0.019	0.054±0.006	0.079±0.006	1.74	0.218
Total Nitrogen (mg/L)	0.902±0.053	0.65±0.046	0.826±0.126	2.4	0.133

The overall physico-chemical parameters were all significantly different ($p<0.05$) among the three study sites (Table 4.10). The pH was significantly lower in LVG than LBA and LKG which had similar values. On the other hand, salinity and specific conductivity were significantly higher in LBA than both LVG and LKG, which had similar values, while total dissolved solids was significantly higher in LBA than LVG and LKG. However, LKG had a significantly higher value for TDS than LVG. Water temperature was significantly lower in LVG than LBA and LKG, which had similar values.

Table 4.10: Overall mean values of physico-chemical parameters of Lakes Victoria, Baringo and Kanyaboli over the study period of September 2016 to January 2017. Mean values with different letter superscripts in a row are significantly different as the SNK test.

	Sampling Sites (Populations)			ANOVA	
Variable	LVG	LBA	LKG	F	P
pH	5.83 ± 0.07^a	6.49 ± 0.030^b	6.37 ± 0.12^b	10.63	0.001
Salinity	0.16 ± 0.04^a	0.42 ± 0.04^b	0.22 ± 0.03^a	13.16	0.001
Specific conductivity (SPC)	0.21 ± 0.02^a	0.59 ± 0.06^b	0.38 ± 0.06^a	36.56	0.001
Total Dissolved Solids (TDS)	13.6 ± 0.46^c	66.2 ± 4.21^a	44.05 ± 6.26^b	12.28	0.001
Temperature (^{o}C)	22.7 ± 0.22^a	25.7 ± 0.16^b	25.35 ± 0.30^b	19.16	0.001

4.4.4. Association between heterozygosity and relative fecundity of the populations of *Clarias gariepinus* from Lakes Victoria, Baringo and Kanyaboli.

There was an association between mean expected heterozygosity and mean relative fecundity of *C. gariepinus* from the three lakes. The Lake Victoria population (LVG), with a higher mean heterozygosity than both LBA and LKG, also reported a higher mean relative fecundity than LBA and LKG. However, although LKG had a higher mean heterozygosity than LBA, had similar mean relative fecundity with the LBA population (Fig. 4.10).
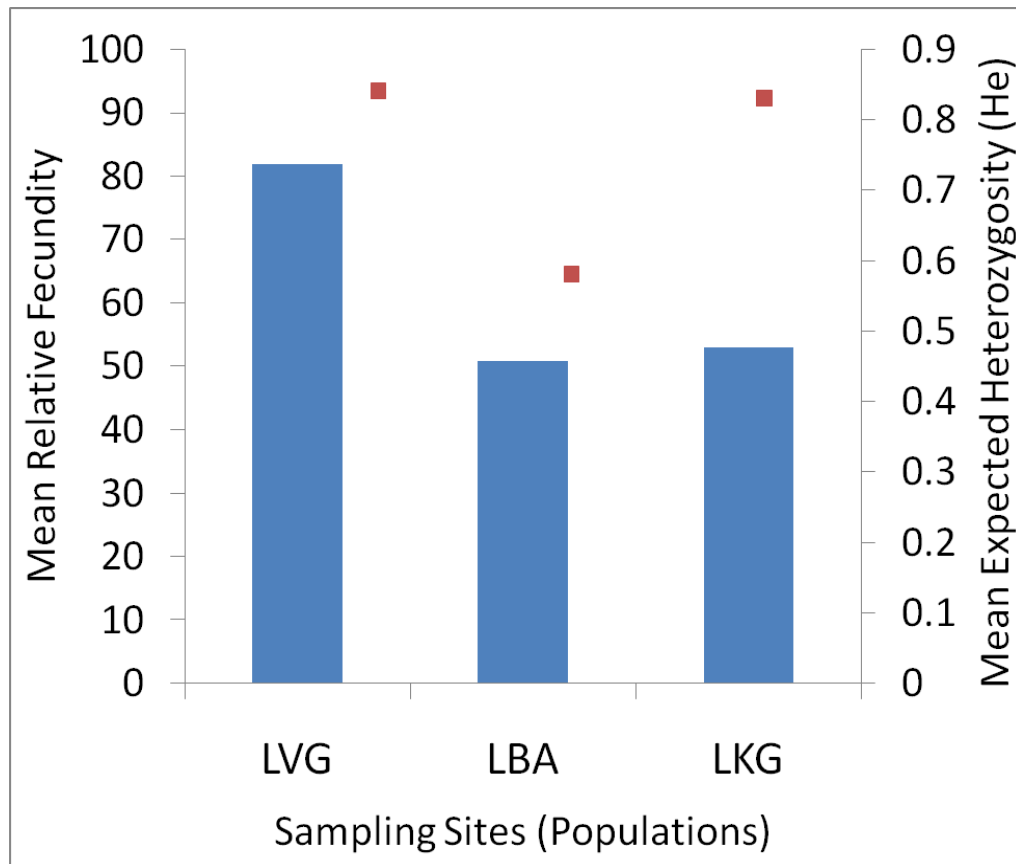
Figure 4.10: Relationship between mean relative fecundity and the expected Heterozygosity (H_E) of *Clarias gariepinus* populations from Lakes Victoria (LVG), Baringo (LBA) and Kanyaboli (LKG). Source: Author, 2017.

For male samples of *C. gariepinus*, the size at first maturity was higher in LBA than in LVG and LKG, although LBA had a lower H_E than both LVG and LKG populations. However, male *C. gariepinus* from LVG had a higher size at first maturity than LKG; consistent with the higher H_E recorded in LVG than LKG populations (Fig. 4.11).
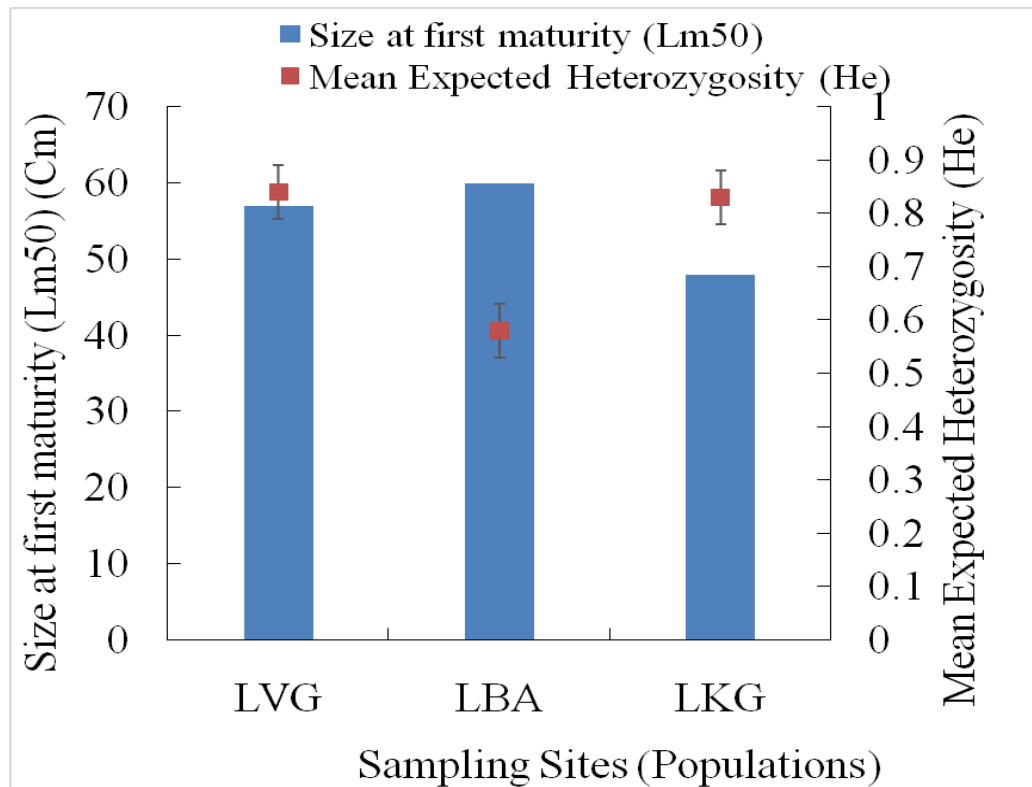
Figure 4.11: Relationship between mean size at first maturity (L_m50) and the mean expected Heterozygosity (H_E) of male samples of *Clarias gariepinus* populations from Lakes Victoria (LVG), Baringo (LBA) and Kanyaboli (LKG). Source: Author, 2017.

The comparison of size at first maturity and H_E of female fish from the three populations showed similar pattern as that observed in male fish samples, with LBA recording higher size at first maturity than both LVG and LKG (Fig. 4.12). A higher size at first maturity was also observed in female fish of LVG than LKG, consistent with the higher H_E in LVG than LKG.
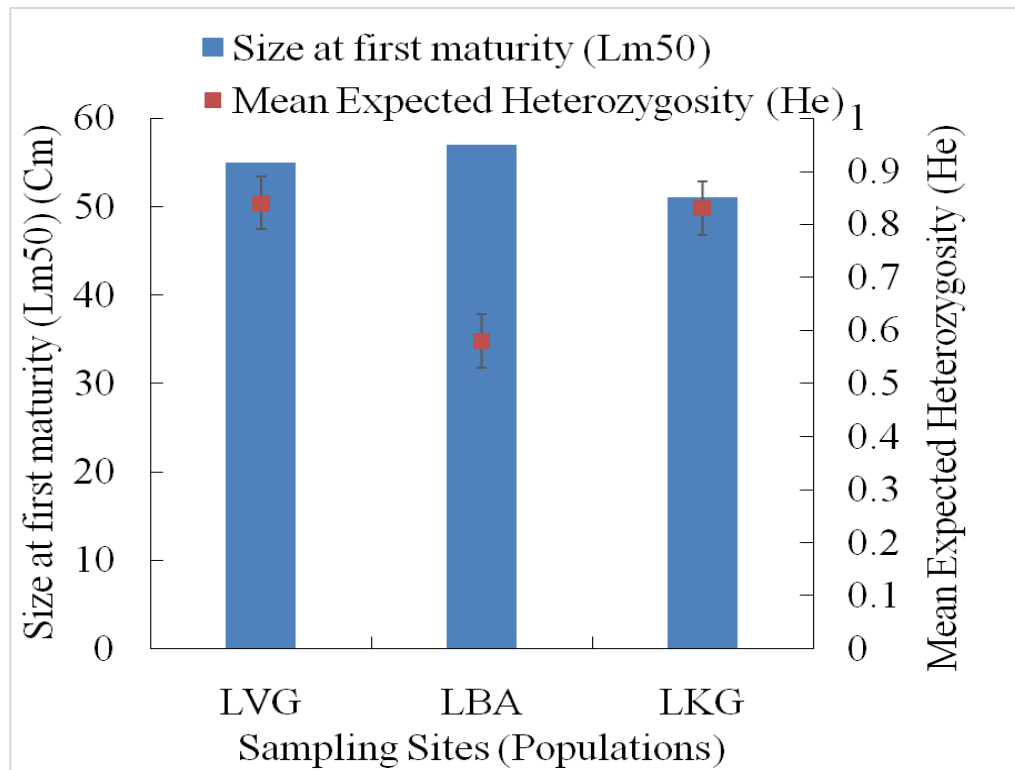
Figure 4.12: Relationship between mean size at first maturity (L_m50) and the mean expected Heterozygosity (H_E) of female samples of *Clarias gariepinus* populations from Lakes Victoria (LVG), Baringo (LBA) and Kanyaboli (LKG). Source: Author, 2017.

CHAPTER FIVE

DISCUSSION

5.1. Genetic diversity of *C. gariepinus* inferred from mitochondrial D-loop control region and microsatellite DNA data

The nucleotide diversity of the catfish populations was low, while haplotype diversity was high, reaching almost 1, with the exception of the SAN, which had low value of 0.087. This shows that genetic variation in the populations could be accounted for by within population variation. However, indices of haplotype and nucleotide diversity were similar to values reported for *C. gariepinus* populations from South Africa, which ranged from 0.838±0.030 to 0.904±0.019 and 0.006±0.003 to 0.008±0.040 respectively (Roodt-Wilding et al., 2010). The presence of shared haplotypes implies there was gene flow among the populations, and this was restricted to farmed populations (UoE, SAG, SAN, WKU and KIB), which were mainly sourced from Lake Victoria, or from other fish farms that initially collected their brood stock from L. Victoria. Translocation of fish populations across drainage basins for aquaculture is common, especially in *C. gariepinus* aquaculture that frequently depends on collection of males from natural populations to provide the pituitary hormone and milt during artificial propagation at hatcheries. In their study of three populations of *C. macrocephalus* in Malaysia, Nazia et al., (2010) reported that human transfer of brood stock across drainage basins was responsible for homogenizing geographically isolated populations of the species.

Apart from reporting a higher number of haplotypes (Table 4.1), SAG also clustered close to LTA in the haplotype spanning network (Figure 4.2), which showed relatively higher genetic diversity for this population compared to samples from different farms (SAN, UoE, KIB and WKU). A possible reason for higher genetic

diversity in SAG could be mixed gene pools, from fish with multiple sources. Artificial propagation of *C. gariepinus* at hatcheries necessitates a collection of male brooders from other natural sites such as swamps, rivers and streams to provide pituitary to induce ovulation, and milt for fertilization of eggs. Similarly, when the number of female brooders at the hatchery decreases, more samples are collected from these natural sites, to augment the number of brood stock. These practices therefore have a similar effect on genetic diversity of brood stock as the deliberate introduction of genetically different fish brood stock by hatcheries to boost genetic variability of brooders that have been kept and used on a farm for many generations (Van der Bank et al., 1992; Grobler et al., 1997).

In addition, farmed populations, except the SAG population, reported lower haplotype diversity while natural populations had higher haplotype diversity values. This could be attributed to the effect of domestication, where farmed fish generally lose genetic diversity. Aquaculture practices like intensive selection for superior traits in a breeding program invariably lead to inbreeding (Norris et al., 1999), because in the absence of pedigree records, closely related families are used for breeding, leading to inbreeding depression. Inbreeding, founder effects and genetic drift reportedly erode genetic variability in farmed catfishes (Van Der Walt et al., 1993; Popoola et al., 2014), as well as other aquaculture species such as salmonids (Su et al., 1996; Bourret et al., 2011) and tilapias (Eknath & Hulata, 2009). Loss of genetic variability potentially affects adaptability, persistence of fish in habitats and productivity of the fish population (Hauser et al., 2002).

Of the 5 natural populations sampled, LKG and LJP had the lowest haplotype diversities. Both lakes are small and isolated (L. Kanyaboli is 10.5 km^2, L. Jipe 30 km^2, L. Baringo 130km^2, L. Turkana 7,000 km^2 while L. Victoria is 69,000 km^2 in

surface area), and higher fishing pressure, especially in LKG population (Aloo, 2003), could have reduced its genetic diversity. Higher fishing pressure is known to reduce genetic diversity in fish populations, through fishing mortality (Van Der Walt et al., 1993). Small and isolated populations also suffer lower genetic diversity due to genetic drift that results from founder effects and lower effective population sizes (Nei et al., 1975). Although the haplotype diversity values of LVG, LBA, LTA and LJP were comparable, at 0.910, 0.877, 0.825 and 0.6794 respectively, LVG had a slightly higher diversity, which was expected, because of its larger population size, as reported by similar studies (Barasa et al., 2014).

On the other hand, 88.2% of the haplotypes were private, distributed in each of the ten populations. The presence of private haplotypes reflects high population differentiation, facilitated by geographical separation of the study sites by distance, and small sizes of both the study populations and samples. For instance, LJP which had the highest number of singletons is small and isolated. Apart from its small size, Lake Kanyaboli is isolated, and fringed by dense papyrus, which restricts the exchange of fish with surrounding watermasses (Abila et al., 2004; Barasa et al., 2016). Small populations and sample sizes often suffer genetic drift (Frankharm et al., 2002), and impact genetic differentiation of populations (Barasa et al., 2016), leading to private haplotypes in the populations. These haplotypes need to be conserved by managing the populations separately, and harnessing the haplotypes into aquaculture programs, as reported by Nazia et al., (2010); Roodt-Wilding et al. 2010; Chemoiwa et al., (2013) and Barasa et al., (2014; 2016; 2017).

Generally, higher genetic variation occurs in natural than farmed fish populations. This is reported in the Indian major carp *Catla catla* (Alam & Islam, 2005; Hansen et al., 2006), the Turbot *Scophthalmus maximus* (Coughlan et al., 1998), Atlantic salmon

(Norris et al., 1999) and the Channel catfish, *I. punctatus* (Perales-Flores et al., 2007). These studies demonstrate the potential impacts of domestication on genetic variability in fish, which occurs by inbreeding that decreases the fitness of populations (Hansen et al., 2006), fixation of deleterious alleles or due to absence of variation at loci showing over-dominance (Hedrick & Kalinowski, 2000). Allelic variation is necessary for maintaining evolutionary potential, important for selective breeding for commercially important traits in captive populations (Frankham et al., 2002).

However, in this study, all farmed samples except SAG had higher number of alleles than natural populations. This could be attributed to artificial propagation practices at hatcheries that source males from natural habitats to provide milt for egg fertilization, and the pituitary gland for induced breeding. Sourcing of male brood stock is not based on any clear guidelines, and brooders are often obtained from a different drainage basin, or a different population of *C. gariepinus*. This could be creating conditions similar to hatcheries that introduce new brood stock from different populations of a fish species to increase genetic variation after several generations of repeated breeding of same individuals. Multiple introductions of different gene pools are often undertaken by hatcheries as a strategy for restoring and maintaining high genetic variation in hatchery reared fish stocks (Van der Bank et al. (1992); Hedrick & Kalinowski, 2000; Wachirachaikarn et al. (2009). However, among the natural populations, LBA had a lower number of alleles (3.80±0.84), compared to other natural populations. This could be attributed to a recent colonization of the lake by *C. gariepinus*, after the lake witnessed frequent drying during the Holocene (Verschuren et al., 2000), especially given its shallow depth (maximum depth 2.1 m) and small surface area of 130 km^2 (Beadle 1974; Bessem et al., 2008). Empirical evidence

shows that Lake Baringo was completely dry about 200 years ago (Bessem et al., 2008). Therefore the Lake Baringo population of *C. garienus* would be evolutionarily youger than the Lakes Victoria and Turkana and Kanyaboli populations. Lower genetic variation is reported in fish with recent colonization history than older and more stable lineages (Barluenga & Meyer, 2010). Although both LTA and LBA are located in the eastern Rift, LTA reported a higher number of alleles and therefore higher genetic variation than LBA, because of a historical connectivity with the Western Nile (Dumont, 1986). Rifting cut off this connectivity, but LTA population retained higher genetic diversity extant in the Nile system, while LBA was seeded by the Kanguen River after re-filling in the late Holocene (Dumont, 1986; Bessem, et al., 2008). Higher genetic variation in LTA compared to LBA could not be revealed by mtDNA since this is a single locus, as opposed to the multi-locus microsatellite DNA markers.

Except for LBA, the number of alleles and H_E among natural catfish populations were uniform, while both the number of alleles (Na) and H_E varied strongly among samples from fish farms. This could be attributed to genetic drift in farmed samples, since fish farms usually hold small sample sizes of fish, which are used for both propagation and grow-out. This is consistent with the results of Hansen et al., (2006), where strong variation in both Na and H_E among farmed samples of the Indian major carp occur due to genetic drift in samples, related to breeding practices. While male brood stock are sacrificed for milt and pituitary, females of preferred features and sizes (200 to 500g) are re-used in artificial propagation, after a reconditioning period of 2-3 months. A re-use of brood stock favors certain traits whose allele frequencies increase at the hatchery, at the expense of traits in brooders that are not used, whose alleles are lost.

On the other hand, LVG, LKG and LTA showed less variable number of alleles and H_E, which were much higher than for LBA. Historical connectivity of Lake Victoria to the western arm of the rift, sharing ichthyofauna with Lakes Kyoga, Albert and George before it was uplifted to 1,000 m by tectonic uplifting (Beadle, 1974; Partridge et al., 1995) could explain higher genetic variation in LVG. This diversity in genetic variability could have been maintained by the large size of the L. Victoria water mass (Barasa et al., 2014), despite predation of LVG by the exotic *L. niloticus*. Similarly, Lake Turkana was connected to the Nile drainage system, before it was cut off by rift (Dumont, 1986), and hence the high genetic variation of the population could be a reflection of historical diversity of *C. gariepinus* in the Nile.

The inbreeding coefficient showed that samples of LKG, SAG, UoE and KIB *C. gariepinus* were inbred, while LVG, LTA, LBA and SAN were not. Of the four inbred populations, only one was natural, with the rest being farmed. Inbreeding in farmed catfishes could be attributed to effects of domestication, where hatchery operators select good looking brooders (females as a source of eggs, and males for milt and pituitary hormone). This selection favours certain genotypes, which are used for propagation, and eliminates others that are considered less desirable for propagation. Also after propagation, female brooders are re-used to spawn eggs in the next propagation, after a reconditioning period of 2 to 3 months. Furthermore, some of the progeny from the brooders are retained on the farms to boost the numbers of brood stock, and so are used as male and female brooders in subsequent generations. This increases the likelihood of progeny sharing alleles by virtue of being identical by descent, and constitutes inbreeding (Norris et al., 1999), which leads to inbreeding depression. Inbreeding in farmed populations is reported not only in catfishes (Van Der Walt et al., 1993; Popoola et al., 2014), but also in other farmed species such as

the Atlantic salmon, *Salmo salar* (Su et al., 1996; Bourret et al., 2011; Perrier et al., 2014), and tilapias (Eknath & Hulata, 2009). Additionally, inbreeding in farmed samples of *C. gariepinus* could result from small numbers of brood stock that farmers usually maintain at hatcheries and farms. Keeping small numbers of brooders is a common practice among *C. gariepinus* farmers because of limited facilities (ponds and tanks), and difficulties of catching and transporting large numbers of live catfish brooders from natural habitats to farms. Furthermore, the number of brooders kept at the farm often reduces naturally over time, because of cannibalism among the brooders kept in the same pond or tank, especially if the fish are inadequately fed, using poor quality diets.

On the other hand, inbreeding in the natural population of LKG, could be attributed to the small size of the lake (Barasa et al., 2014), which could easily cause genetic drift in the population. Similarly high fishing pressure in Lake Kanyaboli (LKG) (Aloo, 2003), to provide catfish for both food and bait for *L. niloticus* (Barasa et al., 2016) could be causing inbreeding in the population by reducing the population size of the fish. Inbreeding is also reported in natural populations of other fish species such as salmonids (Wang et al., 2002; Perrier et al., 2014).

5.2. Population Genetic structure of *C. gariepinus* inferred from mitochondrial D-loop control region and Microsatellite DNA data.

There was differentiation among populations, as illustrated by significantly different F_{ST} values ($p < 0.05$), in a total of 28 pair wise comparisons in mtDNA and 15 pair wise comparisons in microsatellite DNA analyses. Therefore, differences in the populations could be attributed to among population genetic variation. Differentiation among populations could be due to geographic isolation, of the main populations.

According to Beadle (1974), and Giddelo et al., (2002), rifting caused the elevation of Lake Victoria on to an uplifted plateau (1,000 m above sea level), separating it from the connectivity with the western rift. Although both Lakes Baringo and Turkana are in the old eastern or Gregory rift, Lake Turkana and the Omo river were separated from the Nile River system less than 10,000 years ago (Dumont, 1986), when the Kanguen river became affected by tectonic uplifting (Beadle 1974). High genetic differentiation among populations of *C. gariepinus* is reported by Giddelo et al., (2002); Roodt-Wilding et al., (2010); Ojiambo, (2015) and Barasa et al., (2017). The results of this study indicate that gene flow is restricted to samples of *C. gariepinus* from fish farms (UoE, KIB, WKU, SAN and SAG), which are translocated around the country, as sources of seeds, or brood stock. This is so especially for the LVG population, from which most farmed populations except SAG were derived. Similarly, gene flow among the populations could be attributed to the trade in live *C. gariepinus* bait samples (Barasa et al., 2014), where bait traders collect catfish fry from both farms and natural aquatic habitats (such as Lake Kanyaboli) for sale to fishermen along landing beaches of Lake Victoria daily for catching *L. niloticus* by long lines. During the fixing of the bait samples onto hooks by *L. niloticus* fishermen, some of the live samples could escape into the waters of Lake Victoria. Also, some of the samples on the hooks could wriggle off and escape into the water, leading to gene flow.

However, of the 5 clusters identified in the samples (Fig. 4.2), samples from Sagana Aquaculture Center were the only samples from fish farmes that formed a distinct cluster of its own. This showed that the *C. gariepinus* broodstock at Sagana formed a population, while samples from all the other farms sampled did not form a population. This reflects the uniqueness of SAG population, which could be attributed to possible

multiple introductions of *C. gariepinus* from different sites to the farm. Multiple introductions of fish gene pools to a hatchery are known to increase genetic variability of brooders (Van De Bank et al., 1992; Grobler et al., 1997). However, results of this study are not able to tell specific sites from which some of the brooders of SAG were collected from, since field sampling for tis study did not include any samples from around Sagana Aquaculture center.

From the analysis of population genetic structure by STRUCTURE (Fig. 4.4) and STRUCTUREHARVESTER (Fig. 4.5) softwares, it was found that the samples clustered into 4 populations of *C. gariepinus*: LVG, LTA, LBA and SAG. The genetic structuring observed among the first three populations, which are natural populations, could be attributed to geographical separation of the water masses, due to volcanicity and tectonic activity, leading to genetic distinctness of the populations. Although the three lakes belong to the eastern rift (Giddelo et al., 2002), uplifting of Lake Victoria to a plateau (Partridge et al., 1995) disconnected it from Nile system and therefore also Lake Turkana (Giddelo et al., 2002). Further rifting disconnected Lakes Baringo and Turkana, and this led to distinct populations. These populations represent important Catfish genetic resources, which could be utilized in a genetic improvement programme for desirable traits, as recommended by Ponzoni & Nguyen, (2008).

5.3. Life-history parameters of *Clarias gariepinus* from Lakes Victoria, Baringo and Kanyaboli populations of Kenya

5.3.1. Relative fecundity

Relative fecundity, the number of eggs per gram body weight spawned by a fish (Bagenal & Tesch, 1978), is an important parameter in both fisheries and aquaculture. A higher relative fecundity would typically be desirable as it increases persistence and

resilience of the population in the fishery despite fishing pressure (Karjalainen et al., 2015). In aquaculture, a higher relative fecundity increases seed availability for re-stocking ponds in the enterprise, and also for sale to other fish farmers. In the current study, samples of LVG population had a higher relative fecundity than both LBA and LKG, which had similar relative fecundity, despite LKG having a higher heterozygosity than LBA. High plasticity occurs in fecundity as a phenotypic trait (Karjalainen et al., 2015), and this variation can be both intraspecific and interspecific (Murua et al., 2003). Variability in fecundity of *C. gariepinus* populations has been reported in Ethiopia, with the Lake Chamo population (Dadebo et al., 2011) showing a higher fecundity than the L. Awassa population (Dadebo et al., 2000). In the current study, similar relative fecundity of LKG and LBA despite LKG having a higher heterozygosity could be attributed to a higher fishing pressure in Lake Kanyaboli than Lake Baringo. Overfishing is reported in Lake Kanyaboli (Aloo, 2003), and despite lack of information on Lake Baringo, fishing pressure is likely to be higher in Lake Kanyaboli than Baringo. High predation pressure (Reznick et al., 2004) and fishing pressure (Karjalainen et al., 2015) select for earlier and smaller size at maturity. Additionally, Lake Kanyaboli has a smaller watermass compared to both Lakes Baringo and Victoria (Barasa et al., 2017), and so the LKG population was probably smaller than both LBA and LVG populations. Individuals of a smaller population would be distributed over smaller spatial areas (Einum et al., 2003), and since fishing naturally targets bigger and therefore fish of a higher fecundity, this reduces the fecundity of the population. Since fecundity is related to size of the spawner (Kant et al., 2016), fish samples from Lake Kanyaboli probably reach sexual maturity earlier, and so spawn a fewer number of eggs.

Since LVG also had a higher heterozygosity than both LKG and LBA, and nutrient values were similar in the three habitats, the results seem to suggest an association between heterozygosity and relative fecundity as a life history trait in *C. gariepinus*. Therefore the LVG population seems to have a higher reproductive ability than both LBA and LKG, and lower heterozygosity in the evolutionarily younger LBA seems to reduce the reproductive ability of the population. Fecundity is a function of both genetic characteristics (Quattro & Vrijenhoek, 1989; Danzmann et al., 1989; Liskauskas & Ferguson, 1990) and environmental factors (Karjalainen et al., 2015; Vrtilek & Reichard, 2016; Kant et al., 2016). The impact of genetic variation on fitness traits has been demonstrated in salmonids (Wang et al., 2002), in which inbreeding that erodes genetic diversity in a number of salmonids such as the Chinook (*Onchorynchus tshawytscha*), Coho (*O. kisutch*), Chum (*O. keta*) and the Atlantic salmon (*Salmo salar*) has reduced the survival rates of wild populations, prompting the species and populations to be listed under the endangered category in the USA (Knudsen et al., 2000; NRC, 2002). These studies highlight the importance of genetic variation as a primary genetic goal in conservation biology (Loeschcke et al., 1994; Allendorf & Waples, 1996), since it influences complex life histories that ensure persistence of salmonid species in the environment (NRC, 1996; Policansky & Magnuson, 1998), and may be exploited to increase production of farmed fish species such as *C. gariepinus* (Barasa et al., 2016; 2017).

5.3.2. Size at first maturity ($L_m 50$)

It is generally known that evolutionary changes in life history traits affect the viability and future harvests of a fishery (Heino, 1998; Hard et al., 2008). One such trait is the size at first maturity ($L_m 50$) of a fish population. In the current study, LBA had both

sexes of fish maturing at a bigger size than both LVG and LKG. Both sexes of LVG had higher L_m50 than for LKG. Size at first maturity, one of the most variable fitness traits, especially in fish species (Meyer et al., 2003; Hard et al., 2008; Feiner et al., 2017), is an attribute of genetic variability in populations (Thrower et al., 2004; Hard et al., 2008; Feiner et al., 2017), habitat quality and productivity (Meyer et al., 2003) and fishing pressure (Meyer et al., 2003; Hard et al., 2008). The results of this study do not reflect HFC hypothesis, since LBA of lower heterozygosity had higher values of L_m50 than LVG and LKG, both of which had higher heterozygosity than LBA. This could be attributed to higher fishing pressure on LVG and LKG populations of *C. gariepinus* than LBA, which could have induced evolutionary pressure in favour of early maturing fish. Fish in populations under high predation pressure or fishing pressure mature earlier (Vrtilek & Reichard 2016), and this reduces the asymptotic body size, since energy is reallocated from growth to reproduction (Kozlowski, 1992; Heino & Kaitala, 1999; Quince et al., 2008). Higher fishing pressure also removes the bigger fish from the fishery, and induces changes that lead to precocious parents, maturing earlier (Gross, 1996; Locham et al., 2016), and this also reduces fecundity (Hamon et al., 2000; Hamon & Foote, 2005).

High fishing pressure is reported in Lakes Victoria (Pringle, 2005; Turyaheebwa, 2014; LVFO, 2015) and Kanyaboli (Aloo, 2003), although no studies exist comparing fishing pressure in the three lakes. A lower fishing pressure may be expected in Lake Baringo than Lakes Victoria and Kanyaboli, since fishing in Lake Baringo is less commercialized, with fewer vessels and fishermen. Therefore, the results of this study seem to suggest that ecological factors may have a higher impact on L_m50 than

genetic factors. However, genetic characteristics of *C. gariepinus* may be expected to influence L_m50, if ecological factors are constant or comparable in different habitats.

CHAPTER SIX

CONCLUSION AND RECOMMENDATIONS

6.1. Conclusion

From mitochondrial D-loop data that investigated genetic variation in 10 populations of *C. gariepinus*, a total of five populations or clusters were detected. These included LVG, LTA, LBA, LJP and SAG, revealed by both the Maximum likelihood tree and the Minimum spanning network. But a total of four clusters of *C. gariepinus* were detected in the microsatellite DNA analysis, which included only samples from 8 sampling sites. Therefore, it is possible that up to five clusters of *C. gariepinus* could be detected also by microsatellite analysis if LJP and WKU samples were included in the study. Generally, high genetic variation was detected in the samples of *C. gariepinus*. Natural populations of the species had higher genetic variation than farmed samples, and this was revealed by both markers.

Gene flow occurred among populations of *C. gariepinus,* and was mainly restricted to samples from the Lake Victoria basin. This showed that gene flow was promoted mainly by translocation of fish by human activities for aquaculture, since the Lake Victoria basin is a main aquaculture region in the country. This was because most farmed populations had shared haplotypes, and natural populations that were located in isolated and far flung and dry areas (LTA ad LJP), where aquaculture was not practiced, did not have any shared haplotypes.

LTA and LVG had higher genetic variation than LBA, consistent with the fact that LTA and LVG are evolutionarily older lineages than LBA which is younger. Therefore, it appears that genetic variation in *C. gariepinus* increases with evolution, as expected from theory. LVG had higher relative fecundity than LBA and LKG, suggesting that heterozygosity seems to correlate with relative fecundity as a fitness

trait in *C. gariepinus*, although other factors like fishing pressure and inbreeding may erode the potential for high fecundity in the species. There was no correlation between heterozygosity and size at first maturity for the species.

6.2. Recommendations

Following the results of this study, the following recommendations are advanced:

1. Farmers may benefit from higher production if they use brood stock of *C. gariepinus* of higher genetic variation and distinctness in artificial propagation at hatcheries. However, comparative growth and survival of populations of higher genetic variation (LVG, LTA and LKG) and those of lower genetic variation (LBA) should be tested, to establish if growth and survival also correlate with genetic variation in *C. gariepinus*.

2. Interbasin transfer of *C. gariepinus* brood stock and fingerlings should be avoided, to ensure that genetically distinct populations are not homogenized by admixture, or introduction of new alleles or haplotypes.

3. The unique haplotypes and alleles should be conserved, by recruiting these populations into aquaculture.

4. Future research directions should focus on the relationship of heterozygosity and fecundity and size at first maturity in the face of differential environmental factors and fishing pressure.

REFERENCES

Abila, R. Barluenga, M., Engelken, J., Meyer, A. and Salzburger, W. (2004). Population structure and genetic diversity in a Haplochromine fish cichlid of a satellite lake of Lake Victoria. *Molecular Ecology*, **13**: 2589-2602.

Agembe, S. (2012). Estimation of important reproductive parameters for management of the Shoemaker Spine foot Rabbitfish (*Suganus sutor*) in Southern Kenya. *International Journal of Marine Science*, **2**(4): 24-30.

Agnese, J. F. and Teugels, G. G. (2001). Genetic evidence for monophyly of the genus *Heterobranchus* and paraphyly of the genus *Clarias* (Siluriformes, Clariidae). *Copeia*, **2001**: 548-552.

Agnese, J. F. and Teugels, G. G. (2005). Insight into the phylogeny of African Clariidae (Teleostei, Siluriformes): Implications for their body shape evolution, biogeography, and taxonomy. *Molecular Phylogenetics and Evolution*, **36**: 546-553.

Alam, M. S. and Islam, M. S. (2005). Population genetic structure of the major Indian carp *Catla catla* (Hamilton) revealed by microsatellite DNA markers. *Aquaculture*, **246**: 151-160.

Allendorf, F. W. and Waples, R. (1996). Conservation and genetics of salmonid fishes. *In*: Avise, J. C. and Hamrick, J. L. (eds.), Conservation genetics: case histories from nature. New York, Chapman and Hall, pages 238-501.

Aloo, P. A. (2003). Biological diversity of Yala swamp lakes, with special emphasis on fish species composition, in relation to changes in the Lake Victoria basin Kenya: threats and conservation measures. *Biodiversity Conservation* **12**, 905-920.

Ani-Sabwa, J., Mlewa, C. M. and Njiru, J. (2014). Effects of greenhouse and stocking density on growth and survival of African catfish *Clarias gariepinus* (Burchell 1822) fry reared at high altitude. *International Journal of Science and Research*, **3** (9): 1558-1563.

Areerat, S. (1987). *Clarias* culture in Thailand. *Aquaculture*, **63**: 355-362.

Audo, M. C. and Diehl, W. J. (1995). Effect of quality and quantity of environmental stress on multilocus heterozygosity-growth relationships in *Eisnia fetida*. *Heredity*, **75**: 98-105.

Bagenal, T. (1978). Methods for assessment of fish production in fresh waters. Blackwell Scientific Publications Ltd., London, 365 pages.

Bagenal T. and Braum, E. (1978). Eggs and early life history. *In*: Methods for assessment of fish production in freshwaters. IHB Handbook number 3, pages 165-201 (Bagenal T., ed.). Blackwell Scientific Publications, London.

Bagenal, T. B. and Tesch, F. W. (1978). Age and growth. *In*: Methods for assessment of fish production in freshwaters, pages 101-136 (Bagenal, T. ed.). IBP Handbook No. 3. Blackwell Scientific Publications, London.

Barasa, J. E., Abila, R., Grobler, J. P., Dangasuk, O. G., Njahira, M. N. and Kaunda-Arara, B. (2014) Genetic diversity and gene flow in African catfish, *Clarias gariepinus* (Burchell 1822) from Lakes Victoria and Kanyaboli. *African Journal of Aquatic Science*, **39**(3): 287-293.

Barasa J.E., Abila, R., Grobler, J. P., Agaba, M., Chemoiwa, E. J. and Kaunda-Arara, B. (2016). High genetic diversity and population differentiation in *Clarias gariepinus* (Burchell 1822) of Yala swamp: Evidence from mitochondrial DNA sequences. *Journal of Fish Biology*, **89** (6): 2257-22570.

Barasa, J. E., Mdyogolo, S., Abila, R., Grobler, J. P., Skilton, R. A., Bindeman, H., Njahira, M. N., Chemoiwa, E. J., Otto G. D., Kaunda-Arara B and Verheyen, E. (2017). Genetic diversity and population structure of the African catfish, *Clarias gariepinus* (Burchell 1822) in Kenya: implication for conservation and aquaculture. *Belgian Journal of Zoology*, 142 (2): 105-127.

Bandelt H. J., Forster, P. and Rohl, A. (1999). Median-joining networks for inferring intraspecific phylogenies. *Molecular Biology and Evolution*, **16**, 37- 48.

Barluenga, M. and Meyer, A. (2010). Phylogeography, colonization and population history of the Midas cichlid species complex (*Amphilophus* spp.) in the Nicaraguan crater lakes. *BMC Evolutionary Biology*, **10**: 326-346.

Beadle, L. C. (1974). *The Inland Waters of Tropical Africa: An Introduction to Tropical Limnology*. London: Longman.

Berthier, P., Beaumont, M. A., Cornuet, J-M. and Luikart, G. (2002). Likelihood-based estimation of the effective population size using temporal changes in allele frequencies: a genealogical approach. *Genetics*, **160**: 741-751.

Bessem, I., Verschuren, D., Russell, J. M., Hus, J., Mees, F. and Cumming, B. F. (2008). Palaeolimnological evidence for widespread late 18th century drought across equatorial East Africa. *Palaeogeography, Palaeoclimatology and Palaeoecology*, **259**: 107-120.

Blanck, A. and Lamouroux, N. (2007). Large-scale intraspecific variation in life-history traits of European fresh water fish. *Journal of Biogeography*, **34**: 862-875.

Bolivar, R. B., Eknath, A. E., Bolivar, H. L. and Abella, T. A. (1993). Growth and reproduction in individually tagged *Oreochromis niloticus* of different strains. *Aquaculture*, **111**: 159-169.

Bourret, V., O'reilly, P. T., Carr, J. W., Berg, R. P. and Bernatchez, L. (2011). Temporal change in genetic integrity suggests loss of local adaptation in a wild Atlantic Salmon, *Salmo salar* population following introgression by farmed escapes. *Heredity*, **106**: 500-510.

Bowmaker, A. P. (1973). A hydrological study of the Mwenda River and its mouth, Lake Kariba. Ph.D thesis, University of Witwatersrand, South Africa.

Bruton, M. N. (1988). Systematics and biology of clariid catfish. *In*: The culture of sharptooth catfish in Southern Africa. T. Hecht, W. Uys and P. J. Britz (editors), South African National Scientific Programmes, Report Number 153, 146pages, ISBN 0 7988 4498 1. National Programme for Aquaculture, Pretoria, South Africa.

Cambray, J. A. (2003). The need for research and monitoring on the impacts of translocated sharptooth catfish, *Clarias gariepinus*, in South Africa. *African Journal of Aquatic Science*, **28** (2): 191-195.

Cane, M. A. and Molnar, P. (2001). Closing of the Indonesian seaway as a precursor to East African aridification around 3 million years ago. *Nature*, **411**: 157-162.

Cavalli-Sforza, L. L., Menozzi, P. and Piazza, A. (1994). The history and geography of human genes. Princeton University Press, Princeton, NJ.

Chakroborty, L. and Leimar, O. (1987). Genetic variation within a sub-divided population. *In*: N. Ryman and F. Utter, (Eds.) Population genetics and fishery management, pages 89-120. Washington Sea Grant Publications/ University of Washington Press, Seattle.

Clark, W. G. (1991). Ground fish exploitation rates based on life-history parameters. *Canadian Journal of Fisheries and Aquatic Sciences*, **48**: 734-750.

Clay, D. (1979). Sexual maturity and fecundity of the African catfish, *Clarias gariepinus*, with an observation on the spawning behavior of the Nile catfish, *Clarias lazera*. *Zoological Journal of the Linnean society*, **65**: 351-365.

Chemoiwa, E. J., Abila, R., MacDonald, A., Lamb, J., Njenga, E. and Barasa, J. E. (2013). Genetic diversity and population structure of the endangered ripon barbell, *Barbus altianalis* (Boulenger 1900), in Lake Victoria catchment, Kenya, based on mitochondrial DNA sequences. *Journal of Applied Ichythyology*, **29**: 1225-1233.

Chepkirui-Boit, V., Nugi, C. C., Bowman, J., Oyoo, E. O., Rasowo, J., Bundi, J. M. and Cherop, L. (2011). Growth performance, survival, feed utilization and nutrient utilization of the African catfish, *Clarias gariepinus* co-fed *Artemia* and a micro-diet containing atyid shrimp (*Caridina nilotica*) during weaning. *Aquaculture Nutrition,* **17**: e82-e89.

Chitamwebwa, D., Kamanyi, J., Kayungi, J., Nabbongo, H., Ogolla, A. and Ojuok, J. (2009). The present status of the hook fishery and its impact on fish stocks of Lake Victoria. *African Journal of Tropical Hydrobiology and Fisheries*, **12**: 78-82.

Clay, D. (1979). Sexual maturity and fecundity of the African catfish, *Clarias gariepinus*, with an observation on the spawning behavior of the Nile catfish, *Clarias lazera. Zoological Journal of the Linnean society*, **65**: 351-365.

Corbet, P.S. (1961). The food of non-cichlid fishes in the Lake Victoria basin, with remarks on their evolution and adaptation to lacustrine conditions. *Proceedings of the Zoological Society of London*, **136**: 1-101.

Coughlan, J. P., Imsland, A. K., Galvin, P. T., Fitzgerald, R. D., Naevdal, G., and Cross, T. F. (1998). Microsatellite DNA variation in wild populations and farmed strains of turbot from Ireland and Norway: a preliminary study. *Journal of Fish Biology*, **52** (5): 916.

Dadebo, E. (2000). Reproductive biology and feeding habits of the catfish *Clarias gariepinus* (Burchell) in Lake Awassa, Ethiopia. *Ethiopian Journal of Science*, **23** (2): 231-246.

Dadebo, E., Ahlgren, G. and Ahlgren, I. (2003). Aspects of reproductive biology of *Labeo horie* (Heckel) in Lake Chamo, Ethiopia. *African Journal of Ecology*, **41**: 31-38.

Dadebo, E., Gebre-Mariam, Z. and Mengistou, S. (2011). Breeding season, maturation, fecundity and condition factor of the African catfish *Clarias gariepinus* (Burchell 1822) in Lake Chamo, Ethiopia. *Ethiopian Journal of Biological Sciences*, **10**: 1-17.

Daget, J., Gosse, J. P. and Thys van Den Audenaerde, D. F. E. (1984). Checklist of the fresh water fishes of Africa. Vol. 1. ORSTOM, Paris, 410 pages.

Danzmann, R. G., Ferguson, M. M. and Allendorf, F. W. (1988). Heterozygosity and components of fitness in a strain of rainbow trout. *Biological Journal of the Linnean Society*, **33**: 285-304.

David, P. (1998). Heterozygosity-fitness correlations: new perspectives on old problems. *Heredity*, **80**: 531-537.

David, P. and Jarne, P. (1997). Heterozygosity and growth in the marine bivalve, *Spisula ovalis* : testing alternative hypotheses. *Genetic Research*, **70** : 215-223.

de Graaf, G. J., Galemoni, F. and Banzoussi, B. (1995). The artificial reproduction and fingerling of African catfish, *Clarias gariepinus* (Burchell 1822) in protected and unprotected ponds. *Aquaculture Research,* **26**: 233-234.

De Kimpe, P. and Micha, J. –C. (1988). First guidelines for the culture of *Clarias lazera* in Central Africa. *Aquaculture*, **4**: 227-248.

Dumont, H. J. (1986). The Nile River system. In *The ecology of River systems* (Davis, B. R. and Walkers, K. F., eds.), pages 61-74. Dortrecht: Dr. W. Junk Publishers.

Earl, D. A. and vonHoldt, B. M. (2012). STRUCTUREHARVESTER: a website and program for visualizing STRUCTURE output and implementing the Evanno method. *Conservation Genetics Resources*, **4**: 359-361.

Eccles, D. H. (1992). Food and Agriculture Organisation (FAO). Species identification sheets for fishery purposes. Field guide to the freshwater fishes of Tanzania. FAO, Rome. 145 pages.

Echeverria, W. T. (1987). Thirty-four species of Carlifornia Rock fishes: Maturity and seasonality of reproduction. *Fishery Bulletin*, **85** (2): 229-250.

Egna, H. and Boyd, C. E. (1997). Dynamics of pond aquaculture. CRC Press, Boca Raton, 437 pages.

Einum, S., Flemming, I. A., Cote, I. M. and Reynolds, J. D. (2003). Population stability in salmon species: effects of population size and female reproductive allocation. *Journal of Animal Ecology*, **72**, 811-821.

Eknath, A. E. and Hulata, G. (2009). Use and exchange of genetic resources of Nile tilapia (*Oreochromis niloticus*). *Reviews in Aquaculture*, **1**: 197-213.

Eknath, A. E., Tayamen, M. M., Palada de-Vera M. S., Danting, J. C., Reyes, R. A., Dionsio, E. E., Gjedrem, J. B. and Pullin, R. S. V. (1993). Genetic improvement of farmed tilapias: The growth performance of eight strains of *Oreochromis niloticus* tested in eleven different environments. *Aquaculture*, **111**: 171-188.

Erzini, K. (1994). An empirical study of variability in length at age of marine fishes. *Journal of Applied Ichythyology*, **10**: 17-41.

Ewens, W. J. and Spielman, R. S. (1995). The Transmission/Disequilibrium Test: History, Subdivision and Admixture. *American Journal of Human Genetics*, **57**: 455-464.

Excoffier, L., Smouse, P. E. and Quattro, J. M. (1992). Analysis of molecular variance inferred from metric distances among DNA haplotypes: application to human mitochondrial DNA data. *Genetics*, **131**: 479-491.

Excoffier, L., Laval, G. and Schneider S. (2005). Arlequin: an integrated software package for population genetics data analysis. Version 3.0. Computational and Molecular Population Genetics Laboratory (CMPGL). Berne (Switzerland): Institute of Zoology, University of Berne.

Falush, D, Stphens, M. and Pritchard, J. K. (2007). Inference of population structure using multilocus genotype data: dominant markers and null alleles. *Molecular Ecology Notes*, 7: 574-578.

FAO (Food and Agriculture Organization of the United Nations) (2009). Fishstat: Universal software for fishery statistical time series v. 2.3. Data and Statistics Unit, FAO, Rome.

Feiner, Z. S., Dewoody, J. A., Breck, J. E. and Hook, T. O. (2017). Influences of multilocus heterozygosity on size during early life. *Ecology and Evolution*, **7**: 2142-2154.

FishBase, (2003) FAO aquaculture production data of *Clarias gariepinus*. Available source:
http://filaman.unikiel.de/Report/FAO/FAOAquacultureList.cfm?scienti fic= *Clarias gariepinus*. May 13, 2003.

Fisheries Frame Survey-Implementation of a Fisheries Management Plan (2012). Lake Victoria (Kenya) Biennial Fisheries Frame Survey National Report. Frame surveys National Working group. 89 pages. Ministry of Fisheries Development, Nairobi, Kenya.

Frankel, O. H. and Soule, M. E. (1981). Conservation and Evolution. Cambridge University Press, Cambridge.

Frankham, R., Ballou, J. D., and Briscoe, D. (2002). Introduction to Conservation Genetics. Cambridge: Cambridge University Press.

Fryer, G. (2001). On the age and origin of the species flock of haplochromine cichlid fishes of Lake Victoria. *Proceedings of the Royal Society of London, Series B*, **268**: 1147-1152.

Galbusera, P. (1997). The genetic variability of wild and inbred populations of the African catfish, *Clarias gariepinus* (Burchell 1822). Ph.D thesis. Katholieke University, Leuven, Belgium.

Galbusera, P., Volckaert, F. A., Hellemans, B. and Ollevier, F. (1996). Isolation and characterization of microsatellite markers in the African Catfish, *Clarias gariepinus* (Burchell, 1822). *Molecular Ecology,* **5**: 703-705.

Galloway, L. F. and Fenster, C. B. (2000). Population differentiation in an annual legume. Local adapation. *Evolution*, **54** (4): 1173-1181.

Giddelo, C. S., Arndt A. D. and Volckaert F. A. M. (2002). Impact of rifting and hydrography on the genetic structure of *Clarias gariepinus* in eastern Africa. *Journal of Fish Biology*, **60**: 1252-1266.

Goudswaard, K. P. C. and Witte, F. (1997). The catfish fauna of Lake Victoria after the Nile perch upsurge. *Environmental Biology of Fishes*, **49**: 21-43.

Greenwood, P. H. (1957). The reproduction of *Clarias mossambicus* in Lake Victoria. *In*: Second symposium on African Hydrobiology and Inland fisheries, 1956. CSA Pub no. 25: 77-78.

Grobler, J. P., Hoffman, L. C. and Prinsloo, J. F. (1997). A comparison of allozyme heterozygosity and life history variables in four strains of African catfish *Clarias gariepinus*. *South African Journal of Aquatic Science*, **23** (1): 31-41.

Gross, M. R. (1996). Alternative reproductive strategies and tactics: diversity within sexes. *Reviews in Ecology and Evolution*, **11**: 92-98.

Guha, D. and Murkherjee, D. (1991). Seasonal cyclical changes in the gonadal activity of common carp, *Cyprinnus carpio* Linn. *Indian Journal of Fisheries*, **38**: 218-223.

Hallerman, E. M. (2003). Population Genetics: principles and application for Fisheries Scientists. American Fisheries Society, Bethsda, MD. USA, 475 pages.

Hamon, T. R. and Foote, C. J. (2005). Concurrent natural and sexual selection in wild male sockeye salmon, *Onchorynchus nerka*. *Evolution*, **59**: 1104-1118.

Hamon, T. R., Foote, C. J., Hiborn, R. and Rogers, D. E. (2000). Selection on morphology of spawning wild sockeye salmon by gillnet fishery. *Transactions of the American Fisheries Society*, **129**: 1300-1315.

Hansen, M. M., Simonsen, V., Mensberg, K. –L. D., Sarder, MD. R. I. and Ala, MD. S. (2006). Loss of genetic variation in hatchery-reared Indian major carp. *Journal of Fish Biology*, **69** (Supplement B), 229-241.

Hard, J. J., Gross, M. R., Heino, M., Hilborn, R., Kope, R. G., Law, R. and Reynolds, J. D. (2008). Evolutionary consequences of fishing and their implications for Salmon. *Evolutionary Applications*, **1**: 388-408.

Hassanien, H. A. and Gilbey, J. (2005). Genetic diversity and differentiation of Nile tilapia, *O. niloticus*, revealed by DNA. *Aquaculture Research,* **36**: 1450-1457.

Hatfield, T. and Schulter, D. (1999). Ecological speciation in sticklebacks: environment-dependent hybrid fitness. *Evolution*, **53**: 866-873.

Hauser, L., Adcock, G. J., Smith, P. J., Ramirez, J. B. H. and Carvalho, G. R. (2002) Loss of microsatellite diversity and low effective population size in an over-exploited population of New Zealand snapper (*Pagrus auratus*). *Proceedings of National Academy of Science, USA*, **99**: 11742-11747.

He and Stewart, (2001). Age and size at first reproduction of fishes: predictive models based only on growth trajectories. *Ecology*, **82** (3): 784-791.

Hecht, T. (1985). Recent developments in aquaculture in South Africa: sharptooth catfish, *Clarias gariepinus*. In: Hect T. Bruton, M. N. and Safriel, O. (editors) Aquaculture South Africa 1984. Occasion report no. 1. FRD, CSIR, Pretoria. Pages 33-46.

Hecht, T. and Appelbaum, S. (1988). Observations on intraspecific aggression and coeval sibling cannibalism by larval and juvenile *Clarias gariepinus* (Clariidae: Pisces) under controlled conditions. *Journal of Zoology, London*, **214**: 21-44.

Hecht, T. and Britz, P. J. (1988). An overview of the development of clariid catfish culture, with particular reference to Southern Africa. *In*: The culture of sharptooth catfish in Southern Africa. T. Hecht, W. Uys and P. J. Britz (editors), South African National Scientific Programmes, Report Number 153, 146pages, ISBN 0 7988 4498 1. National Programme for Aquaculture, Pretoria, South Africa.

Hedrick, P. W. and Kalinoswski S. T. (2000). Inbreeding depression in conservation biology. *Annual Review of Ecology and Systematics*, **39**: 139-162.

Heino, M. (1998). Management of evolving fish stocks. *Canadian Journal of Fisheries and Aquatic Sciences*, **55**: 171-12.

Heino, M. and Kaitala, V. (1999). Evolution of resource allocation between growth and reproduction in animals with indeterminate growth. *Journal of Evolutionary Biology*, **12**: 423-429.

Hogendoorn, H. (1977). Progress in the controlled propagation of the African catfish, *Clarias lazera* (Cuvier and Valenciennes). Third meeting of the ICES Working Group on mariculture, Brest, France, May 1977. *Actes de Colloques du CNEXE*, **4**: 123-130.

Hogendoorn, H. (1980). Controlled propagation of the African catfish, *Clarias lazera*. III. Feeding and growth of fry. *Aquaculture*, **21**: 233-241.

Huisman, E. A. and Richter, C. J. J. (1987). Reproduction, growth, health control and aquacultural potential of the African catfish, *C. gariepinus* (Burchell 1822). *Aquaculture*, 63: 1-14.

Huff, D. D., Miller, M. L., Chizinski, J. C. & Bruce, V. (2011). Mixed-source reintroductions lead to outbreeding depression in second-generation descendants of a native North-American fish. *Molecular Ecology*, 2011.

Hutchings, J. A. and Jones, M. E. B. (1998). Life history variation and growth rate thresholds for maturity in Atlantic salmon, Salmo salar. *Canadian Journal of Fisheries and Aquatic Sciences*, **55** (Supplement 1): 22-47.

Joanna, G., Dariusz, P., Miroslaw, P., Serhan, T. A., Lidia, M. and Magdalena, L. K. (2011). Life-history traits of Amur sleeper, *Perccottus glenii*, in the invaded Vistula River: early investment in reproduction but reduced growth rate. *Hydrobiologia*, **661**: 197-210.

Johnson, C. T., Scholz, C. A., Talbot, M. R., Kelts, K., Ricketts, R. D., Ngobi, G., Beuning, K., Ssemmanda I. and McGill J. W. (1996). Late Pleistocene desiccation of Lake Victoria and rapid evolution of cichlid fishes. *Science*, **273**: 1091-1093.

Kana, S. K. and Panda, S. (2011). Growth estimation and length at maturity of a commercially important fish, *Dayscieaena albida* (Boroga) in Chilika lagoon, India. *European Journal of Experimental Biology*, **1**(2): 84-91.

Kant, K. R., Gupta, K. and Langer, S. (2016). Fecundity in fish *Puntius sophore*, and relationship of fecundity and fish length, weight and ovary weight from Jammu water bodies J and K, India. *International Journal of Fisheries and Aquaculture Sciences*, **6** (2): 99-110.

Karjalainen, J., Urpanen, O., Keskinen, T., Huuskonen, H., Sarvala, J., Valkeajrvi, P. and Marjomaki, T. J. (2016). Phenotypic plasticity in growth and fecundity induced by strong population fluctuations affects reproductive traits of female fish. *Ecology and Evolution*, **6** (3): 779-790.

Kaufman, L. and Ochumba, P. (1993). Evolutionary and conservation biology of cichlid fishes as revealed by faunal remnants in the Northern Lake Victoria. *Conservation Biology*, **7** (3): 719-730.

Kelleher, M. K. and Vinke, M. (1976). Preliminary results of studies on the survival of *Clarias lazera* in ponds. FAO CIFA Technical paper 4, (Supplement 1). Pages 487-496.

King, M. (1995). Fisheries biology, assessment and management. Fishing News Books, Blackwell Science, Oxford, UK, 342 pages.

Knaepkens, G., Knapen, D., Bervoets, L., Hanfling, B., Verheyen, E. and Eens, M. (2002). Genetic diversity and condition factor: a significant relationship in Flemish but not in German populations of the European bullhead (*Cottus gobio*). *Heredity* **89**, 280-287.

Knudsen, E. E., MacDonald, D. D. and Steward, C. R. (2000). Setting the stage for a sustanaible Pacific salmon fisheries strategy. *In*: Knudsen, E. E., Steward, C. R., MacDonald, D. D., Williams, J. E. and Reiser, D. W. (eds.), Sustainable Fisheries Management: Pacific Salmon, New York, Lewis Publishers, CRC Press LLC, pages 3-11.

Kolding, J. (1993). Population dynamics and life history styles of *Oreochromis niloticus*, in Ferguson's Gulf, Lake Turkana, Kenya. *Environmental Biology of Fishes*, **37**: 25-46.

Kozlowski, J. (1992). Optimal allocation of resources to growth and reproduction: implications for age and size at maturity. *Trends in Ecology and Evolution*, **7**: 15-19.

Lal, K. K., Singh, R. K., Mohindra, V., Singh, B. and Ponniah, A. G. (2003). Genetic make-up of exotic Catfish *Clarias gariepinus* in India. *Asian Fisheries Science*, **16**: 229-234.

Lesica, P. and Allendorf, F. W. (1995). When are peripheral populations viable for conservation? *Conservation Biology*, **9**: 753-760.

Librado, P. and Rozas, J. (2009). DnaSP v5: A software for comprehensive analysis of DNA polymorphism data. *Bioinformatics*, **25**: 1451-1452.

Lind, C. E, Brummett, R. E. and Ponzoni, R. W. (2012). Exploitation and conservation of fish genetic resources in Africa: issues and priorities for aquaculture development and research. *Reviews in Aquaculture*, **4**: 125-141.

Link, J. S. and Burnnett, J. (2001). The relationship between stomach contents and maturity state for major northwest Atlantic fishes: new paradigms. *Journal of Fish Biology*, **59**: 788-794.

Liskauskas, A. P. and Ferguson, M. M. (1990). Enzyme heterozygosity and fecundity in a naturalized population of Brook trout (*Salvelinus fontinalis*). *Canadian Journal of Fisheries and Aquatic Sciences*, **47**: 2010-2015.

Locham, A. G., Kaunda-Arara, B., Wakibia, J. G. and Muya, S. (2014). Phenotypic divergence in reproductive traits of the Marbled Parrotfish, *Leptoscarus vaigiensis* (Quoy and Gaimard 1824) on variably protected reefs in Kenya. *Western Indian Ocean Journal of Marine Science*, **13** (1): 69-80.

Lockard, L. L. (1975). Some relationships between water fertility and egg production in brown water trout, Salmo trutta from Montana rivers. *Great Basin Naturalist*, **35** (4): 435-441.

Loeschcke, V., Tomiuk J. and Jain, S.K. (1994). Introductory remarks: Genetics and conservation biology. *In*: Loeschcke, V., Tomiuk J. and Jain, S.K. (eds.), Conservation genetics. Basel/Switzerland: Birkhauser verlag, pages 3-8.

Lung'ayia, H. B. O. (1989). Some observations on the African catfish, *Clarias gariepinus* (Burchell, 1822), in the Sondu-Miriu River of Lake Victoria, Kenya. *In*: ……

LVFO (2015). Lake Victoria Fisheries Organization, Stock assessment report- status of the fish stocks 2014. LVFO Secretariat, Jinja, Uganda. 47 pages.

Macharia, S. K., Ngugi, C. C. and Rasowo, J. (2005). Comparative study of the hatching rates of African catfish, *Clarias gariepinus*, eggs on different substrates. *NAGA*, *World Fish Center Q.*, vol. **28** (3 and 4): 23-26.

Magondu, E. W., Rasowo, J., Oyoo-Okoth, E. and Charo-Karisa, H. (2011). Evaluation of sodium chloride (Nacl) for potential prophylactic treatment and its short term toxicity to African catfish *Clarias gariepinus* (Burchell 1822) yolk sac and swim-up fry. *Aquaculture*, **319**: 307-310.

Maithya, J., Njiru, M., Okeyo-Owuor, J. B. and Gichuki, J. (2012). Some aspects of the biology and life history strategies of *Oreochromis variabilis* (Boulenger 1906) in the Lake Victoria basin. *Lakes & Reservoirs: Research and Management*, **17**: 65-72.

Maruyama, T. and Fuerst, P. A. (1985). Population bottlenecks and non equilibrium models in population genetics. III. Genic homozygosity in populations which experience periodic bottlenecks. *Genetics*, 111: 691-703.

Matsuishi, T., Muhoozi, L., Mkumbo, O., Budeba, Y., Njiru, M., Asila, A., Othina, A., and Cowx, I. G. (2006). Are the exploitation pressures on the Nile perch fisheries resources of Lake Victoria a cause for concern? *Fisheries Management and Ecology*, 13: 53-71.

McBride, R. S., Vidal, T. E. and Cadrin, S. X. (2013). Changes in size and age of northern stock of Tile fish, *Lopholatilus chamaeleonticeps*) after a period of overfishing. *Fisheries Bulletin*, **111**: 161-174.

Meyer, A. (1993). The evolution of of mitochondrial DNA in fishes. *In*: Mochachka, P. W. and Mommsen, T. P. Eds. Biochemistry and Molecular Biology of Fishes. Elsevier Press Amsterdam, New York, pages 1-38.

Meyer, K. A., Schill, D. J., Elle, F. S., and Lamansky, J. A. (2003). Reproductive demographics and factors that influence length at sexual maturity in Yellowstone cutthroat trout in Idaho. *Transactions of the American Fisheries Society*, **132**: 183-195.

Miller, L. M. and Kapuscinski, A. R. (2003). Genetic guidelines for hatchery supplementation programs. *In*: Population genetics: Principles and Applications for Fisheries scientists (Edited by E. M. Hallerman). Pages 329-355. American Fisheries Society, Bethesda, MD, USA.

Miller, L. M., Close T. and Kapuscinski, A. R. (2004). Lower fitness of a hatchery and a hybrid rainbow trout compared to naturalized populations in Lake Superior tributaries. *Molecular Ecology*, **13**: 3379-3388.

Mkumbo, O. C. and Mlaponi, E. (2007). Impact of the baited hook fishery on the recovering endemic fish species in Lake Victoria. *Aquatic Ecosystem Health and Management*, **10** (4): 458-466.

Mookherjee, H. K. and Mazumdar, S. R. (1959). Some aspects of life history of *Clarias batrachus*. *Proceedings of the Zoological society of Bengal*, **3**: 71-79.

Moreau, J., Bambino, C., and pauly, D. (1986). A comparison of four indices of fish growth performance based on 100 tilapia populations (family Cichlidae). In: The first Asian Fisheries Forum, Asian Fisheries Society, Manila, Philippines, pages 201-206.

Munro, J. L. (1965). Feeding relationships and production of fish in a southern Rhodesian lake. Ph.D thesis, University of London.

Murua, H., Kraus, G., Saborido-Rey, F., Witthames, P. R., Thorsen, A. and Junguera, S. (2003). Procedures to estimate fecundity in marine fish speciies in relation to their reproductive strategy. *North Western Atlantic Fisheries Science*, **33**: 33-54.

Musa, S. M., Aura, C. M., Ngugi, C. C. and Kundu, R. (2012). The effect of three different feed types on growth performance and survival of *Clarias gariepinus* fry reared in a hatchery. *ISRN Zoology*, **2012**: 1-6.

Mwita, C. J. and Ngwengulila, G. (2008). Molecular phylogeny of the clariid fishes of Lake Victoria, Tanzania, inferred from cytochrome *b* DNA sequences. *Journal of Fish Biology,* **73**: 1139-1148.

Nagl, S., Tichy, H., Mayer, W. F., Takezaki, N., Takahata, N. and Klein J. (2000). The origin and age of haplochromine fishes in Lake Victoria, East Africa. *Proceedings of the Royal Society London*, Series B, **267**, (1447): 1049-1061.

Na-Nakorn, U., Kamonrat, W., and Ngamsiri, T. (2004). Genetic diversity of walking catfish, *Clarias macrocephalus*, in Thailand and evidence of genetic introgression from introduced farmed *C. gariepinus*. *Aquaculture,* **240**: 145-163.

Na-Nakorn, U. and Brummett, R. E. (2009). Use and exchange of aquatic genetic resources for food and aquaculture: *Clarias* catfish. *Reviews in Aquaculture*, **1**: 214-223.

Nazia, A. K., Suzana, M., Azhar, H., Nguyen Thuy, T. T. and Siti Azizah, M. N. (2010). No genetic differentiation between geographically isolated populations of *Clarias macrocephalus* in Malaysia revealed by sequences of mtDNA cytochrome *b* and D-loop gene regions. *Journal of Applied Ichthyology*, **26**: 568-570.

Nei, M. Maruyama, T. and Chakraborty R. (1975). The bottleneck effect and genetic variability in populations. *Evolution*, **29**(1): 1-10.

Ngugi, C. C., Omolo, B., Langdon, C. and Bowman, J. (2005). Studies on strategies for increasing the growth and survival of African Catfish, *Clarias gariepinus* juveniles reared for stocking or for use as bait. In: 25th Annual Technical Report- Vol.II, Oregon state University, Snell Hall 400 Corvallis, Oregon 97331-1641, USA.

Nicola, G. G. and Almodovar, A. (2002). Reproductive traits of stream dwelling brown-trout *Salmo trutta* in contrasting neighboring rivers of central Spain. *Freshwater Biology*, **47**: 1353-1365.

Njiru, M., Ojuok, J. E., Okeyo-Owuor, J. B., Muchiri, M., Ntiba, J. M. and Cowx, I. G. (2006). Some biological aspects and life history strategies of Nile tilapia, *Oreochromis niloticus* (L), in Lake Victoria, Kenya. *African Journal of Ecology*, **44**: 30-37.

Norris, A. T., Bradley, D. G. and Cunningham, E. P. (1999). Microsatellite genetic variation between and within farmed and wild Atlantic salmon (*Salmo salar*) populations. *Aquaculture*, **180**: 247-264.

NRC (National Research Council) (1996). Upstream: salmon and society in the Pacific North west. Washington D. C., National Academic Press, 452 pages.

NRC (National Research Council) (2002). Genetic status of Atlantic salmon in Maine. Washington D. C., National Academic Press, 62 pages.

Nyina-Wamwiza, L., Wathelet, B., Richir, J., Rollin, X. and Ketemont, P. (2010). Partial or total replacement of fish meal by local agricultural by-products in diets of juvenile African catfish, *C. gariepinus*: growth performance, feed efficiency and digestibility. *Aquaculture Nutrition*, **16** (3): 237-247.

Ojiambo, D. (2015). Population genetics structure of wild and domestic African catfish (*Clarias gariepinus*) in Victoria and Albertine drainage basins. MSc. thesis, Makerere Univerisity, Uganda, 53 pages.

Onyando, J. O., Kisoyan, P. and Chemelil, M. C. (2005). Estimation of potential soil erosion for River Perkerra catchment in Kenya. *Water resources management*, **19** (2): 133-143.

Owiti, D. O. and Dadzie, S. (1989). Maturity, fecundity and the effect of reduced rainfall on the spawning rhythm of a siluroid catfish, *Clarias mossambicus* (Peters). *Aquaculture and Fisheries Management*, **20**: 355-368.

Ozorio, R. O. A., Uktoseja, J. L. A., Huisman, E. A. and Verreth, J. A. J. (2001). Changes in fatty acid concentrations in tissues of African catfish, *Claris gariepinus* Burchell, as a consequence of dietary carnitine, fat and lysine supplementation. *British Journal of Nutrition*, **86**: 623-636.

Quattro, J. M. and Vrijenhoek, R. C. (1989). Fitness differences among remnant populations of the endangered sonoran topminnow. *Science*, **245**: 976-978.

Papageorgiou, N. K. (1979). The length weight relationship, age, growth and reproduction of the roach, *Rutilus rutilus* (L.) in Lake Volvi. *Journal of Fish Biology*, **14**: 529-538.

Park, S. D. E. (2001). Trypanotolerance in West African cattle and the population genetic effects selection. PhD Thesis, University of Dublin, Dublin.

Partridge, T. C., Wood, B. A. and deMenocal, P. A. (1995). The influence of global climatic change and regional uplift on large-mammalian evolution of East and Southern Africa. *In* Palaeoclimate and Evolution, with emphasis on human origins. Vrba ES, Denton, G. H., Partridge, T. C. and Burkle T. H. eds., pages 331-355. London, New Haven: Yale University Press.

Peakall, R. and Smouse, P. E. (2012). GenAlEx 6.5. Genetic analysis in Excel. Population genetic software for teaching and research- Bioinformatics 28: 2537-2539.

Perales-Flores, L. E., Sifuentes-Rincon, A. M., and Garcia de Leon, F. J. (2007). Microsatellite variability analysis in farmed catfish (*Ictalurus punctatus*) from Tamaulipas, Mexico. *Genetics and Molecular Biology*, **30** (3): 570-574.

Perrier, C., Normandeau, E., Dionne, M., Richard, A. and Bernatchez, L. (2014). Alternative reproductive tactics increase effective population size and decrease inbreeding in wild Atlantic salmon. *Evolutionary Applications*, **7**: 1094-1106.

Pojular, S. M., Maes, G. E., Vancoillie, C. and Volckaert, F. A. M. (2006). Environmental stress and life stage-dependence on the detection of Heterozygosity-fitness correlations in the European eel, *Anguilla Anguilla*. *Genome*, **49** (11): 1428- 1437.

Policansky, D. and Magnuson, J. J. (1998). Genetics, metapopulations, and ecosystem management of fisheries. *Ecological Applications*, **8**(Supplement 1): S119-S123.

Ponzoni, R. W. and Nguyen, H. N. (2008). Foreword. *In*: Ponzoni and Nguyen (eds.), Proceedings of a workshop on the development of a genetic improvement program for the African catfish, *Clarias gariepinus*. WorldFishcenter conference proceedings number 1889. The WorldFish center, Penang, Malaysia, 130 pages.

Popoola, M. O., Fasakin, E. A. and Awopetu, J. I. (2014). Genetic variability in wild and cultured populations of *Clarias gariepinus* using Random Amplified Polymorphic DNA (RAPD) marker. Accepted for publication in the *Croatian Journal of Fisheries*. Online.

Post, G. (1987). Textbook of fish health. Revised and Expanded edition. T. F. H. Publications, Neptune city New Jersey.

Pringle, R. M. (2005). The origins of the Nile perch in Lake Victoria. Bioscience, 55 (9): 780-787.

Pritchard, J. K. and Rosenberg, N. A. (1999). Use of unlinked genetic markers to detect stratification in association studies. *American Journal of Human Genetics*, 65: 220-228.

Pritchard, J. K., Stephens, M., Donnelly, P. (2000). Inference of population structure using multi-locus genotype data. Genetics, **155**: 945-959.

Quince, C., Abrams, P. A., Shuter, P. J. and Lester, N. P. (2008). Biphasic growth in fish I: Theoretical Foundations. *Journal of Theoretical Biology*, **254**: 197-206.

Rasowo, J., Oyoo, E. O. and Ngugi, C. C. (2007). Effects of formaldehyde, sodium chloride, potassium permanganate, and hydrogen peroxide on hatch rate of African catfish, *Clarias gariepinus* eggs. *Aquaculture*, **269**: 271-277.

Rasowo, J., Auma, E., Ssanyu, G. and Ndunguru, M. (2008). Does African catfish (*Clarias gariepinus*) affect rice in integrated rice-fish culture in Lake Victoria Basin, Kisumu? *African Journal of Environmental Science and Technology*, **2**(**10**): 336-341.

Reynolds, J. D., Dulvy, N. K., Goodwin, N. B.and Hutchings, N. B. (2005). Biology of extinction risk in marine fishes. *Proceedings of the Royal Society B*, **272**: 2337-2344.

Reznick D.N., M. J. Bryant, D. A., Roff, C. K., Ghalambor, and D. E. Ghalambor (2004). Effect of extrinsic mortality on the evolution of senescence in gubbies. *Nature*, **431**: 1095-1099.

Roeder, K., Escobar, M., Kadane, J. B. and Balazs, I. (1998). Measuring heterogeneity in forensic databases using hierarchical Bayes models. *Biometrika*, **85**: 269-287.

Roodt-Wilding, R, Swart, B. L., and Impson, N. D. (2010). Genetically distinct Dutch- domesticated *Clarias gariepinus* used in aquaculture in Southern Africa. *African Journal of Aquatic Science*, **35**: 241-249.

Salzburger, W. and Meyer, A. (2004). The species flocks of East African cichlid fishes: recent advances in molecular phylogenetics and population genetics. *Naturwissenschaften,* **91**: 277-290.

Savolainen, O. and Hedrick, P. (1995). Heterozygosity and fitness: no association in Scots Pine. *Genetics*, **140**: 755-766.

Schwartz, M. K., Luickart, G. and Waples, R. S. (2006). Genetic monitoring as a promising tool for conservation and management. *Trends in Ecology and Evolution*, **22** (1): 25-34.

Scott, T. M. and Koehn, R. K. (1990). The effect of environmental stress on the relationship of heterozygosity to growth rate in the coot clam, *Mulinia lateralis* (Say). *Journal of Experimental Marine Biology and Ecology*, **135**: 109-116.

Senanan, W., Kapuscinski, A. R., Na-Nakorn, U. and Miller, L. M. (2004). Genetic impacts of hybrid Catfish farming (*Clarias macrocephalus*Clarias gariepinus*) on native Catfish populations in Central Thailand. *Aquaculture*, **235**: 167-184.

Sibly, R. M., Grimm V., Martin, B. T., Johnston, A. S. A., Kulakowski, K. Topping C. J., Calow, P., Nabe-Nielsen, Thorbek, P. and DeAngelis, D. L. (2013). Representing the acquisition and use of energy by individuals in agent-based models of animal populations. *Methods in Ecology and Evolution*, **4**: 151-161.

Skelton, P. (1993). <u>A complete guide to the freshwater fishes of Southern Africa.</u> Johannesburg: Southern Book Publishers.

Smith, M. K. and Chesser, R. K. (1981). Rationale for conserving genetic variation of fish gene pools. *Ecological Bulletin*, **34**: 13-26.

Smith, G. A. and de Beer, K. (1988). Managing the marketing of *Clarias gariepinus* in South Africa. *In*: The culture of sharptooth catfish in Southern Africa. T. Hecht, W. Uys and P. J. Britz (editors), South African National Scientific Programmes, Report Number 153, 146 pages, ISBN 0 7988 4498 1. National Programme for Aquaculture, Pretoria, South Africa.

Smith, A. A. and Walker, F. K. (2004). Spawning dynamics of common carp in the River Murray, South Australia, shown by macroscopic and histological staging of gonads. *Journal of Fish Biology*, **64**: 336-354.

Spiegel, M. R. (1991). Theory of statistics applications. McGraw-Hill, Paris, 358 pages.

State Department of Fisheries (2010). Fisheries statistical Bulletin, 2010. Ministry of Fishreis DevelopmentNairobi.

State Department of Fisheries (2011). Fisheries statistical Bulletin, 2011. Ministry of Fisheries Development, Nairobi, 54 pages.

State Department of Fisheries (2012). Fisheries statistical Bulletin, 2012. Ministry of Fisheries Development, Nairobi, 66 pages.

Stearns, C. S. (1976). Life history tactics: a review of the ideas. *The Quarterly Review of Biology*, **51** (1).

Stearns, S.C. and Crandall, R. E. (1984). Plasticity for age and size at sexual maturity: a life history response to unavoidable stress, pages 2-33, In: G. W. Potts and R. J. Wootton (Eds.) Fish reproduction: strategies and tactics. Academic Press, New York, NY.

Souza, U. P., Ferreira, F. C., Braga, M. F. D. S. and Winemiller, K. O. (2015). Feeding, body condition and reproductive investment of *Astyanax intermedius* (Characiformes, Characidae), in relation to rainfall and temperature in a Brazilian Atlantic forest stream. *Ecology of Freshwater fish*, **24**: 123-132.

Su, G. S., Liljedahl, L. E. and Gall, G. A. E. (1996). Effects of inbreeding on growth and reproductive traits in rainbow trout (*O. mykiss*). *Aquaculture*, **142**: 139-148.

Sudarto, H. (2007). Systematic revision and phylogenetic relationships among populations of Clariid species in Southeast Asia. Thesis, University of Indonesia, Depok, West Java, Indonesia.

Sulem, Y. S., Tomedi, E. T., Mounchili, S., Tekeng, S. and Brummet, R. S. (2006). Survival of *Clarias gariepinus* fry in earthen ponds: effects of composts and leaks. *Aquaculture*, **260** (1-4): 139-144.

Tampuboloon, P. A. R. P., Jatmiko I., Hartaty, H., and Bahtiar, A. (2014). Reproductive biology of Skipjack Tuna (*Katsuwonis pelamis*) in Eastern Indian Ocean. Indian Ocean Tuna Commission, WPTT 16-35.

Tamura, K., Dudley, J., Nei, M. and Kumar, S. (2007). MEGA 4: Molecular Evolutionary Genetics Analysis and (MEGA) software version 4.0. *Molecular Biology and Evolution*, **24**: 1596-1599.

Tautz, D. (1989). Hypervariability of simple sequences as a general source of polymorphic DNA markers. *Nucleic acid Research*, **17**: 6463-6471.

Teugels, G. G., Guyomard, R. and Legendre, M. (1992). Enzymatic variation in African Clariid Catfishes. *Journal of Fish Biology*, **40**: 87-96.

Thelen, G. C. and Allendorf, F. W. (2001). Heterozygosity-fitness correlations in rainbow trout: effects of allozyme loci or associative overdominance? *Evolution*, 55: 1180-1187.

Thrower, F. P., Hard, J. J. and Joyce, J. E. (2004). Genetic architecture of growth and early life history transitions in anadromous and derived freshwater populations of steelhead. *Journal of Fish Biology*, **65**: 286-307.

Twiddle, D. and Turner, T. L. (1977). Age, growth and natural mortality rates of some cichlid fishes of Lake Malawi. *Journal of Fish Biology*, **10**: 385-398.

Turyaheebwa, N. (2014). Perception on fishery trends in Lake Victoria. MSc. thesis, Arctic University of Norway, Tomso, Norway. 75 pages.

Udupa, K. S. (1986). Statistical method of estimating the size at first maturity in fishes. ICLARM, Metro Manilla, *Fishbyte*, **4**(2): 8-10.

Uthice, S. and Benzie, A. H. (2003). Gene flow and population history in high dispersal marine invertebrates: mitochondrial DNA of *Holothuria nobilis* (Echinodermata: Holothuroidae) populations from the Indo-Pacific. *Molecular Ecology*, **12**: 2635-2648.

Van der Bank, F. H., Grobler, J. P. and Du Preez, H. H. (1992). A comparative biochemical genetic study of three populations of domesticated and wild African Catfish, *Clarias gariepinus*. *Comparative Biochemistry and Physiology*, **101**B: 387-390.

Van der Waal, B. C. W. (1978). Some and production experiments with *Clarias gariepinus* in the Transvaal. *South African Journal of Wildlife Research*, **8**: 13-18.

Van Der Walt, L. D., Van Der Bank, F. H. and Steyn, G. J. (1993). The suitability of using cryopreservation of spermatozoa for the conservation of genetic diversity in African catfish, *Clarias gariepinus*. *Comparative Biochemistry and Physiology*, **106** (2): 313-318.

Vehvilainen, H., Kause, A., Kuuka-Antilla, H., Koskinen, H. and Paananen, T. (2012). Untangling the positive genetic correlation between rainbow trout growth and survival. *Evolutionary Applications*, **5**: 732-745.

Verschuren, D., Laird, K. R. and Cumming, B. F. (2000). Rainfall and drought in equatorial East Africa during the past 1,100 years. *Nature*, **403**: 410-413.

Vila-Gispert, A and Moreno-Avich, R. (2002). Life history patterns of 25 species in European freshwater fish communities. *Environmental Biology of Fishes*, **65**: 387-400.

Vrtilek, M. and Reichard, M. (2016). Female fecundity traits in wild populations of African annual fish: the role of the aridity gradient. *Ecology and Evolution*, **6** (16): 5921-5931.

Wachirachaikarn, A., Rungsin, W., Srisapoome, P. and Na-Nakorn, U. (2009). Crossing of African Catfish, *Clarias gariepinus* (Burchell, 1822), strains based on strain selection using genetic diversity data. *Aquaculture* **290**: 53-60.

Wallace, W. J. and Aarsjord P. (1984). An investigation of the consequences of the egg size for the culture of Arctic charr, *Salvelinus alpines*. *Journal of Fish Biology*, **24**: 427- 435.

Wang, S., Hard, J. J. and Utter, F. (2002). Salmonid inbreeding: a review. *Reviews in Fish Biology and Fisheries*, **11**: 301-319.

Withler, R. E., Nelson, R. J., Miller, K. M. and Beacham, T. D. (2000). Intact genetic structure and high levels of genetic diversity in bottlenecked sockeye salmon (*Onchorynchus nerka*) populations of the Fraser River, British Columbia, Canada. *Canadian Journal of Fisheries and Aquatic Sciences*, **57**: 1985-1998.

Wootton, R. T. (1998). Ecology of teleost fishes. Second edition. Kluwer Academic Publishers, London, 386 pages.

Wright, S. (1965). The interpretation of population structure by F-statistics with special regard to systems of mating. *Evolution*, **19**: 395-420.

Wright, S. (1978). Evolution and the Genetics of Populations. Vol. 4. Variability within and among Natural Populations. University of Chicago Press, Chicago.

Wudneh, T. (1998). Biology and management of fish stocks in Bahir Dar Gulf, Lake Tana, Ethiopia. Ph.D thesis, Wageningen Agricultural University, The Netherlands, 150 pages.

Yalcin, S., Solak, K. and Akyut, I. (2001). Certain reproductive characteristics of the catfish (*Clarias gariepinus* Burchell, 1822) living in the Asi River, Turkey. *Turkish Journal of Zoology*, **25**: 453-460.

Yue, G. H., Kovacs, B. and Orban, L. (2003). Microsatellites from *Clarias batrachus* and their polymorphism in seven additional catfish species. *Molecular Ecology Notes*, **3**: 465- 468.

Zouros, E. (1987). On the relationship between heterozygosity and heterosis: an evaluation of the evidence from marine mollusks. *Isozymes*, **15**: 255-270.

APPENDICES

Appendix I: Concentration of genomic DNA at 50 ng/μl, volume of DNA and water required to dilute the DNA to 20 ng/ μl and concentration of DNA in purified PCR products of Lake Victoria (LVG) population of *C. gariepinus*

Sample	Genomic DNA (ng/μl)	Volume of gDNA (μl) for dilution to 20 ng/μl	Volume of water (μl)	DNA concentration (ng/μl) of purified PCR products
LVG1	1594.1	0.6	49.4	29
LVG2	853.6	1.2	48.8	12.6
LVG3	157.9	6.3	43.7	14.7
LVG4	234.6	4.3	45.7	28.2
LVG5	1250.8	0.8	49.2	23.6
LVG6	276.3	3.6	46.4	40.3
LVG7	106.9	9.4	40.6	55.8
LVG8	365.3	2.7	47.3	42.9
LVG9	236.8	4.2	45.8	12.6
LVG10	201.2	5.0	45.0	19.6
LVG11	104.1	9.6	40.4	35.5
LVG12	193.4	5.2	44.8	22.2
LVG13	453.7	2.2	47.8	48.9
LVG14	257.4	3.9	46.1	19.3
LVG15	167.8	6.0	44.0	45.8
LVG16	744.1	1.3	48.7	31.1
LVG17	278	3.6	46.4	24.8
LVG18	175.7	5.7	44.3	36.6
LVG19	246	4.1	45.9	23.8
LVG20	233.7	4.3	45.7	38.2
LVG21	78.5	13.0	37.0	1.6
LVG22	190.4	5.3	44.7	27.2
LVG23	196.4	5.1	44.9	27.2
LVG24	99.1	10.0	40.0	22.9
LVG25	83.6	12.0	38.0	25.4

Appendix II: Concentration of genomic DNA at 50 ng/µl, volume of DNA and water required to dilute the DNA to 20 ng/ µl and concentration of DNA in purified PCR products of Lake Turkana (LTA) population of *C. gariepinus.*

Sample	Genomic DNA (ng/µl)	Volume of gDNA (µl) for dilution to 20 ng/µl	Volume of water (µl)	DNA concentration (ng/µl) of purified PCR products
LTA1	160.5	6.2	43.8	49
LTA2	213.7	4.7	45.3	26.9
LTA3	250.5	4.0	46.0	38.6
LTA4	181.7	5.5	44.5	46.3
LTA5	173.2	5.8	44.2	77
LTA6	282	3.5	46.5	73.8
LTA7	1187.9	0.8	49.2	33.4
LTA8	229.8	4.4	45.6	39.6
LTA9	156.1	6.4	43.6	27.4
LTA10	545.1	1.8	48.2	103.8
LTA11	152.4	6.6	43.4	62.1
LTA12	54.6	18	32	43
LTA13	765.4	1.3	48.7	53.9
LTA14	346	2.9	47.1	31.2
LTA15	756	1.3	48.7	24.9
LTA16	178	5.6	44.4	26.9
LTA17	205.8	4.9	45.1	61.4
LTA18	337.2	3.0	47.0	23
LTA19	301.4	3.3	46.7	50.3
LTA20	644.7	1.6	48.4	26.5
LTA21	510.7	2.0	48.0	16.7
LTA22	865.2	1.2	48.8	16
LTA23	189	5.3	44.7	26.2
LTA24	1617	0.6	49.4	39.8
LTA25	409.5	2.4	47.6	17.6
LTA26	1055.2	0.9	49.1	62.7
LTA27	510.9	2.0	48.0	60.5
LTA28	302.1	3.3	46.7	16.3

Appendix III: Concentration of genomic DNA at 50 ng/µl, volume of DNA and distilled water required to dilute the DNA to 20 ng/ µl and concentration of DNA in purified PCR products of Lake Baringo (LBA) population of *C. gariepinus*.

Sample	Genomic DNA (ng/µl)	Volume of DNA used to dilute genomic DNA to 20 ng/µl	Volume of water (µl)	DNA Concentration of purified PCR products (ng/µl)
LBA 1	812.1	1.2	48.8	32.9
LBA 2	442.8	2.3	47.7	67.1
LBA 3	170.5	5.9	44.1	30.8
LBA 4	1044.2	1.0	49.0	51.2
LBA 5	878	1.1	48.9	37.5
LBA 6	1123	0.9	49.1	44.2
LBA 7	802.1	1.2	48.8	55.2
LBA 8	2795	0.4	49.6	54.7
LBA 9	159.3	6.3	43.7	27.3
LBA 10	349.2	2.9	47.1	29.3
LBA 11	712.7	1.4	48.6	69.6
LBA 12	687.7	1.5	48.5	108.6
LBA 13	242.1	4.1	45.9	70.2
LBA 14	73.3	13.6	36.4	89.3
LBA 15	285.7	3.5	46.5	24.3
LBA 16	89.4	11.2	38.8	24
LBA 17	194.4	5.1	44.9	32.8
LBA 18	350.5	2.9	47.1	25.1
LBA 19	297.4	3.4	46.6	11.1
LBA 20	426.6	2.3	47.7	22.7
LBA 21	250.1	4	46.0	10.2
LBA 22	160.7	6.2	43.8	6
LBA 23	228.5	4.4	45.6	19.7
LBA 24	30.9	32.4	17.6	29
LBA 25	809.1	1.2	48.8	26.4

Appendix IV: Concentration of genomic DNA at 50 ng/µl, volume of DNA and distilled water required to dilute the DNA to 20 ng/ µl and concentration of DNA in purified PCR products of Lake Kanyaboli (LKG) population of *C. gariepinus*.

Sample	Genomic DNA (ng/µl)	Volume of gDNA (µl) for dilution to 20 ng/µl	Volume of water (µl)	DNA Concentration (ng/µl)
LKG1	399.3	2.5	47.5	43.1
LKG2	135.6	7.4	42.6	43.7
LKG3	573.8	1.7	48.3	92.8
LKG4	725.5	1.4	48.6	107
LKG5	17.5	57.1	42.9	93.3
LKG6	385	2.6	47.4	143.5
LKG7	366.1	2.7	47.3	122.6
LKG8	515.7	1.9	48.1	3.7
LKG9	170.9	5.9	44.1	0.7
LKG10	466.3	2.1	47.9	95.7
LKG11	513.1	1.9	48.1	128
LKG12	533.6	1.9	48.1	10.8
LKG13	327.1	3.1	46.9	112.5
LKG14	269.3	3.7	46.3	1
LKG15	1216.5	0.8	49.2	0.1
LKG16	348.4	2.9	47.1	3.1
LKG17	552.6	1.8	48.2	76.6
LKG18	641.2	1.6	48.4	8.7
LKG19	105.9	9.4	40.6	9.8
LKG20	132.3	7.6	42.4	4.8
LKG21	65	15.4	34.6	8.2
LKG22	160.9	6.2	43.8	2.6
LKG23	367	2.7	47.3	16
LKG24	125.8	7.9	42.1	6.5
LKG25	111.1	9.0	41.0	25.3
LKG26	138.4	7.2	42.8	16.9
LKG27	87.2	11.5	38.5	22.3
LKG28	107.2	9.3	40.7	7
LKG29	215.7	4.6	45.4	5.4
LKG30	90.2	11.1	38.9	9.3

Appendix V: Concentration of genomic DNA at 50 ng/µl, volume of DNA and distilled water required to dilute the DNA to 20 ng/ µl of final volume 50 µl, and the concentration of DNA in purified PCR products of Lake Jipe (LJP) population of *C. gariepinus*.

Sample	Genomic DNA (ng/µl)	Volume of gDNA (µl) for dilution to 20 ng/µl	Volume of water (µl)	DNA Concentration of purified PCR products (ng/µl)
LJP1	450.1	2.2	47.8	106.8
LJP2	379	2.6	47.4	104.8
LJP3	758.2	1.3	48.7	78.7
LJP4	607.6	1.6	48.4	80.1
LJP5	622	1.6	48.4	46.7
LJP6	375.8	2.7	47.3	77.1
LJP7	300.1	3.3	46.7	84.5
LJP8	381	2.6	47.4	59.5
LJP9	282.4	3.5	46.5	74.2
LJP10	298.1	3.4	46.6	90.1
LJP11	413.2	2.4	47.6	90.7
LJP12	401.3	2.5	47.5	84.2
LJP13	168.4	5.9	44.1	33.8
LJP14	685	1.5	48.5	73.7
LJP15	320.9	3.1	46.9	63.8
LJP16	246.9	4.1	45.9	47.9
LJP17	222.1	4.5	45.5	60.2
LJP18	577.6	1.7	48.3	58.6
LJP19	54	18.5	32.5	74.6
LJP20	145.2	6.9	43.1	34.3
LJP21	192.2	5.2	44.8	57.3
LJP22	221.3	4.5	45.5	57.7
LJP23	443.7	2.3	47.7	68
LJP24	253.4	4.0	46.0	48.3
LJP25	572.2	1.7	48.3	69.5
LJP26	415.5	2.4	47.6	60.5
LJP27	165.3	6.0	44.0	62.8
LJP28	233.3	4.3	45.7	60.2
LJP29	608.1	1.6	48.4	73.8
LJP30	323	3.1	46.9	61.5
LJP31	192.6	5.2	44.8	88.6
LJP32	646.4	1.5	48.5	91.3
LJP33	236.7	4.2	45.8	110
LJP34	546.5	1.8	48.2	61
LJP35	291.3	3.4	46.6	86.7

Appendix VI: Concentration of genomic DNA at 50 ng/µl, volume of DNA and distilled water required to dilute the DNA to 20 ng/ µl of final volume 50 µl, and the concentration of DNA in purified PCR products of Sagana Aquaculture Centre (SAG) population of *C. gariepinus*

Sample	Genomic DNA (ng/µl)	Volume of gDNA (µl) for dilution to 20 ng/µl	Volume of water (µl)	DNA concentration (ng/µl)
SAG1	172.8	5.8	44.2	33.2
SAG2	143.3	7.0	43.0	25.1
SAG3	142.6	7.0	43.0	85.1
SAG4	260.2	3.8	46.2	6.2
SAG5	191	5.2	44.8	3.7
SAG6	151.7	6.6	43.4	1.4
SAG7	171.4	5.8	44.2	0.1
SAG8	302.8	3.3	46.7	4.8
SAG9	110	9.1	40.9	11.6
SAG10	289.8	3.5	46.5	5.4
SAG11	86.1	11.6	38.4	4.6
SAG12	603.9	1.7	48.3	24.9
SAG13	236.7	4.2	45.8	16.2
SAG14	86	11.6	38.4	10.3
SAG15	832.9	1.2	48.8	6.7
SAG16	122.7	8.1	41.9	15.6
SAG17	244.2	4.1	45.9	10.8
SAG18	321.8	3.1	46.9	3.4
SAG19	448.9	2.2	48.8	11.7
SAG20	103.8	9.6	40.4	1.2
SAG21	748.6	1.3	48.7	70.8
SAG22	181.2	5.5	44.5	24.7
SAG23	264.2	3.8	46.2	85.7
SAG24	238.1	4.2	45.8	0.1
SAG25	131.8	7.6	42.4	37.3
SAG26	117.9	8.5	41.5	2.8
SAG27	96.9	10.3	39.7	22.6
SAG28	200.7	5.0	45.0	14.8
SAG29	208.1	4.8	45.2	3.2
SAG30	102.8	9.7	40.3	10.8

Appendix VII: Concentration of genomic DNA at 50 ng/μl, volume of DNA and distilled water required to dilute the DNA to 20 ng/ μl of final volume 50 μl, and the concentration of DNA in purified PCR products of University of Eldoret (UoE) population of *C. gariepinus*.

Sample	Genomic DNA (ng/μl)	Volume of gDNA (μl) for dilution to 20 ng/μl	Volume of water (μl)	DNA Concentration (ng/μl)
UoE1	632.8	0.9	49.1	61.5
UoE2	501.8	1.3	48.7	46.1
UoE3	213.2	1.3	48.7	42.7
UoE4	685.6	0.8	49.2	61
UoE5	772.1	0.8	49.2	59.4
UoE6	370.7	0.8	49.2	48.2
UoE7	231.6	1.3	48.7	40.1
UoE8	268.1	1.0	49	55.8
UoE9	269.6	1.9	48.1	43.2
UoE10	1087.3	0.9	49.1	71.5
UoE11	1075.8	0.9	49.1	40.5
UoE12	508.2	2.0	48	51.3
UoE13	659.9	1.5	48.5	52.2
UoE14	1016.9	1.0	49	62.3
UoE15	889.9	1.1	48.9	64.8
UoE16	1087	0.9	49.1	59.4
UoE17	1373.7	0.7	49.3	38.1
UoE18	700.5	1.4	48.6	38.8
UoE19	1963.7	0.5	49.5	52.8
UoE20	422.2	2.4	47.6	12.6
UoE21	1234.7	0.8	49.2	35.2
UoE22	1097	0.9	49.1	18.1
UoE23	928.7	1.1	48.9	49.5
UoE24	901	1.1	48.9	49.7
UoE25	919	1.1	48.9	24.6
UoE26	458.2			70.2
UoE27	459			52.6
UoE28	366.9			29.6
UoE29	220.7			11.1
UoE30	189.6			17.2

Appendix VIII: Number and distribution of haplotypes in samples of *Clarias gariepinus* collected from 10 different sites in Kenya, inferred from sequences of mtDNA D-loop control region.

SITE	HAPLOTYPES	TOTAL NUMBER OF HAPLOTYPES	NUMBER OF SHARED HAPLOTYPES	NUMBER OF PRIVATE HAPLOTYPE
Lake Victoria (LVG)	Hap_2, 4, 5, 8, 9, 14, 44, 45, 46, 47, 48, 49 and 50.	13	6	7 (Hap_44, 45, 46, 47, 48, 49, and 50).
Lake Turkana (LTA)	Hap_36, 37, 38, 39, 40, 41, 42, and 43.	8	4	4 (Hap_37, 41, 42 and 43).
Lake Baringo (LBA)	Hap_10, 11, 12, 13, 14, 15, 16 and 17	8	5	3 (Hap_13, 16 and 17).
Lake Jipe (LJP)	Hap_18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29.	12	2	10 (Hap_18, 20, 21, 23, 24, 25, 26, 27, 28, 29)
Lake Kanyaboli (LKG)	Hap_2, 3, 28, 29, 30, 31, 32, 33, 34, 35	10	5	5 (Hap_29, 30, 31, 34, and 35).
Sangoro Aquaculture Center (SAN)	Hap_2, 4, 5, 8, 14, 61, 62, 63, and 64.	10	7	3 (Hap_62, 63, and 64).
Sagana Aquaculture Center (SAG)	Hap_2, 4, 5, 9, 51, 52, 53, 54, 55, 56, 57, 58, 59, and 60.	14	7	7 (Hap_51, 52, 54, 55, 56, 57 and 60).
Wakhungu Fish Farm (WKU)	Hap_1, 2, 3, 4, 8 and 68.	6	5	1 (Hap_68)
University of Eldoret Fish Farm (UoE)	Hap_2, 5, 6, 14, 65, 66, 67	7	6	1 (Hap_66)
Kibos Fish Farm (KIB)	Hap_1, 2, 3, 4, 5, 6, 7, 8, and 9	9	7	2 (Hap_7 and 9)

Appendix IX: Values of allelic diversity and heterozygosity at 6 microsatellite loci used to genotype samples of *Clarias gariepinus* from 8 different sites in Kenya.

Population	Cga1				Cga3				Cga9				Cga10			
	N	Allele	H_O	H_E	N	Allele	H_O	H_E	N	Allele	H_O	H_E	N	Allele	H_O	H_E
LVG	23	5	0.79	0.78	23	10	0.81	0.87	23	4	0.78	0.66	23	10	0.72	0.75
LKG	20	7	0.44	0.67	20	9	0.6	0.88	20	7	0.45	0.64	20	4	1	0.70
LTA	20	5	0.5	0.73	20	8	0.67	0.83	20	5	0.56	0.63	20	9	0.85	0.89
LBA	18	3	0.41	0.57	18	4	0.39	0.56	18	3	0.4	0.43	18	5	0.5	0.66
SAN	20	8	0.68	0.79	20	10	0.75	0.88	20	7	0.55	0.65	20	12	0.9	0.9
SAG	20	4	0.32	0.67	20	8	0.59	0.78	20	6	0.25	0.72	20	9	0.6	0.79
UoE	20	8	0.75	0.7	20	6	0.8	0.83	20	6	0.47	0.72	20	10	0.9	0.89
KIB	20	8	0.44	0.70	20	10	0.70	0.82	20	6	0.37	0.82	20	8	0.88	0.88

Population	Cba2				Cba19			
	N	Allele	H_O	H_E	N	Allele	H_O	H_E
LVG	23	6	1	1	23	13	0.85	0.93
LKG	20	14	0.90	0.92	20	8	0.95	0.80
LTA	20	12	1	0.93	20	9	0.88	0.87
LBA	18	-	-	-	18	4	0.63	0.67
SAN	20	-			20	7	0.89	0.85
SAG	20	12	0.95	0.91	20	7	0.56	0.67
UoE	20	12	0.9	0.92	20	11	0.6	0.87
KIB	20	13	0.92	0.93	20	13	0.90	0.93

Appendix X: Single locus statistics for samples of *Clarias gariepinus* from 8 different sites in Kenya genotyped with 6 microsatellite loci. N is sample size, Na is the mean number of alleles, H_E is expected heterozygosity, H_o is observed heterozygosity.

Locus	Parameter	LVG	LKG	LTA	LBA	SAN	SAG	UoE	KIB
Cga1	N	23	20	20	18	20	20	20	20
	Na	5	7	5	3	8	4	8	8
	He	0.7802	0.7254	0.7250	0.5686	0.7909	0.6699	0.7000	0.6955
	Ho	0.5714	0.4444	0.5000	0.4117	0.6842	0.3157	0.7500	0.4375
	P(HW)	0.266	0.001	0.050	0.037	0.180	0.0003	0.7655	0.0079
Cga3	N	23	20	20	18	20	20	20	20
	Na	10	9	8	4	10	8	6	10
	He	0.8729	0.8756	0.8254	0.5619	0.8833	0.7789	0.8256	0.8205
	Ho	0.8125	0.6000	0.6666	0.3888	0.7500	0.5882	0.8000	0.7000
	P(HW)	0.041	0.002	0.082	0.148	0.012	0.0254	0.857	0.3741
Cga9	N	23	20	20	18	20	20	20	20
	Na	4	7	5	3	7	6	6	6
	He	0.6601	0.6397	0.7124	0.4321	0.6448	0.7231	0.7240	0.8208
	Ho	0.7777	0.4500	0.5555	0.4000	0.5500	0.2500	0.4736	0.3684
	P(HW)	0.398	0.001	0.030	0.052	0.087	0.0002	0.0011	0.000
Cga10	N	23	20	20	18	20	20	20	20
	Na	10	4	9	5	13	9	10	8
	He	0.7809	1.000	0.8862	0.6619	0.9000	0.7923	0.8859	0.8841
	Ho	0.6666	1.000	0.8461	0.5000	0.9000	0.6000	0.9000	0.8823
	P(HW)	0.045	1.000	0.064	0.285	0.0130	0.0033	0.5453	0.627
Cba2	N	23	20	20	18	20	20	20	20
	Na	6	14	12	0	17	12	12	13
	He	1.000	0.9189	0.9307	0.000	0.9388	0.9132	0.9218	0.9275
	Ho	1.000	0.8947	1.000	-	1.0000	0.9473	0.9000	0.9167
	P(HW)	1.000	0.435	0.787	-	0.7318	0.5715	0.7682	0.1310
Cba19	N	23	20	20	18	20	20	20	20
	Na	13	8	9	4	10	7	11	13
	He	0.9262	0.7923	0.8681	0.6633	0.8524	0.8667	0.8667	0.9331
	Ho	0.8461	0.8947	0.8823	0.5000	0.8888	0.5789	0.6000	0.8947
	P(HW)	0.002	0.414	0.674	0.292	0.262	0.3316	0.0187	0.2757

Appendix XI: Gel electrophoresis of genomic DNA for *Clarias gariepinus* **of the Lake Victoria (LVG) population. The genomic DNA was electrophoresed in 0.8% agarose gel at 100 W for 35 minutes.**
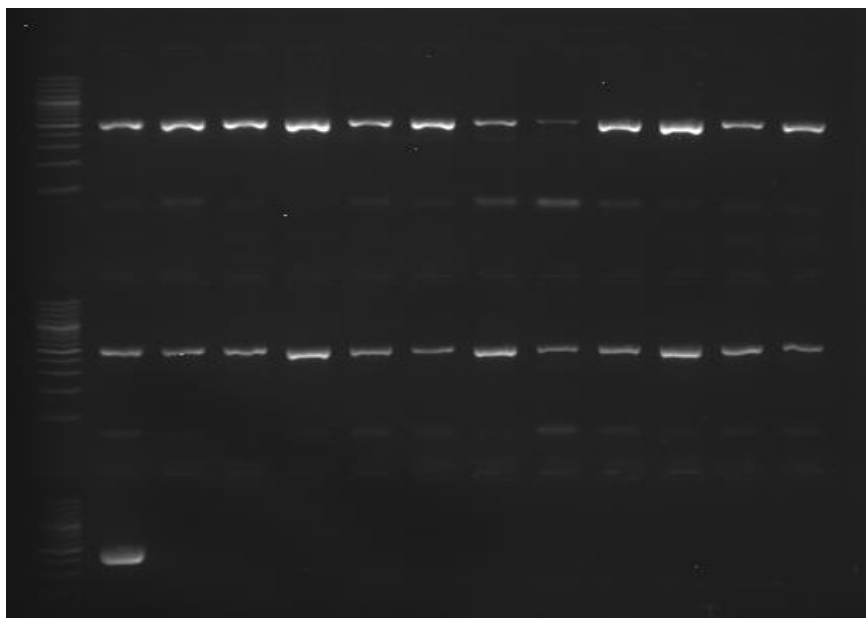
Appendix XII: Gel electrophoresis of purified PCR products for *Clarias gariepinus* from Sangoro Fish Farm (SAN), Kenya. The products were electrophoresed in 2% agarose gel at 100 W for 35 minutes. The size of the products, as determined by the DNA ladder (L) is 500 b
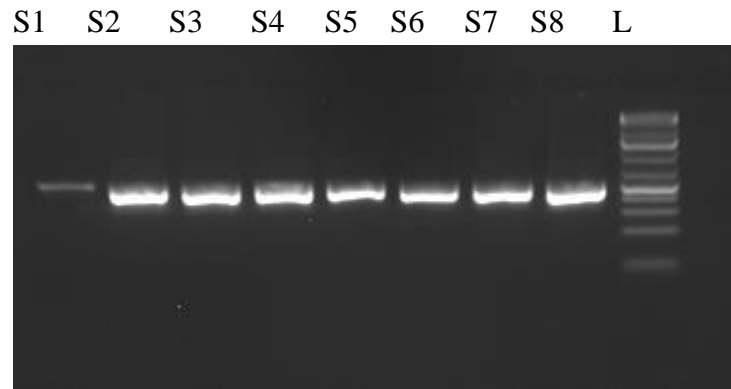
Appendix XIII: The length, weight, sex of fish, gonadal maturity stage, weight of gonads, gonado-somatic index (GSI), number of eggs per gram of eggs, and fecundity of fish samples of LVG population in September 2016.

S N	Length (Cm)	Weight (g)	Sex	Maturity st	Gonad Wt (g)	GSI (%)	Eggs/g	Fecundity
1	67	1872	F	5	46.23	2.47		
2	58	1668	F	3	6.85	0.411		
3	73	1205	M	5	2.95	0.245		
4	85	4561	F	5	193.76	4.248	192.2*1164	223,721
5	25.5	99.75	M	2	0.1	0.1		
6	28	123.93	M	2	0.11	0.089		
7	24	84.71	M	2	0.04	0.047		
8	21	51.82	M	1	0.06	0.116		
9	30	163.68	M	1	0.01	0.006		
10	41	329.6	M	3	0.09	0.027		
11	28	162.49	F	1	0.14	0.086		
12	24	72	F	2	0.08	0.111		
13	23.5	54	M	1	0.06	0.111		
14	23	61	M	1	0.07	0.115		
15	22.5	55.5	M	1	0.08	0.144		
16	31	204.78	F	1	0.12	0.059		
17	107	3,762	M	5	38.17	1.015		
18	63	1,015	F	5	53.93	5.313		
19	67	1,230	M	5	2.52	0.205		
20	38	228	M	2	0.06	0.026		
21	72	1,119	M	4	0.94	0.084		
22	78	1,220	M	5	4.73	0.388		
23	61	791	M	5	2.17	0.274		
24	40	426	F	2	0.53	0.124		
25	86	4,307	M	5	2.35	0.055		
26	29	173	F	1	0.17	0.098		
27	29	181	F	1	0.23	0.127		
28	48	346	F	2	0.76	0.22		
29	35	254	F	2	0.56	0.221		
30	32	224	F	2	0.5	0.224		
31	31	212	M	1	0.08	0.038		
32	31	198	F	1	0.09	0.045		
33	68	1,308	F	5	28.36	2.168	27*984	26,568
34	52.5	755	F	3	3.49	0.462		
35	53	1,054.60	F	6	62.64	5.94	Spend	
36	58	1,157.70	M	4	1.84	0.159		
37	56	831	M	5	1.8	0.217		
38	69	2,228	F	5	133.04	5.971	131.5*725	95,338
39	53	1,157	F	2	4.51	0.39		
40	32	231	F	1	0.32	0.14		
41	28	177	F	1	0.17	0.1		
42	68	2,145	F	5	159	7.413	158*710	112180
43	38	398	M	1	0.06	0.02		

44	54	921	F	3	3.16	0.34		
45	60	1,521	F	4	3.72	0.24		
46	72	2,748	F	5	178.12	6.482	177*836	147,972
47	64	1,980	F	5	128.85	6.508	126*1010	127,260
48	44	609	F	2	0.69	0.11		
49	74	1,885	F	5	298.6	15.84	298*856	255,088
50	84	2,960	M	5	6.61	0.22		
51	45	465	M	2	0.21	0.045		
52	39	379	F	3	0.95	0.251		
53	48	535	F	3	0.78	0.146		
54	32	196	M	1	0.06	0.031		
55	72	2,549	M	4	4.83	0.189		
56	76	2,671	M	5	6.04	0.226		
57	59	674	F	3	2.68	0.398		
58	61	704	M	4	4.85	0.689		
59	43	580	F	3	2.83	0.488		
60	28	156	M	2	0.3	0.192		
61	71	2,370	M	5	5.83	0.246		
62	29	167	F	1	0.09	0.054		
63	31	197	M	2	0.02	0.01		
64	27	137	F	2	0.23	0.168		
65	42	601	F	2	1.01	0.168		
66	31	262	F	2	0.26	0.099		
67	34	273	M	1	0.02	0.007		
68	40	459	M	3	0.87	0.19		
69	60	688	F	4	10.3	1.497		
70	28	178	F	2	0.47	0.264		
71	33	275	F	2	0.75	0.273		
72	65	1,719	M	4	0.76	0.044		
73	54	921	F	3	3.16	0.343		
74	60	2,351	F	4	8.95	0.381		
75	75	2,705	F	4	7.09	0.262		
76	34	370	M	2	0.12	0.032		
77	55	964	M	4	4.86	0.504		
78	50	720	F	3	3.02	0.419		
79	47	667	M	4	4.7	0.705		
80	39	443	M	2	0.48	0.108		
81	34	291	F	2	0.16	0.055		
82	27	105	F	1	0.09	0.086		
83	61	2,389	F	5	178.4	7.468	177*1086	192,222
84	68	2,763	M	5	5.7	0.206		
85	30	206	F	1	0.06	0.029		
86	31	217	M	1	0.12	0.055		
87	28	167	F	1	0.08	0.048		
88	57	1,260	M	4	4.3	0.341		
89	47	660	F	3	6.2	0.939		
90	42	468	F	2	0.18	0.038		
91	54	902	M	3	2.7	0.299		
92	50	784	M	4	3.86	0.492		
93	61	1,983	M	5	5.8	0.292		
94	31	180	F	1	0.08	0.044		

95	30	170	M	1	0.05	0.029		
96	45	609	M	3	0.98	0.161		
97	40	580	M	2	0.43	0.074		
98	34	317	F	2	0.1	0.032		
99	43	480	M	2	0.25	0.052		
100	67	2,086	M	4	3.08	0.148		
101	28	115	M	1	0.08	0.07		
102	59	1,064	F	4	6.8	0.639		
103	30	185	M	1	0.09	0.049		

Appendix XIV: The length, weight, sex of fish, gonadal maturity stage, weight of gonads, gonado-somatic index (GSI), number of eggs per gram of eggs, and fecundity of fish samples of LVG population in October 2016.

SN	Length (cm)	Weight (g)	Sex	Maturity Stage	Gonad weight (g)	GSI	Eggs/g	Fecundity
1	60	1418	M	5	3.45	0.243		
2	33	278	F	2	0.28	0.101		
3	79	2937	M	5	5.36	0.182		
4	65	1859	F	5	183.54	9.873	181*1172	212,132
5	43	458.4	F	2	0.48	0.105		
6	52	821	M	3	3.21	0.391		
7	58	1221	F	4	49.05	4.017		
8	55	1159	M	4	1.21	0.104		
9	50	746	F	2	1.3	0.174		
10	46	498.3	F	2	1.05	0.211		
11	39	390	M	2	1.06	0.272		
12	56.5	1455	F	4	2.04	0.14		
13	49	746	F	2	1.99	0.267		
14	55.5	887	M	5	3.82	0.431		
15	47.5	706	M	2	0.44	0.062		
16	49	715	M	2	0.56	0.078		
17	52	884.6	M	3	0.68	0.077		
18	47	881	F	2	2.11	0.24		
19	50	902	M	3	0.94	0.104		
20	62	1285	F	5	66.18	5.15	64*884	56,576
21	41	587	M	2	0.23	0.039		
22	36	368	M	1	0.18	0.049		
23	47	598	M	2	0.21	0.035		
24	41	420	F	2	0.81	0.193		
25	77	2290	M	5	6.59	0.288		
26	92	3201	M	5	7.74	0.242		
27	75	2098	M	5	5.02	0.239		
28	76	2220	M	5	7.53	0.339		
29	75	2162	M	4	3.67	0.17		
30	62	1796	M	4	1.3	0.072		
31	56	912	M	3	0.26	0.029		
32	24	98	M	1	0.02	0.02		
33	30	195	M	1	0.06	0.031		
34	65	2016	F	5	145.85	7.235	143*976	139,568
35	59	1482	F	4	4.78	0.323		
36	81	4112	M	4	4.43	0.108		
37	73	2659	M	5	2.63	0.099		
38	68	2128	F	5	152.45	7.164	151*814	122,914
39	43	456	M	2	0.21	0.046		
40	71	2378.2	F	5	190.45	8.008	188*1182	222,216
41	59	1094.7	M	2	0.79	0.072		

42	46	675	F	2	1.26	0.187		
43	42	527	F	2	0.82	0.156		
44	58	1214	F	2	1.75	0.144		
45	60	1138	M	5	4.88	0.429		
46	44	560	M	2	0.13	0.023		
47	39	536	M	4	0.58	0.108		
48	43	541	M	2	0.05	0.009		
49	57	1273	F	2	3.25	0.255		
50	32	310	F	1	0.19	0.061		
51	28	176	M	1	0.08	0.045		
52	38.5	370	F	2	0.73	0.197		
53	37.6	368	M	4	1.56	0.424		
54	56	1018.2	F	2	2.48	0.244		
55	35.4	308.6	F	1	0.35	0.113		
56	32	238	M	1	0.01	0.004		
57	29	172	M	1	0.04	0.023		
58	40	498	M	3	0.36	0.072		
59	37	354	F	2	0.52	0.147		
60	28	155	F	1	0.72	0.465		
61	65	1859	F	5	182.54	9.819	180*1062	191,160
62	44	568.4	M	2	0.31	0.055		
63	67	1987.3	F	3	5.06	0.255		
64	74	2722	F	5	227.29	8.35	225*1042	234,450
65	30	201	M	1	0.08	0.04		
66	61	1334	F	5	76.5	5.735	74*990	73,260
67	66	2251	F	5	156.4	6.948	154.2*1008	155,433
68	61	1347	F	3	5.4	0.401		
69	36	384	F	2	0.24	0.063		
70	35	320	F	2	0.32	0.1		
71	26.5	153	M	2	0.02	0.013		
72	31	227	F	2	0.64	0.282		
73	45	733	M	3	0.25	0.034		
74	57	1089	F	2	2.47	0.227		
75	40	478	F	2	0.81	0.169		
76	37	287	F	2	0.49	0.171		
77	32.5	238	F	1	0.35	0.147		
78	29	184	M	1	0.03	0.016		
79	48	571.4	M	2	0.27	0.047		
80	34.5	278	F	1	0.34	0.122		
81	33.6	231.7	M	1	0.04	0.017		
82	39	418	F	2	0.36	0.086		
83	33	258	M	3	0.28	0.109		
84	41	560	F	2	0.49	0.088		
85	42	580	F	3	0.87	0.15		
86	34	302	M	1	0.14	0.046		
87	33	227	M	2	0.1	0.044		
88	33	271	M	1	0.09	0.033		
89	30	185	F	1	0.18	0.097		

90	45	640	F		2	0.51	0.08		
91	63	1160	M		5	3.41	0.294		
92	47.5	710	M		5	1.14	0.161		
93	74	2320	F		5	218.4	9.414	216*1074	231,984
94	72	2384	F		5	99.23	4.162		
95	46	758	F		3	1.95	0.257		
96	60	1139	F		5	121.75	10.69	119*1025	121,975
97	72	2267	M		5	4.51	0.199		
98	77	2564	F		5	278.36	10.86	276.2*1104	304,925
99	70	2240	F		5	119.76	5.346	118*1122	132,396
100	56	1486.7	M		3	0.34	0.023		
101	29	188	M		1	0.05	0.027		
102	30	198	F		2	0.08	0.04		
103	61	1910	F		4	3.79	0.198		
104	79	2862	F		4	11.53	0.403		
105	48	1100	M		3	0.25	0.023		
106	36	295.4	F		2	0.35	0.118		
107	50	1025	M		3	0.28	0.027		
108	28	168	M		1	0.06	0.036		
109	30	178	M		1	0.07	0.039		
110	32	201	F		1	0.1	0.05		
111	35	310	F		2	0.23	0.074		
112	39	395	F		2	0.54	0.137		
113	43	619	M		2	0.26	0.042		
114	73	2,535	F		5	138.43	5.461	137*1086	148,782
115	71	2,340	F		5	122.71	5.244	121*1034	125,114

Appendix XV: The length, weight, sex of fish, gonadal maturity stage, weight of gonads, gonado-somatic index (GSI), number of eggs per gram of eggs, and fecundity of fish samples of LVG population in November 2016.

SN	Length (cm)	Weight (g)	Sex	Maturity Stage	Gonad Wt (g)	GSI (%)	Eggs/g	Fecundity
1	44	415	M	2	0.23	0.055		
2	63	1958	F	5	171.46	8.757	175.5*1235	216,743
3	58.5	1542	F	4	3.2	0.208		
4	56	1438	M	3	2.06	0.143		
5	59	1551	M	4	0.34	0.022		
6	60	1739	F	5	70.82	4.072	70*1089	76,230
7	51	1361	M	4	0.38	0.028		
8	37	302.6	F	2	0.15	0.05		
9	68	2,356.80	F	3	4.29	0.182		
10	43	610	F	2	0.46	0.075		
11	28	168	F	1	0.09	0.054		
12	59	1590	M	4	3.76	0.236		
13	61	1,622	M	3	2.86	0.176		
14	32	210	F	2	0.13	0.062		
15	58	1559.6	M	3	3.2	0.205		
16	64	1905.4	F	5	94.4	4.954	93*894	83,142
17	72	2,648.30	M	3	2.68	0.101		
18	53	1203	F	5	102	8.479	101*1068	107,868
19	44	528	M	5	2.12	0.402		
20	31	209	M	1	0.03	0.014		
21	24	110.5	M	1	0.02	0.018		
22	67	2,450	F	4	3.81	0.156		
23	39	346	M	1	0.1	0.029		
24	63	1440	F	5	289.7	20.12	288*1160	334,080
25	54	1422	M	4	3.14	0.221		
26	28	178.6	F	1	0.08	0.045		
27	58	1784.6	F	2	0.24	0.013		
28	59	1842	M	3	3.41	0.185		
29	60	2,104	M	2	0.34	0.016		
30	44	432	F	5	68.5	15.86	67*706	47,302
31	54	1427	M	4	4.87	0.341		
32	76	2803	F	3	4.05	0.144		
33	68	2,552	M	3	5.6	0.219		
34	28	165	F	1	0.07	0.042		
35	40.5	280	F	5	72.6	25.93	71.6*827	58,882
36	42	324	F	4	3.36	1.037		
37	41	332	F	5	19.91	5.997	19*785	14,915
38	43	426	M	4	3.04	0.714		
39	37	248	F	4	8.81	3.552		
40	43	356	F	5	22.78	6.399	22*986	21,692
41	38	263	F	5	17.28	6.57	16.8*1004	16,867
42	48	462	M	4	1.42	0.307		
43	44	460	F	5	36.18	7.865	35*710	24,850
44	69	2,629	M	4	3.28	0.125		
45	51	1342	F	4	2.08	0.155		
46	55	1437	M	4	1.46	0.102		

47	47	690	F	5	117.2	16.99	116*1104	128,064
48	44	670	M	4	1.04	0.155		
49	46	554	M	4	2.62	0.473		
50	77	2,940	M	4	3.74	0.127		
51	40	399.7	F	2	0.57	0.143		
52	52	1,377	M	3	1.07	0.078		
53	66	2,482.10	F	4	6.63	0.267		
54	29	185.2	M	1	0.04	0.022		
55	46	245	M	3	0.18	0.073		
56	41	410.2	M	2	0.1	0.024		
57	39.5	462.5	F	2	0.68	0.147		
58	66	1834	F	5	70.16	3.826	69.3*1045	72,419
59	55	1200	F	3	3.15	0.263		
60	73	2,690	F	4	7.82	0.291		
61	38	387	M	2	0.17	0.044		
62	59	1249.6	M	5	3.68	0.294		
63	69	2289	F	5	113.87	4.975	112*1129	126,448
64	26	110	M	1	0.05	0.045		
65	33	264.2	F	2	0.18	0.068		
66	27	96.5	M	1	0.07	0.073		
67	71	2,781	M	3	3.65	0.131		
68	54	1123.5	F	2	0.42	0.037		
69	61	1,920	M	4	4.7	0.245		
70	40	330	F	5	28.8	8.727	27*1034	27,918
71	45	327	M	5	2.17	0.664		
72	43	478	M	4	2.22	0.464		
73	44	442	M	4	2.86	0.647		
74	68	2,461	M	5	4.61	0.187		
75	60	1,942	M	5	5.44	0.28		
76	52	504	M	5	3.66	0.726		
77	45.7	589	M	4	2.4	0.407		
78	46	626	F	2	0.31	0.05		
79	43	394	M	5	2.61	0.662		
80	67.5	2271	F	5	280	12.33	279*858	239,382
81	39	328	M	4	0.98	0.299		
82	46	470	M	5	1.78	0.379		
83	42	340	M	4	0.98	0.288		
84	43	350	F	4	20.4	5.829		
85	43	476	M	5	1.48	0.311		
86	30	212	F	1	0.07	0.033		
87	34	278	M	2	0.32	0.115		
87	49.2	537	F	2	0.27	0.05		
88	78	2,782	F	3	3.4	0.122		
89	68	2180	M	5	3.16	0.145		
90	51	558	F	2	2.06	0.369		

Appendix XVI: The length, weight, sex of fish, gonadal maturity stage, weight of gonads, gonado-somatic index (GSI), number of eggs per gram of eggs, and fecundity of fish samples of LVG population in December 2016.

SN	Length (Cm)	Weight (g)	Sex	Maturity stage	Gonad wt	GSI (%)	No. of Eggs/g	Fecundity
1	32	243	M	2	0.09	0.037		
2	27	138	F	1	0.25	0.181		
3	60	1674.3	M	3	2.17	0.13		
4	35	278	M	1	0.09	0.032		
5	56	990	F	2	0.1	0.01		
6	26	118	F	1	0.09	0.076		
7	34	256	M	1	0.09	0.035		
8	45	633	M	3	1.22	0.193		
9	28	158	F	1	0.1	0.063		
10	56	985.7	F	3	2.08	0.211		
11	41	460	M	2	0.58	0.126		
12	64	1,437	M	4	5.18	0.36		
13	48	826	M	4	0.45	0.054		
14	38	336	M	4	0.34	0.101		
15	68	1,743.50	F	3	5.19	0.298		
16	39	423	M	2	0.28	0.066		
17	62	1158	M	4	2.43	0.21		
18	59	1052	M	3	0.19	0.018		
19	65	1290	F	4	50.72	3.932		
20	63	984	F	5	61.8	6.28	60*1276	76,560
21	36	659	F	2	1.96	0.297		
22	73	2011	M	5	5.28	0.263		
23	76	2294	M	4	4.45	0.194		
24	51	1219	F	3	4.21	0.345		
25	78	2472	M	5	6.27	0.254		
26	73	1710	M	4	1.36	0.08		
27	59	1237	F	3	6.08	0.492		
28	74	2020	M	4	8.12	0.402		
29	75	2201	M	5	5.7	0.259		
30	66	1920	M	3	0.93	0.048		
31	75	2206	M	5	6.67	0.302		
32	43	491.3	F	2	0.26	0.053		
33	42	470	M	2	1.35	0.287		
34	69	1603	M	4	1.98	0.124		
35	66	1324	M	4	1.68	0.127		
36	61	876	M	4	1.89	0.216		
37	79	2330	M	5	4.15	0.178		

38	87	3367	M	5	5.24	0.156		
39	75	2919	M	5	6.2	0.212		
40	60	1703	M	4	4.7	0.276		
41	72	2465	M	5	4.56	0.185		
42	66	1985.4	F	5	171.4	8.633	168*1418	238,224
43	79	2389	M	4	4.26	0.178		
44	75	2213	F	5	72.8	3.29	70*1130	79,100
45	27	125	F	1	0.1	0.08		
46	25	127	M	1	0.03	0.024		
47	49	724	F	2	1.48	0.204		
48	45	680	F	2	1.16	0.171		
49	38	456	F	2	1.08	0.237		
50	46	604	M	4	4.89	0.81		
51	68	2076	F	5	205.92	9.919	204*1009	205,836
52	66	1918	F	2	1.05	0.055		
53	76	2,871	F	4	8.04	0.28		
54	47	578	M	2	0.32	0.055		
55	65	1549	F	2	3.2	0.207		
56	36	374	F	2	0.41	0.11		
57	37	397	M	2	0.24	0.06		
58	34	301	M	1	0.2	0.066		
59	44	68.25	M	2	0.68	0.996		
60	42	506	F	2	0.4	0.079		
61	35	344	F	2	0.2	0.058		
62	64	1823.6	F	3	5.63	0.309		
63	26	129	F	1	0.05	0.039		
64	23	87	F	1	0.06	0.069		
65	22	90	M	1	0.01	0.011		
66	21.5	72	F	1	0.03	0.042		
67	21	71	M	1	0.01	0.014		
68	54	1310	M	3	3.28	0.25		
69	69	1593	M	4	3.18	0.2		
70	73	2129	M	5	4.65	0.218		
71	71	2017	M	4	10.92	0.541		
72	60	1,734	F	2	0.63	0.036		
73	52	1237	M	3	1.38	0.112		
74	48	702	F	2	0.4	0.057		
75	49	728	M	4	0.85	0.117		
76	56	1124	M	3	1.84	0.164		
77	40	451	F	2	0.39	0.086		
78	56	1100	M	4	5.48	0.498		
79	67	2,658	M	3	2.8	0.105		

80	69	1778	M	4	3.03	0.17		
81	30	196	M	1	0.01	0.005		
82	36	329	F	2	0.27	0.082		
83	37	372	F	2	0.24	0.065		
84	29	169	F	1	0.09	0.053		
85	42	812	F	2	1.64	0.202		
86	56	1314	M	5	2.53	0.193		
87	45	475	F	2	1.48	0.312		
88	72	2016	F	5	15.94	0.791		
89	51	1034	M	3	3.61	0.349		
90	65	1989	M	5	8.64	0.434		
91	71	2,783.40	M	5	5.32	0.191		
92	34	267	F	2	0.16	0.06		
93	76	2486	F	5	263.3	10.59	261*1078	281,358
94	26	101	M	1	0.04	0.04		
95	58	1347	M	3	0.96	0.071		
96	79	3,480	F	4	11.5	0.33		
97	28	173	F	1	0.09	0.052		
98	54	1243	F	3	2.6	0.209		
99	60	1627	M	4	5.6	0.344		
100	56	1300	F	4	5.81	0.447		
101	60	1385	M	4	4	0.289		
102	31	238	F	2	0.13	0.055		
103	61	2186	F	2	0.27	0.012		
104	73	2564	F	5	286.3	11.17	285*1126	320,910
105	78	3390	F	4	8.92	0.263		

.

Appendix XVII: The length, weight, sex of fish, gonadal maturity stage, weight of gonads, gonado-somatic index (GSI), number of eggs per gram of eggs, and fecundity of fish samples of LVG population in January 2017.

SN	Length (Cm)	Weight (g)	Sex	Maturity St	Gonad Wt (g)	GSI (%)	Eggs/g	Fecundity
1	49	815	M	2	0.13	0.016		
2	34	172	M	2	0.06	0.035		
3	28	87	F	1	0.17	0.195		
4	24	67.5	F	1	0.1	0.148		
5	23	68	F	1	0.19	0.279		
6	27	82	F	1	0.07	0.085		
7	26	74	F	1	0.06	0.081		
8	35	149.5	F	2	0.26	0.174		
9	39	270	F	2	0.18	0.067		
10	56	612.5	F	3	2.31	0.377		
11	39	239	F	1	0.16	0.067		
12	43	316	F	2	0.7	0.222		
13	44	297.5	F	2	0.64	0.215		
14	56	610	M	5	2.16	0.354		
15	50	445	M	2	0.72	0.162		
16	64	1210	F	4	9.67	0.799		
17	46	310	M	2	0.22	0.071		
18	39	237	F	2	0.89	0.376		
19	36	202.5	F	3	1.43	0.706		
20	33	146	M	2	0.95	0.651		
21	35	204	M	2	0.21	0.103		
22	45	468	M	1	0.07	0.015		
23	33	172	F	2	0.24	0.14		
24	31	139	F	2	0.29	0.209		
25	25	79	F	1	0.05	0.063		
26	32	145	F	1	0.09	0.062		
27	44	427	F	2	0.86	0.201		
28	44	298	F	5	24.84	8.336	23*804	18,492
29	40	267	M	2	0.17	0.064		
30	37	233.5	F	1	0.48	0.206		
31	44	296	F	2	0.84	0.284		
32	35	184	M	2	0.07	0.038		
33	33	143	F	1	0.12	0.084		
34	66	1,854	F	5	71.42	3.852	70*1062	74,340
35	76	2670	M	4	7.4	0.277		
36	31	208	M	2	0.1	0.048		

37	59	723	F	4	8.41	1.163		
38	28	199	M	1	0.08	0.04		
39	43	270	M	2	0.3	0.111		
40	72	2,568	F	5	86.38	3.364	85.2*1109	94,487
41	50	471	M	3	3.2	0.679		
42	49	465.8	F	2	0.79	0.17		
43	61	983	F	4	4.03	0.41		
44	30	186	F	1	0.08	0.043		
45	36	334	M	2	0.47	0.141		
46	41	367	F	2	0.28	0.076		
47	39	351.8	F	2	0.19	0.054		
48	71	2,738	M	5	6.04	0.221		
49	75	2,856	F	4	11.05	0.387		
50	42	380	M	3	2.5	0.658		
51	37	345.9	F	2	1.68	0.486		
52	30	176.2	F	2	0.23	0.131		
53	77	2,948.30	F	4	6.3	0.214		
54	56	621.8	M	3	2.06	0.331		
55	40	360	M	2	0.35	0.097		
56	47	450.1	F	2	0.18	0.04		
57	40	421	M	2	0.14	0.033		
58	53	504	F	3	2.6	0.516		
59	60	2245.3	M	4	4.21	0.188		
60	42	370	M	2	0.93	0.251		
61	69	1819	F	5	137.9	7.581	136.1*1110	151,071
62	50	721	M	3	1.49	0.207		
63	46	560	M	2	0.08	0.014		
64	43	490	M	4	0.72	0.147		
65	36	314	M	2	0.19	0.061		
66	36	342	F	5	25.43	7.436		
67	38.5	472	F	2	0.47	0.1		
68	34	293	F	2	0.39	0.133		
69	30	213	F	1	0.08	0.038		
70	60	1785	F	4	2.05	0.115		
71	63	1,884	F	5	119.65	6.351	118*1084	127,912
72	28	128	M	1	0.08	0.063		
73	40	436	M	2	0.14	0.032		
74	39	427	M	2	0.12	0.028		
75	77	2,985	M	3	3.07	0.103		
76	69	2,430	M	4	5.62	0.231		
77	38	475	F	2	0.24	0.051		

78	28	145.8	F	1	0.09	0.062		
79	62	2,153.40	F	5	98.36	4.568	97*964	93,508
80	32	186	M	1	0.07	0.038		
81	37	198.5	M	2	0.2	0.101		
82	54	874.6	M	3	0.73	0.083		
83	60	1361	F	5	154.71	11.37	1186*152.5	180,865
84	27	94.3	M	1	0.07	0.074		
85	46	621.5	F	3	2.06	0.331		

Appendix XVIII: The length, weight, sex of fish, gonadal maturity stage, weight of gonads, gonado-somatic index (GSI), number of eggs per gram of eggs, and fecundity of fish samples of LBA population in September 2016.

SN	Length (cm)	Weight (g)	Sex	Maturity stage	Gonad weight (g)	GSI (%)	Eggs/g	Fecundity
1	58	1750	F	5	60.74	3.471		
2	56	975	M	4	0.54	0.055		
3	85.5	4532	F	5	281.34	6.208		
4	90.5	6000	F	5	180.27	3.005		
5	80	3500	F	5	249.42	7.126		
6	72	1607	F	2	3.35	0.208		
7	52	523	F	2	1.75	0.335		
8	49	416.5	M	3	0.12	0.029		
9	41.5	285.5	M	3	0.23	0.081		
10	78.5	3.14	M	2	0.4	12.74		
11	49.5	587.3	F	2	1.06	0.18		
12	54	1640.5	M	4	0.5	0.03		
13	74	1652.7	M	4	3.98	0.241		
14	57.5	698.4	F	5	55.67	7.971		
15	67.5	1524.5	M	3	0.42	0.028		
16	37	192	M	1	0.02	0.01		
17	51.5	513.3	F	2	1.82	0.355		
18	72	1626.4	F	4	8.15	0.501		
19	54	668.4	M	2	0.05	0.007		
20	44.5	380.4	M	2	0.05	0.013		
21	44	323	M	2	0.24	0.074		
22	49	484	F	2	0.41	0.085		
23	45	308	M	2	0.03	0.01		
24	67.5	1389.2	M	3	0.67	0.048		
25	38	233	F	2	0.93	0.399		
26	52.5	558	F	2	1.32	0.237		
27	65	1128	M	5	2.46	0.218		
28	35	178.5	F	1	0.45	0.252		
29	65.5	1179.8	M	2	0.6	0.051		
30	67	1427.6	F	5	69.2	4.847		
31	60	1087.6	F	2	3.23	0.297		
32	68	1487.9	F	5	70.36	4.729		
33	46	587	F	2	1.72	0.293		
34	57	769	F	2	1.05	0.137		
35	54	707.4	M	2	0.01	0.001		
36	62	672.4	M	5	1.74	0.259		
37	58.5	736.2	M	5	4.65	0.632		
38	63	1142.3	M	2	0.03	0.003		

39	56	956	M	2	0.08	0.008		
40	62.5	924	M	4	0.67	0.073		
41	82	4250	F	4	31.03	0.73		
42	52	1532.5	F	2	3.72	0.243		
43	67	1532	M	3	1.71	0.112		
44	68.5	1498.8	F	5	49.06	3.273		
45	77.4	2160	F	5	185.78	8.601		
46	48	425	F	4	9.35	2.2		
47	49.5	471.5	F	2	1.54	0.327		
48	58	737.5	F	3	2.43	0.329		
49	44.5	592.5	F	4	6.7	1.131		
50	50	572.3	F	2	1.9	0.332		
51	50.4	454.5	F	5	43.51	9.573		
52	52.5	503.5	F	5	27.61	5.484		
53	50.5	318.5	F	2	2.89	0.907		
54	50.5	500.5	F	5	38.91	7.774		
55	71	1793.6	M	2	0.63	0.035		
56	53	537.3	M	4	1.96	0.365		
57	69	1528.3	M	2	0.36	0.024		
58	68.5	1298.7	F	5	59.64	4.592		
59	61	1202.3	F	2	7.04	0.586		
60	75.5	1266	M	5	5.3	0.419		
61	59.5	1487	F	5	146.63	9.861		
62	66	1048.4	F	2	3.89	0.371		
63	58.5	1109	F	5	43.39	3.913		
64	67	1379	F	2	4.06	0.294		
65	66.5	1745.03	M	5	3.95	0.226		
66	72	1702.44	F	4	32.01	1.88		
67	67	1220.5	F	5	99.87	8.183		
68	60	955.1	M	3	0.54	0.057		
69	36	180	F	1	0.26	0.144		
70	44.5	459.6	F	2	1	0.218		
71	37	210.5	M	1	0.06	0.029		
72	35.5	180.5	M	1	0.02	0.011		
73	68	1529.5	F	5	46.64	3.049	45*783	35,235
74	71	1722.6	M	2	0.37	0.021		
75	68.5	1323.4	F	4	39.46	2.982		
76	69	1231.2	M	5	3.21	0.261		
77	59	907	F	2	3.61	0.398		
78	63	1193.5	F	5	32.35	2.711	31*1063	32,953
79	53	1315	F	5	62.93	4.786	61*1169	71,309
80	57	631	M	4	1.53	0.242		
81	56	714.5	M	3	0.86	0.12		

82	58.5	842.5	M	2	0.16	0.019		
83	51	554	F	2	2.26	0.408		
84	58.5	776.4	F	2	3.75	0.483		
85	61	1011.5	F	5	78.85	7.795	77.3*1046	80,856
86	62	1133	M	2	0.77	0.068		
87	32	133.5	F	1	0.64	0.479		
88	31	133.5	M	1	0.39	0.292		
89	31.5	131	F	1	0.59	0.45		
90	44.5	312.5	M	2	0.38	0.122		
91	60	915.5	M	5	3.33	0.364		
92	46	390.1	F	2	1.66	0.426		
93	75	1631	F	4	39.88	2.445		
94	41	350	F	5	14.03	4.009		
95	54	298	F	5	32.42	10.88	31*1000	31,000
96	49	799	M	2	1.06	0.133		
97	61	1397	M	3	0.74	0.053		
98	62.5	1105	F	5	74.61	6.752	73*1052	76796
99	46	363.5	M	4	1.04	0.286		
100	51	385.4	M	4	1.35	0.35		
101	57	763.4	M	2	0.15	0.02		
102	57.5	859	F	2	2.93	0.341		
103	34	177	F	1	0.5	0.282		
104	37	238.5	F	1	0.78	0.327		
105	33.5	175	M	1	0.04	0.023		
106	45.5	378	F	5	97.45	25.78	96*1120	107,520
107	35	189	F	1	0.85	0.45		
108	57	966	F	4	25.6	2.65		
109	63	1088	M	4	2.06	0.189		
110	38	191	F	2	1.11	0.581		
111	42	313	F	2	1.36	0.435		
112	50	474	F	2	2.2	0.464		

113	65	1,394	M	1	0.16	0.011		
114	50.4	484.3	F	2	1.45	0.299		
115	33	163.5	F	4	8.29	5.07		
116	56	821	F	5	43.87	5.343	42*859	36,078

Appendix XIX: The length, weight, sex of fish, gonadal maturity stage, weight of gonads, gonado-somatic index (GSI), number of eggs per gram of eggs, and fecundity of fish samples of LBA population in October 2016.

SN	Length (cm)	Weight (g)	Sex	Maturity stage	Gonad wt (g)	0.14	Eggs/g	Fecundity
1	77.5	2880	M	5	4.1	0.14		
2	41	501	F	2	1.08	0.22		
3	46	588	M	2	0.1	0.02		
4	37	304	F	2	0.84	0.28		
5	36	277	F	2	1.03	0.37		
6	40	389	F	4	7.33	1.88		
7	76	3151	F	3	5.84	0.19		
8	52	896	F	2	1.6	0.18		
9	58	1279	M	2	0.16	0.01		
10	50	827	M	2	0.05	0.01		
11	50.5	866	F	2	1.28	0.15		
12	49	581	M	3	0.14	0.02		
13	56	1124	F	5	85.8	7.633	84*702	58,968
14	31	176	M	1	0.12	0.07		
15	32.5	219	F	2	1.17	0.53		
16	36	320	M	1	0.52	0.162		
17	35	257	F	2	0.5	0.19		
18	31	170	M	5	0.41	0.24		
19	30	188	M	2	0.14	0.07		
20	37.5	295	M	2	0.13	0.04		
21	67	1,865	F	5	120.33	6.452	1080*119	128,520
22	53	751	F	2	1.88	0.25		
23	43	452	F	2	0.91	0.201		
24	62	1582	M	2	0.1	0.01		
25	72	2750	M	4	4.06	0.147		
26	53	785	M	3	2.54	0.324		
27	32	127	F	1	0.06	0.047		
28	37	314	F	1	0.07	0.02		
29	33.5	276	F	2	0.59	0.21		
30	34	276	M	2	0.12	0.04		
31	35	327	F	2	0.81	0.25		
32	33	321	F	2	0.5	0.16		
33	36.5	353	F	2	0.98	0.28		
34	76	1358	F	5	32.76	2.412	31*689	21,359
35	80	3087	M	5	7.4	0.24		
36	46	694	F	5	20.12	2.9	19.40*613	11,892
37	46.5	592	F	2	1.32	0.22		
38	46	687	M	2	0.02	0		
39	41	371	F	2	2.66	0.72		
40	59.5	718	M	3	0.22	0.03		
41	48	856	F	2	1.56	0.18		
42	45.5	697	F	4	5.53	0.79		
43	40.5	420	F	2	0.62	0.15		
44	64	1610	F	2	2.01	0.12		
45	69	1825	F	2	1.53	0.08		

46	76.5	2290	M	2	0.56	0.02		
47	57.5	1272	F	2	2.31	0.18		
48	58	1360	F	2	3.2	0.24		
49	61	2210	M	4	1.3	0.06		
50	39.5	437	F	2	0.73	0.17		
51	53	1018	M	1	0.23	0.02		
52	75	2222	M	4	2.61	0.12		
53	47	708	M	1	0.26	0.04		
54	43	542	F	1	2.18	0.4		
55	36	318	F	2	0.8	0.25		
56	39	356	M	2	0.04	0.01		
57	35	244	F	2	0.41	0.17		
58	43	488	M	2	0.04	0.01		
59	46	609	F	1	0.11	0.02		
60	43	513	M	1	0.03	0.01		
61	38.5	406	F	2	1.91	0.47		
62	58	1545	F	3	2.4	0.16		
63	41	490	F	2	1.25	0.26		
64	34	210	M	2	0.12	0.057		
65	35	226	M	1	0.09	0.039		
67	56	1305	F	5	49.56	3.797	48*947	45,456
68	70	2831	F	4	5.78	0.204		
69	50	994	F	2	0.71	0.071		
70	54	1271	F	5	72.86	5.732	71*1160	82,360
71	29	136	M	1	0.08	0.058		
72	59	1630	F	2	0.54	0.033		
73	37	216	M	3	1.06	0.491		
74	60	1540	M	3	2.08	0.135		
75	62	1789	F	5	90.76	5.073	89*1100	97900
76	40	307	M	2	0.48	0.156		
77	45	613	F	3	2.18	0.355		
78	76	2934	M	5	5.67	0.196		
79	30	186	M	1	0.08	0.043		
80	53	1112	F	5	46.31	4.165	45*784	35280
81	48	743	F	2	0.15	0.0201		

Appendix XX: The length, weight, sex of fish, gonadal maturity stage, weight of gonads, gonado-somatic index (GSI), number of eggs per gram of eggs, and fecundity of fish samples of LBA population in November 2016.

SN	Length (Cm)	Weight (g)	Sex	Maturity Sta	Gonad Wt (g)	GSI (%)	Eggs/g	Fecundity
1	28.5	93	M	1	0.03	0.032		
2	32.5	130.5	F	1	0.35	0.268		
3	53	551	F	3	2.17	0.394		
4	60.5	731	M	4	1.71	0.234		
5	65	999.5	F	5	22.89	2.29	21*1290	27,090
6	48	205	F	4	2.45	1.195		
7	43	261.5	M	3	0.4	0.153		
8	29.5	93.5	F	1	0.2	0.214		
9	37	571	M	2	0.21	0.037		
10	30	176	F	1	0.74	0.42		
11	55	635	M	4	2.05	0.323		
12	75	1852.8	F	5	9.08	0.49	Spent	
13	83	3,740	M	5	3.32	0.089		
14	54	581.5	M	3	0.5	0.086		
15	56	707.5	M	2	0.28	0.04		
16	79	3369	M	4	1.47	0.044		
17	43	293.5	M	2	0.25	0.085		
18	55	624.5	M	4	0.35	0.056		
19	53	578	F	2	1.04	0.18		
20	53	624.6	M	4	1.78	0.285		
21	43	332	M	4	0.67	0.202		
22	62	982	F	3	5.17	0.526		
23	66	1065	M	4	1.12	0.105		
24	62	977.5	F	3	3.67	0.375		
25	61.5	869	F	5	74.68	8.594	74*1143	84,582
26	78	2,803.50	M	5	3.15	0.112		
27	76	2121	M	5	2.64	0.124		
28	63	1,140	F	3	4.22	0.37		
29	52	566	M	2	0.04	0.007		
30	79	3,172	M	4	1.99	0.063		
31	56	688	F	5	38.65	5.618	37.68*1065	40,129
32	49	399	F	2	1.72	0.431		
33	83	2,442	M	5	1.78	0.073		
34	74	2,663	M	2	0.42	0.016		
35	58	884	F	5	74.92	8.475	74*1121	82,954
36	84	3,780	F	5	11.95	0.316	Spent	
37	79	3,636	M	4	5.05	0.139		

38	80	3,641	M	4	2.72	0.075		
39	56	690	M	4	1.96	0.284		
40	35	174	M	1	0.02	0.012		
41	37	174	F	2	1.44	0.83		
42	65	589	M	3	0.29	0.049		
43	45	320	M	2	0.08	0.025		
44	55	585	F	2	1.8	0.308		
45	56	667	M	2	0.24	0.036		
46	49	449	M	5	0.93	0.207		
47	82	3,894	F	5	292.18	7.503	291*1018	296,238
48	44	314	F	2	0.09	0.029		
49	54	601	M	3	0.74	0.123		
50	67	1,112	M	4	0.7	0.063		
51	32	132	M	1	0.03	0.023		
52	50	375	M	3	0.38	0.101		
53	70	2,637	F	4	2.93	0.111		
54	74	2,725.50	M	3	0.47	0.017		
55	76	2,980	F	5	248.15	8.327	247*974	240,578
56	65	1,336	M	3	0.76	0.057		
57	75	2,738	M	5	5.2	0.19		
58	73	2,629	F	5	158.08	6.013		
59	51	440	F	3	0.43	0.098		
60	39	233	M	4	1.51	0.648		
61	56	865	F	4	3.74	0.433		
62	42	308	F	2	1.19	0.386		
63	49	805	M	3	0.35	0.043		
64	42	510	F	2	1	0.196		
65	44.5	479	F	2	1.1	0.23		
66	46	611	F	2	1.23	0.2		
67	41	440	M	4	0.39	0.09		
68	38	354	F	2	1.76	0.5		
69	37	303	F	2	0.79	0.26		
70	67	1,536	F	5	63.04	4.1	62*1104	68448
71	64	1,391	F	3	3.75	0.27		
72	37	303	F	2	0.87	0.29		
73	38	382	F	2	1.37	0.36		
74	41	402	F	2	0.91	0.23		
75	29	245	F	1	0.26	0.11		
76	79	2,470	F	5	241.34	9.77	246*1098	270,108
77	53	1189	F	2	1.69	0.14		
78	50	912	F	3	2.67	0.29		

79	52	1,215	M	2	0.27	0.02		
80	50	1,053	M	2	0.21	0.02		
81	53	1,037	F	2	0.87	0.08		
82	51	973	F	2	1.71	0.18		
83	46	726	M	1	0.15	0.02		
84	45	822	M	2	0.14	0.02		
85	45	586	M	2	0.05	0.009		
86	50	899	F	4	11.26	1.25		
87	84	4,006	M	3	0.68	0.017		
88	47	769	M	2	0.05	0.007		
89	36	311	F	2	1.02	0.32		
90	41	533	M	1	0.03	0.005		
91	43	563	F	4	13.75	2.44		
92	37.5	395	M	2	0.05	0.012		
93	52	895	F	2	2.95	0.329		
94	64	1,749	M	4	0.59	0.033		
95	44	612	M	4	0.47	0.076		
96	35	223	F	1	0.21	0.094		
97	41	435	M	2	0.08	0.018		
98	35.5	284	M	1	0.03	0.01		
99	64	1,893	M	3	0.3	0.015		
100	64	1,873	M	2	0.36	0.019		
101	63	1,662	F	3	4.27	0.257		
102	59	1,362	M	2	0.15	0.011		
103	58.5	1,459	F	5	36.07	2.472	35*850	29,750
104	46	649	M	5	1.65	0.254		
105	60	1,126	F	5	82.67	7.342	81*912	73,872

.

Appendix XXI: The length, weight, sex of fish, gonadal maturity stage, weight of gonads, gonado-somatic index (GSI), number of eggs per gram of eggs, and fecundity of fish samples of LBA population in December 2016.

SN	Length (cm)	Weight (g)	Sex	Maturity Stage	Gonad Weight (g)	GSI (%)	No. of Eggs/g	Fecundity
1	58	1094	M	5	2.71	0.248		
2	65	1834	F	5	44.35	2.418	43*1208	51,944
3	64	1749	M	5	4.84	0.277		
4	65	1429	M	5	5.27	0.369		
5	59	1549	F	5	43.94	2.837	43*1164	50,052
6	52	854	F	5	21.12	2.473	20*785	15,700
7	55	1182	F	5	24.16	2.044	23*1006	23,138
8	58	1184	M	4	3.49	0.295		
9	63	1749	F	5	30.52	1.745	29*1056	30,624
10	74	2659	M	5	7.43	0.279		
11	75	3007	M	5	8.42	0.28		
12	77	3504	M	5	12.25	0.350		
13	48	710	F	3	1.71	0.241		
14	37.5	285	F	2	0.8	0.2817		
15	45	633	F	2	1.59	0.251		
16	60	1459	M	3	0.54	0.037		
17	50	1266	M	3	0.36	0.028		
18	38	369	M	4	1	0.271		
19	72	2258	M	3	0.48	0.021		
20	58	2478	F	3	2.81	0.113		
21	68	2616	M	3	0.69	0.026		
22	69	2592	F	5	187.02	7.215	186*1027	191,022
23	72	3591	F	5	99.79	2.779	99*1109	109,791
24	85	4061	M	5	8.76	0.216		
25	83	4719	M	3	1.75	0.037		
26	50	1374	F	3	2.35	0.171		
27	70	2600	M	3	1.35	0.052		
28	84	4582	M	3	0.76	0.017		
29	78	3579	M	3	0.57	0.016		
30	40	441	F	2	0.83	0.188		
31	46	673	F	2	1.46	0.217		
32	40	430	M	3	0.33	0.077		
33	62	1758	M	3	0.38	0.022		

34	62	1557	M	5	2.65	0.170		
35	49	871	M	3	0.39	0.045		
36	34	242	M	2	0.21	0.087		
37	80	4000	M	5	7.04	0.176		
38	65	3506	M	5	5.36	0.153		
39	68	2507	M	4	6.45	0.257		
40	56	1547	F	5	100.69	6.509	100*1062	106,200
41	60	2565	F	5	79.49	3.099	78.6*1105	86,853
42	68	2392	M	5	8.08	0.338		
43	73	2683	M	5	6.97	0.260		
44	83	4,540	M	5	10.18	0.224		
45	82	4538	M	5	10.69	0.236		
46	66	2651	F	5	76.75	2.895	76*1,135	86,260
47	88	5,908	M	5	7.01	0.1187		
48	72	2,958	M	5	13.64	0.461		
49	95	5,568	M	5	6.55	0.118		
50	79	3,892	F	5	305.63	7.853	304.2*1283	390,289
51	41	681	M	4	1.43	0.21		
52	100	7,865	M	5	14.01	0.178		
53	94	4,056	M	5	10.2	0.252		
54	87	4,608	M	5	7.33	0.159		
55	93	5,549	M	5	11.18	0.202		
56	95	6,568	M	5	19.76	0.301		
57	96	6,582	M	5	10.7	0.163		
58	78	3,834	F	5	80.05	2.088	79*877	69,283
59	87	4,576	M	5	6.41	0.140		
60	63	1,809	M	5	4.24	0.234		
61	88.4	5548	F	5	165.19	2.978	164*1,174	192,536
62	82.6	4568	M	5	5.95	0.130		
63	45	655	M	4	0.66	0.101		
64	58	1474	M	2	0.34	0.023		
65	66	1356	M	5	4.07	0.300		
66	72.5	1867	M	5	6.8	0.364		
67	49	793	F	5	29.99	3.782	29*1030	29,870
68	54	876	F	5	10.72	1.224		
69	56	886	M	4	1.89	0.213		
70	51	692	F	5	35.48	5.127	34*996	33,864
71	50	870	F	5	18.78	2.159		
72	40	419	F	5	20.94	4.998	20*848	16,960

73	48	443	M	4	2.02	0.456		
74	49	623	M	6	5.01	0.804		
75	46	461	M	4	1.99	0.432		
76	43	483	M	4	0.98	0.203		
77	43	416	F	5	8.2	1.971		
78	59	329	M	4	0.66	0.201		
79	44	412	M	4	1.6	0.388		
80	72.5	2980	M	3	0.72	0.024		
81	70.5	2548	M	3	0.58	0.023		
82	86	5,007	M	3	1.28	0.026		
83	51.5	1020	F	2	1.15	0.113		
84	51.5	986	F	3	1.88	0.191		
85	70	2560	F	3	4.16	0.163		
86	48.5	662	M	2	0.06	0.009		
87	46	633	M	3	0.12	0.019		
88	44	732	M	3	0.99	0.135		
89	53	1156	F	2	1.87	0.162		
90	55.5	497	M	4	0.36	0.072		
91	56.5	1188	M	3	0.32	0.027		
92	42	448	F	3	1.18	0.263		
93	40	419	F	3	1.9	0.454		
94	70	2181	M	3	0.77	0.035		
95	58	1600	F	3	2.7	0.169		
96	71	2831	M	3	0.48	0.017		
97	76.5	3,634	M	5	5.42	0.149		
98	74	3,006	F	5	38.15	1.269		
99	54	1,040	F	5	24.74	2.379		
100	74	3,908	F	5	176.65	4.520	176*786	138,336
101	76	3540	M	5	9.18	0.259		

Appendix XXII: The length, weight, sex of fish, gonadal maturity stage, weight of gonads, gonado-somatic index (GSI), number of eggs per gram of eggs, and fecundity of fish samples of LBA population in January 2017.

SN	Length (Cm)	Weight (g)	Sex	Maturity Stage	Gonad Wt (g)	GSI (%)	Fecundity	Fecundity
1	42	365.5	F	2	1.38	0.378		
2	55	1032.5	F	2	3.19	0.309		
3	84	4,109	F	5	38.36	0.934	Spent	
4	48	443.8	F	5	24.61	5.545	23.60*900	21,240
5	32	130.5	M	1	0.04	0.031		
6	46	205	F	1	0.43	0.21		
7	45	265.5	F	5	18.87	7.107	17.50*1080	18,900
8	49	648.6	M	1	0.05	0.008		
9	67.5	1123.5	M	3	5.59	0.498		
10	58	702.5	F	2	2.86	0.407		
11	84	4,300	M	4	3.7	0.086		
12	73	2,330	M	2	0.17	0.007		
13	40	291	F	2	2.31	0.794		
14	63	1247	F	3	3.74	0.3		
15	65	1223	M	2	0.11	0.009		
16	56	655	F	2	1.05	0.16		
17	67	993	M	2	0.19	0.019		
18	47	481.5	M	2	0.04	0.008		
19	49	567.5	F	2	1.44	0.254		
20	60	885	M	1	0.24	0.027		
21	51	485	M	2	0.07	0.014		
22	61	882	M	2	0.03	0.003		
23	62	888	F	5	25.48	2.869	24*1269	30,456
24	61.5	1061	M	4	1.08	0.102		
25	58	818.5	F	3	1.87	0.228		
26	62.5	953.6	M	2	0.14	0.015		
27	77	1711	M	4	2.59	0.151		
28	33	141	M	1	0.04	0.028		
29	32	130.5	M	1	0.05	0.038		
30	32	126.5	F	1	0.12	0.095		
31	40	227.5	M	1	0.01	0.004		
32	69	1271	M	3	0.76	0.06		
33	67	1174	F	3	2.71	0.231		
34	58	641	M	5	5.47	0.853		
35	47	365.5	F	2	0.92	0.252		
36	44	264	M	2	0.12	0.045		

37	36	170	F		2	0.45	0.265		
38	45	324	F		2	1.09	0.336		
39	41	211	M		2	0.02	0.009		
40	37	205	F		2	0.77	0.376		
41	42	311	M		2	0.18	0.058		
42	52	493	M		4	0.3	0.061		
43	56	673	F		3	4.77	0.709		
44	57	601	M		3	0.34	0.057		
45	71	900	F		4	2.86	0.318		
46	56	889	M		5	3.75	0.422		
47	74	1506	F		5	15.76	1.046	14*870	12,180
48	59	1905	F		5	56.94	2.989	55.3*1182	65,364
49	51	566.5	F		2	2.29	0.404		
50	43	255.5	M		2	0.1	0.039		
51	46	314	F		1	0.15	0.048		
52	37	111	F		5	5.47	4.928	Spent	
53	28	76	M		1	0.02	0.026		
54	40	240.5	M		1	0.04	0.017		
55	33	148.5	M		2	2.24	1.508		
56	48	452	F		2	2.27	0.502		
57	47.5	473.5	F		2	1.93	0.408		
58	44	347.5	M		2	0.02	0.006		
59	53	580	M		2	0.13	0.022		
60	63	814	M		3	0.41	0.05		
61	36	203	M		2	0.13	0.064		
62	50	436	F		2	0.18	0.041		
63	62	1358	F		5	31.87	2.347		
64	43	328.5	M		3	1.06	0.323		
65	70	2607	F		4	4.86	0.186		
66	37	320	F		2	0.14	0.044		
67	30	215	F		2	0.96	0.447		
68	28	128	M		2	0.08	0.063		
69	34	245.6	F		2	0.61	0.248		
70	45	348.5	M		3	0.4	0.115		
71	52	524	F		4	2.09	0.399		
72	35	300.5	M		1	0.09	0.03		
73	60	1290.5	F		3	3.21	0.249		
74	38	407	M		2	0.74	0.182		
75	52	603	M		4	0.74	0.123		
76	45	449	F		2	0.23	0.051		
77	76	2274	F		3	0.62	0.027		
78	30	198	F		1	0.08	0.04		

79	56	965	F	5	41.34	4.284	40*1108	44,320
80	60	1348	M	3	0.48	0.036		
81	62	1473	M	1	0.69	0.047		
82	47	640	F	1	0.84	0.131		
83	40	378	F	3	1.37	0.362		
84	33	405	M	1	0.02	0.005		
85	41	494	M	4	0.82	0.166		
86	46	514	F	2	1.74	0.339		
87	58	765	F	3	2.05	0.268		
88	60	934	F	4	4.57	0.489		
89	72	2708	M	5	3.89	0.144		
90	70	2600	M	5	3.04	0.117		
91	46	661	F	2	1.34	0.203		
92	38	360	M	4	0.92	0.256		
93	33	209	M	2	0.2	0.096		
94	44	461	F	2	1.8	0.39		
95	42	464	M	2	0.06	0.013		
96	32	156	M	1	0.05	0.032		
97	84	4562	F	5	294.89	6.464	294*1143	336,042
98	67	2732	F	5	59.56	2.18	58.1*1012	58,797
99	56	1196	F	2	1.55	0.13		
100	44	556	F	3	1.93	0.347		
101	61	1178	M	2	0.4	0.034		
102	50	849	M	2	0.14	0.016		
103	45	595	M	4	0.8	0.134		
104	39	349	M	1	0.02	0.006		
105	38	300	F	2	1.09	0.363		
106	74	2199	F	3	9.07	0.412		
107	44	521	F	2	1.86	0.357		
108	47	713	M	4	0.57	0.08		
109	45	606	M	2	0.25	0.041		
110	35	244	F	1	0.32	0.131		
111	58	1357	M	3	0.28	0.021		
112	56	979	M	2	0.18	0.018		
113	68	2289	M	4	4.5	0.197		
114	60	2156	F	3	0.81	0.038		
115	52	1543	F	3	0.6	0.039		
116	46	576	M	3	0.48	0.083		
117	78	2784	M	4	4.53	0.163		
118	72	2,409	F	4	4.21	0.175		
119	38	335	F	2	0.09	0.027		

120	35	308	F	1	0.08	0.026		
121	51	1516	F	3	0.24	0.016		
122	56	1715	M	3	0.2	0.012		
123	50	1108	F	5	34.67	3.129	33*783	25,839
124	32	127	F	1	0.07	0.055		
125	63	2165	F	5	67.81	3.132	66.1*1268	83,815

Appendix XXIII: The length, weight, sex of fish, gonadal maturity stage, weight of gonads, gonado-somatic index (GSI), number of eggs per gram of eggs, and fecundity of fish samples of LKG population in September 2016.

SN	Length (Cm)	Weight (g)	Sex	Maturity Stage	Gonad Wt (g)	GSI (%)	Eggs/g	Fecundity
1	59	749.5	F	3	5.1	0.68		
2	40.1	317	F	2	1.11	0.35		
3	37	266	F	2	1.18	0.444		
4	33	148.5	F	1	0.15	0.101		
5	28	97	F	1	0.33	0.34		
6	27	76.5	F	1	0.14	0.183		
7	52	460.24	M	4	1.74	0.378		
8	56	450.4	F	5	75.19	16.69	73.6*778	57,261
9	41	262	M	4	0.86	0.328		
10	37	279.1	M	1	0.03	0.011		
11	54	754	M	4	3.28	0.435		
12	28	91.5	F	2	0.08	0.087		
13	49	619.5	F	2	20	3.228		
14	43.5	417	M	4	1.85	0.444		
15	57	1355	M	5	4.03	0.297		
16	39	240	M	3	0.58	0.242		
17	61	1,199	F	4	1.37	0.114		
18	35	197	F	2	0.09	0.046		
19	45	468.3	F	3	2.05	0.438		
20	56	890	M	3	2.87	0.322		
21	63	1238.6	F	3	3.61	0.291		
22	70	1724.5	M	5	4.82	0.28		
23	26	89	F	1	0.04	0.045		
24	34	219	F	1	0.06	0.027		
25	44	432	M	2	0.28	0.065		
26	39	256	F	2	0.16	0.063		
27	45	457.2	F	5	60.46	13.22	59*826	48,734
28	51	653	F	4	8.12	1.243		
29	54	738	F	5	69.43	9.408	68*900	61,200
30	40	408	M	2	0.34	0.083		
31	29	197	F	1	0.08	0.041		
32	63	1523.4	F	5	89.41	5.869	88*1082	95,216
33	38	261	M	2	0.41	0.157		
34	31	190	F	1	0.12	0.063		
35	49	578	F	4	6.23	1.078		
36	51	658.7	M	5	5.19	0.788		
37	48	549	F	3	2.76	0.503		
38	57	946	F	5	49.38	5.22	48*962	46,176

39	34	340	M	1	0.06	0.018		
40	33	328.2	M	1	0.05	0.015		
41	44	480	F	3	2.3	0.479		
42	52	710	M	4	3.71	0.523		
43	27	93	F	1	0.06	0.065		
44	67	1659	F	5	86.72	5.227	84*874	73,416
45	76	2205	M	5	6.21	0.282		
46	30	207	M	1	0.09	0.043		
47	28	142	F	1	0.07	0.049		
48	41	421	F	3	2.17	0.515		
49	59	1012	M	4	3.65	0.361		
50	64	1801	F	4	8.32	0.462		
51	40	400	F	2	0.24	0.06		
52	33	339	M	3	2.1	0.619		
53	29	191	F	1	0.09	0.047		
54	60	1135	F	3	3.61	0.318		
55	53	762.4	M	4	4.06	0.533		
56	37	346	F	2	0.85	0.246		
57	66	1682.4	M	3	5.67	0.337		

Appendix XXIV: The length, weight, sex of fish, gonadal maturity stage, weight of gonads, gonado-somatic index (GSI), number of eggs per gram of eggs, and fecundity of fish samples of LKG population in October 2016.

SN	Length (cm)	Weight (g)	Sex	Maturity stage	Gonad weight (g)	GSI (%)	Eggs/g	Fecundity
1	82	3,780	M	5	4.5	0.119		
2	74	2,917	M	3	1	0.034		
3	37	209.5	F	2	0.62	0.296		
4	37	202.7	F	2	0.72	0.355		
5	41	321.5	M	2	0.14	0.044		
6	31	179.5	F	2	0.72	0.401		
7	27.8	140.5	M	1	0.03	0.021		
8	25.6	115.5	F	2	0.64	0.554		
9	40.2	248.5	M	4	0.75	0.302		
10	43.1	292.6	M	3	0.29	0.099		
11	39.8	258.1	F	4	17.04	6.598		
12	37	180.3	F	2	1.5	0.832		
13	34	155.5	F	2	0.33	0.212		
14	32	132	M	2	0.08	0.061		
15	53	1028	M	5	3.34	0.325		
16	52	632	M	5	3.16	0.5		
17	45	347	F	5	32.33	9.317	31*890	27,590
18	41	327.5	M	3	0.39	0.119		
19	43	324.5	F	5	34.59	10.66	33.2*674	22,376
20	41	305.4	M	2	0.12	0.039		
21	35.6	186	M	2	0.57	0.306		
22	56.7	667.4	M	5	2.85	0.427		
23	43	325	F	5	30.39	9.351	29*1064	30,856
24	62	1146	F	6	11.21SPENT	0.978		
25	46	360.15	M	4	0.64	0.178		
26	54	479.5	F	3	4.57	0.953		
27	51	737.5	F	3	4.02	0.545		
28	33	149.5	F	2	0.57	0.381		
29	30	129	M	1	0.2	0.155		
30	23	60.5	M	1	0.03	0.05		
31	21	39	F	1	0.04	0.103		
32	66	1,260.5	M	5	2.96	0.235		
33	63	1145	M	5	4.64	0.405		
34	67	1153.6	M	4	0.94	0.081		
35	69	1,380.4	F	4	10.64	0.771		
36	28	90.5	F	2	0.39	0.431		
37	26	80.5	F	1	0.03	0.037		
38	45	375.5	M	2	0.1	0.027		
39	24	57	F	1	0.02	0.035		
40	57	784.1	M	3	0.19	0.024		
41	42	290	F	2	0.85	0.293		
42	41	310.2	M	2	0.15	0.048		
43	42	360.2	M	2	0.18	0.05		
44	60	1986	F	5	47.87	2.41	46*779	35,834
45	65	2,397	F	5	56.8	2.37	55.1*1124	61,932
46	34	197.6	M	2	0.18	0.091		

47	28	124	M	1	0.04	0.032		
48	70	2,561	M	3	4.2	0.164		
49	56	656	M	2	0.48	0.073		
50	52	629	M	4	2.54	0.404		
51	50	587.6	F	5	43.9	7.471	42.2*1008	42,537
52	40	398.7	F	5	39.65	9.945	38*1054	40,052
53	47	532.5	M	3	1.28	0.24		
54	37	256	M	2	0.53	0.207		
55	35	210	F	2	1.06	0.505		
56	73	2,704	F	4	6.83	0.253		
57	27	105	F	1	0.05	0.048		
58	49	570	M	5	3.21	0.563		
59	44	456	M	2	0.8	0.175		
60	52	758	F	5	40.67	5.365	39.1*910	35,581
61	53	776	F	5	35.84	4.619	34*800	27,200
62	40	386	M	3	2.09	0.541		
63	35	218	F	2	0.12	0.055		
64	32	199	M	1	0.08	0.04		
65	31	156	M	2	0.1	0.064		
66	49	564	M	2	0.48	0.085		
67	62	2,756	F	4	5.32	0.193		
68	43	410.4	F	3	1.05	0.256		
69	48	540	F	2	0.28	0.052		
70	49	526.3	M	3	1.62	0.308		
71	60	2,645	F	5	48.01	1.815	47*1100	51,700

Appendix XXV: The length, weight, sex of fish, gonadal maturity stage, weight of gonads, gonado-somatic index (GSI), number of eggs per gram of eggs, and fecundity of fish samples of LKG population in November 2016.

SN	Length (cm)	Weight (g)	Sex	Maturity	Gonad Wt (g)	GSI (%)	No. of Eggs/g	Fecundity
1	36	173.5	M	3	0.3	0.173		
2	45	329	F	5	27.54	8.371	26*1012	26,312
3	55.2	931.7	F	5	45.63	4.897	44*1000	44,000
4	71	1362	M	4	1.48	0.109		
5	47	442	F	5	42.06	9.516	41*974	39934
6	49	544.6	F	4	6.95	1.276		
7	42	356	M	3	1.2	0.337		
8	82	3176	M	5	15.52	0.489		
9	37	254.5	F	5	7.71	3.029	7*708	4,956
10	44	257.5	F	5	39.31	15.27	38*1072	40,736
11	36	248.5	M	2	0.1	0.04		
12	41	321.5	F	3	2.94	0.914		
13	35	216.5	F	3	3.08	1.423		
14	40	309.5	M	2	0.48	0.155		
15	39	220.5	M	2	0.56	0.254		
16	41	287.5	M	5	5.71	1.986		
17	43	320.5	M	4	3.41	1.064		
18	31	139	M	1	0.07	0.05		
19	28	84.5	F	1	0.06	0.071		
20	53	596.7	F	5	54.78	9.18	53.1*866	45,984
21	50.1	598.7	M	4	5.03	0.84		
22	38	238	M	2	0.08	0.034		
23	36	236	M	1	0.07	0.03		
24	43	386	M	4	2.3	0.596		
25	29	120.6	M	1	0.04	0.033		
26	54	555.5	M	4	1.84	0.331		
27	52	514.4	M	4	3.01	0.585		
28	45	388.2	M	3	4.89	1.26		
29	45	368	F	5	32.79	8.91	31*1189	36,859
30	41	392.5	M	2	1.34	0.341		
31	64	1743.5	F	5	3.3	0.189		
32	50	651.5	F	5	30.74	4.718	28.75*1100	31,625
33	51	549.5	F	2	3.34	0.608		
34	49	505.5	F	3	3.72	0.736		
35	42	272	F	2	1.2	0.441		
36	39.2	269	M	2	0.13	0.048		
37	47	432	F	3	3.69	0.854		
38	46	397	M	2	0.05	0.013		

39	51	470.5	M	3	0.93	0.198		
40	48.6	496.8	F	3	2.5	0.503		
41	55	826	M	4	0.48	0.058		
42	52	585	M	4	0.64	0.109		
43	62	1025	M	5	1.44	0.14		
44	56	575.5	M	4	0.5	0.087		
45	55	646	M	5	1.71	0.265		
46	42	317.5	F	5	4.6	1.449	3.2*705	2,256
47	30	288	M	3	0.09	0.031		
48	59	1059	M	4	1.49	0.141		
49	33	152.5	M	3	0.15	0.098		
50	32	136	F	1	0.4	0.294		
51	42	293.5	M	2	0.04	0.014		
52	40	288.3	F	2	0.88	0.305		
53	30	109.5	M	1	0.01	0.009		
54	60	1272	M	3	1.74	0.137		
55	32	144.5	F	2	0.08	0.055		
56	35	177	F	1	0.07	0.04		
57	23	51	F	1	0.06	0.118		
58	44	352	F	2	0.14	0.04		
59	28	98	F	2	0.04	0.041		
60	56	679	F	5	58.04	8.548	57*932	53,124
61	78	2870	M	4	3.6	0.125		
62	70	2490	M	5	4.39	0.176		
63	33	210	M	2	0.08	0.038		
64	34	248	M	2	0.2	0.081		
65	62	1438	F	4	3.76	0.261		
66	65	1598	F	5	78.3	4.9	77*1135	87,395
67	59	710	F	4	5.61	0.79		
68	60	1254	F	3	3.1	0.247		
70	54	573	M	3	4.2	0.733		
71	48	391	M	2	0.21	0.054		
72	32	201	F	2	0.08	0.04		
73	57	644.5	F	4	5.62	0.872		
74	39	340	F	3	0.16	0.047		
75	31	196.7	M	1	0.09	0.046		
76	28	94.2	M	2	0.05	0.053		
77	78	2905	F	5	65.81	2.265	65*1101	71,565

Appendix XXVI: The length, weight, sex of fish, gonadal maturity stage, weight of gonads, gonado-somatic index (GSI), number of eggs per gram of eggs, and fecundity of fish samples of LKG population in December 2016.

SN	Length (cm)	Weight (g)	Sex	Maturity	Gonad Wt (g)	GSI (%)	Eggs/g	Fecundity
1	49	473	F	5	31.45	6.649	30*1110	33,000
2	33	141	F	2	0.29	0.206		
3	32	158	M	1	0.08	0.051		
4	52	667	M	4	1.04	0.156		
5	78	2924	M	5	2	0.068		
6	39	246	F	5	4.5	1.829	3*821	2,463
7	52	596	F	5	14.5	2.433	13*986	12,818
8	51	581	F	5	30	5.164	28.5*1082	30,837
9	43	342	M	2	0.35	0.102		
10	46	427	F	3	4.91	1.15		
11	29	117	M	1	0.02	0.017		
12	47	442	M	4	1	0.226		
13	44	357	F	2	1.02	0.286		
14	88	3146	M	5	6.77	0.215		
15	57	796.5	M	4	1.14	0.143		
16	51	515.4	M	4	1.43	0.277		
17	59	936.4	M	4	1.91	0.204		
18	51	665	M	3	0.08	0.012		
19	45	348	F	2	0.95	0.273		
20	36	180.5	M	2	0.08	0.044		
21	56	791.5	M	2	0.1	0.013		
22	33	120.5	M	1	0.04	0.033		
23	33	117.8	F	1	0.02	0.017		
24	55	876	M	5	2.8	0.32		
25	47	578.4	F	5	44.57	7.706	43*1050	45,150
26	32	120.5	F	2	0.09	0.075		
27	43	366	F	2	1.22	0.333		
28	49	625	M	4	0.64	0.102		
29	41	228.5	M	4	0.51	0.223		
30	59	1031.5	M	4	2.37	0.23		
31	42	375.5	F	3	4.2	1.119		
32	36	209.5	F	5	30.35	14.49	28*900	25,200
33	33	140.5	M	2	0.1	0.071		
34	33	150	F	2	0.11	0.073		
35	65	1890	M	5	5.51	0.292		
36	54	940	F	5	18.43	1.961	17*662	11,254
37	44	372	F	5	25.52	6.86	24*880	21,120
38	60	1365.5	M	5	1.27	0.093		
39	32	128.5	M	2	0.1	0.078		
40	47	463	M	4	1.13	0.244		
41	51	510.5	M	5	1.6	0.313		
42	36	128.5	F	2	0.36	0.28		
43	49	471.5	M	2	0.52	0.11		
44	33	150	F	2	0.6	0.4		

45	39	278.5	F	3	1.67	0.6		
46	34	160	M	2	0.1	0.063		
47	38	242.5	F	3	2.14	0.882		
48	35	175.5	M	2	0.24	0.137		
49	45	457	M	3	0.42	0.092		
50	49	489	M	2	0.3	0.061		
51	60	1123	F	4	9.4	0.837		
52	76	3028	F	5	8.56	0.283		
53	39	368	F	3	0.58	0.158		
54	30	175	M	2	0.05	0.029		
55	56	720	F	4	6.03	0.838		
56	57	731	F	4	7.63	1.044		
57	70	2840	M	5	3.4	0.12		
58	40	381	M	2	0.13	0.034		
59	29	117	F	1	0.04	0.034		
60	57	721	F	3	1.3	0.18		
61	38	340	M	2	0.13	0.038		
62	45	440	M	2	0.26	0.059		
63	62	2230	F	3	0.85	0.038		
64	33	205	F	1	0.04	0.02		
65	63	2100	M	4	4.68	0.223		
66	70	2801	F	5	9.43	0.337		
67	71	2841	F	4	4.6	0.162		
68	28	99	M	1	0.02	0.02		
69	70	2759	F	5	15.6	0.565		
70	44	436	M	4	2.74	0.628		
71	42	400	F	3	1.3	0.325		
72	45	445	F	2	0.93	0.209		
73	67	2540	F	5	56.84	2.238	55*1108	60,940
74	64	2123	M	4	2.59	0.122		
75	65	2178	M	5	4.67	0.214		
76	48	589	F	5	46.8	7.946	45*1002	45,090
77	50	658	M	4	3.4	0.517		
78	49	615	F	3	0.29	0.047		
79	68	2254	M	3	0.83	0.037		
80	31	209	F	2	0.08	0.038		

Appendix XXVII: The length, weight, sex of fish, gonadal maturity stage, weight of gonads, gonado-somatic index (GSI), number of eggs per gram of eggs, and fecundity of fish samples of LKG population in January 2017.

SN	Length (Cm)	Weight (g)	Sex	Maturity Stage	Gonad weight (g)	GSI (%)	Number of eggs/g of eggs	Fecundity
1	34	134	M	2	0.23	0.172		
2	33	435	F	2	0.48	0.11		
3	31	115	F	2	0.41	0.357		
4	28	190	M	1	0.22	0.116		
5	38	142	F	5	6.37	4.486	758*5.1	3,866
6	34	110	M	1	0.09	0.082		
7	54	990	M	3	0.4	0.04		
8	53	791	M	5	2.3	0.291		
9	48	531	F	3	1.18	0.222		
10	38	425	F	5	12.08	2.842	825*11	9,075
11	39	235	M	1	0.2	0.085		
12	34	170	M	1	0.18	0.106		
13	60	2250	M	5	2.21	0.098		
14	60	2761	M	5	2.04	0.074		
15	59	1830	M	4	1.01	0.055		
16	61	1421	M	2	0.32	0.023		
17	53	1875	F	5	53.76	2.867	1026*52	53,352
18	45	816	M	4	0.84	0.103		
19	49	1485	M	4	2.7	0.182		
20	44	1285	F	5	32.53	2.532	964*31	29,884
21	35	675	M	3	0.19	0.028		
22	53	1635	M	4	0.96	0.059		
23	53	835	M	3	0.39	0.047		
24	60	2960	M	5	4.4	0.149		
25	52	1920	M	4	0.91	0.047		
26	53	606	M	5	1.36	0.224		
27	51	717	F	5	26.17	3.65	1084*25	27,100
28	49	285	F	5	19.26	6.758	1010*18	18,180
29	52	610	M	3	0.46	0.075		
30	49	810	M	5	0.97	0.12		
31	47.2	407	F	5	9.46	2.324	982*8	7,856
32	58	864	F	5	94.84	10.98	1048*93.1	97,569
33	44	646	M	2	0.13	0.02		
34	43	567	F	5	9.46	1.668	1058*8	8,464
35	42	621	F	5	11.61	1.87	1034*10.1	10,443
36	35	160.5	F	2	0.66	0.411		
37	49	656.5	M	5	1.48	0.225		
38	42	558	M	4	0.64	0.115		
39	47	539	F	5	10.12	1.878	770*9	6,930

40	57	1030	F	5	37.68	3.658	800*36	28,800
41	49	510.3	F	5	43.58	8.54	1108*42.3	46868
42	47	516.7	F	5	7.74	1.498	790*6.2	4,898
43	49	456.7	F	5	25.6	5.605	1188*24	28,512
44	48	495.5	M	5	1	0.202		
45	54	904.5	F	5	8	0.884	868*7	6,076
46	60	1975	F	5	20.76	1.051	992*19.1	18,947
47	67	2300	M	4	4.2	0.183		
48	32	188	M	1	0.07	0.037		
49	28	114	F	1	0.08	0.07		
50	34	190	F	1	0.08	0.042		
51	56	2403	F	5	31.6	1.315	1008*30.2	30,442
52	48	538	M	3	0.72	0.134		
53	49	548	F	2	0.53	0.097		
54	70	2571	M	3	1.86	0.072		
55	62	2015	M	5	4.57	0.227		
56	65	2386	M	4	2.4	0.101		
57	72	2624	F	5	38.28	1.459	800*37	29,600
58	45	594	F	5	11.65	1.961	720*10.1	7,272
59	30	170	F	1	0.05	0.029		
60	33	198	F	1	0.06	0.03		
61	38	286	F	2	0.16	0.056		
62	71	2754	F	3	2.56	0.093		
63	29	134	M	1	0.08	0.06		
64	54	1962	M	3	1.34	0.068		
65	43	574.8	F	2	0.93	0.162		
66	56	2101	F	2	0.81	0.039		
67	67	2683	M	3	1.53	0.057		
68	78	2976.6	F	3	3.2	0.108		
69	42	435.7	F	3	1.94	0.445		
70	40	392.5	M	3	0.84	0.214		

Appendix XXVIII: Length, maturity stage of gonads and maturity status of male *Clarias gariepinus* samples of the Lake Victoria (LVG) population. Fish samples were collected for 5 months, from septemeber 2016 to January 2017. All the fish with gonads in maturity stage 3

Serial Number	Length of Fish (Cm)	Maturity stage	Maturity status
1	73	5	Mature
2	25.5	2	Immature
3	28	2	Immature
4	24	2	Immature
5	21	1	Immature
6	30	1	Immature
7	41	3	Mature
8	23.5	1	Immature
9	23	1	Immature
10.	22.5	1	Immature
11.	107	5	Mature
12.	67	5	Mature
13.	38	2	Immature
14.	72	4	Mature
15.	78	5	Mature
16.	61	5	Mature
17.	86	5	Mature
18.	31	1	Immature
19.	58	4	Mature
20.	56	5	Mature
21.	38	1	Immature
22.	84	5	Mature
23.	45	2	Immature
24.	32	1	Immature
25.	72	4	Mature
26.	76	5	Mature
27.	61	4	Mature
28.	28	2	Immature
29.	71	5	Mature
30.	31	2	Immature
31.	34	1	Immature
32.	40	3	Mature
33.	65	4	Mature
34.	34	2	Immature
35.	55	4	Mature
36.	47	4	Mature
37.	39	2	Immature
38.	68	5	Mature
39.	31	1	Immature
40.	57	4	Mature
41.	54	3	Mature
42.	50	4	Mature

43.	61	5	mature
44.	30	1	Immature
45.	45	3	Mature
46.	40	2	Immature
47.	43	2	Immature
48.	67	4	Mature
49.	28	1	Immature
50.	30	1	Immature
51.	60	5	Mature
52.	79	5	Mature
53.	52	3	Mature
54.	55	4	Mature
55.	39	2	Immature
56.	55.5	5	Mature
57.	47.5	2	Immature
58.	49	2	Immature
59.	52	3	Mature
60.	50	3	Mature
61.	41	2	Immature
62.	36	1	Immature
63.	47	2	Immature
64.	77	5	Mature
65.	92	5	Mature
66.	75	5	Mature
67.	76	5	Mature
68.	75	4	Mature
69.	62	4	Mature
70.	56	3	Mature
71.	24	1	Immature
72.	30	1	Immature
73.	81	4	Mature
74.	73	5	Mature
75.	43	2	Immature
76.	59	2	Immature
77.	60	5	Mature
78.	44	2	Immature
79.	39	4	Mature
80.	43	2	Immature
81.	28	1	Immature
82.	37.6	4	Mature
83.	32	1	Immature
84.	29	1	Immature
85.	40	3	Mature
86.	44	2	Immature
87.	30	1	Immature
88.	26.5	2	Immature
89.	45	3	Mature
90.	29	1	Immature

91.	48	2	Immature
92.	33.6	1	Immature
93.	33	3	Mature
94.	34	1	Immature
95.	33	2	Immature
96.	33	1	Immature
97.	63	5	Mature
98.	47.5	5	Mature
99.	72	5	Mature
100.	56	3	Mature
101.	29	1	Immature
102.	48	3	Mature
103.	50	3	Mature
104.	28	1	Immature
105.	30	1	Immature
106.	43	2	Immature
107.	44	2	Immature
108.	56	3	Mature
109.	59	4	Mature
110.	51	4	Mature
111.	59	4	Mature
112.	61	3	Mature
113.	58	3	Mature
114.	72	3	Mature
115.	44	5	Mature
116.	31	1	Immature
117.	24	1	Immature
118.	39	1	Immature
119.	54	4	Mature
120.	59	3	Mature
121.	60	2	Immature
122.	54	4	Mature
123.	68	3	Mature
124.	43	4	Mature
125.	48	4	Mature
126.	69	4	Mature
127.	55	4	Mature
128.	44	4	Mature
129.	46	4	Mature
130.	77	4	Mature
131.	52	3	Mature
132.	29	1	Immature
133.	46	3	Mature
134.	41	2	Immature
135.	38	2	Immature
136.	59	5	Mature
137.	26	1	Immature
138.	27	1	Immature

139.	71	3	Mature
140.	61	4	Mature
141.	45	5	Mature
142.	43	4	Mature
143.	44	4	Mature
144.	68	5	Mature
145.	60	5	Mature
146.	52	5	Mature
147.	45.7	4	Mature
148.	43	5	Mature
149.	39	4	Mature
150.	46	5	Mature
151.	42	4	Mature
152.	43	5	Mature
153.	34	2	Immature
154.	68	5	Mature
155.	32	2	Immature
156.	60	3	Mature
157.	35	1	Immature
158.	34	1	Immature
159.	45	3	Mature
160.	41	2	Immature
161.	64	4	Mature
162.	48	4	Mature
163.	38	4	Mature
164.	39	2	Immature
165.	62	4	Mature
166.	59	3	Mature
167.	73	5	Mature
168.	76	4	Mature
166.	78	5	Mature
167.	73	4	Mature
168.	74	4	Mature
169.	75	5	Mature
170.	66	3	Mature
171.	75	5	Mature
172.	42	2	Immature
173.	69	4	Mature
174.	66	4	Mature
175.	61	4	Mature
176.	79	5	Mature
177.	87	5	Mature
178.	75	5	Mature
179.	60	4	Mature
180.	72	5	Mature
181.	79	4	Mature
182.	25	1	Immature
183.	46	4	Mature

184.	47	2	Immature
185.	37	2	Immature
186.	34	1	Immature
187.	44	2	Immature
188.	22	1	Immature
189.	21	1	Immature
190.	54	3	Mature
191.	69	4	Mature
192.	73	5	Mature
193.	71	4	Mature
194.	52	3	Mature
195.	49	4	Mature
196.	56	3	Mature
197.	56	4	Mature
198.	67	3	Mature
199.	69	4	Mature
200.	30	1	Immature
201.	56	5	Mature
202.	51	3	Mature
203.	65	5	Mature
204.	71	5	Mature
205.	26	1	Immature
206.	58	3	Mature
207.	60	4	Mature
208.	60	4	Mature
209.	49	2	Immature
210.	34	2	Immature
211.	56	5	Mature
212.	50	2	Immature
213.	46	2	Immature
214.	33	2	Immature
215.	35	2	Immature
216.	45	1	Immature
217.	40	2	Immature
218.	35	2	Immature
219.	76	4	Mature
220.	31	2	Immature
221.	28	1	Immature
222.	43	2	Immature
223.	50	3	Immature
224.	36	2	Immature
225.	71	5	Immature
226.	42	3	Immature
227.	56	3	Immature
228.	40	2	Immature
229.	40	2	Immature
230.	60	4	Immature
231.	42	2	Immature

232.	50	3	Immature
233.	46	2	Immature
234.	43	4	Immature
235.	36	2	Immature
236.	28	1	Immature
237.	40	2	Immature
238.	39	2	Immature
239.	77	3	Immature
240.	69	4	Immature
241.	32	1	Immature
242.	37	2	Immature
243.	54	3	Immature
244.	27	1	Immature

Appendix XXIX: Length, gonad maturity stages and maturity status of Clarias gariepinus female fish samples of the Lake Victoria (LVG) population. Fish samples were collected for 5 months, from September 2016 to January 2017. All the fish with gonads in maturity stag

Serial Number	Length of Fish (Cm)	Maturity stage	Maturity status
1	67	5	Mature
2	58	3	Mature
3	85	5	Mature
4	28	1	Immature
5	24	2	Immature
6	31	1	Immature
7	63	5	Mature
8	40	2	Immature
9	29	1	Immature
10.	29	1	Immature
11.	48	2	Immature
12.	35	2	Immature
13.	32	2	Immature
14.	31	1	Immature
15.	68	5	Mature
16.	52.5	3	Mature
17.	53	5	Mature
18.	69	5	Mature
19.	53	2	Immature
20.	32	1	Immature
21.	28	1	Immature
22.	68	5	Mature
23.	54	3	Mature
24.	60	4	Mature
25.	72	5	Mature
26.	64	5	Mature
27.	44	2	Immature
28.	74	5	Mature
29.	39	3	Mature
30.	48	3	Mature
31.	59	3	Mature
32.	43	3	Mature
33.	29	1	Immature
34.	27	2	Immature
35.	42	2	Immature
36.	31	2	Immature

37.	60	4	Mature
38.	28	2	Immature
39.	33	2	Immature
40.	54	3	Mature
41.	60	4	Mature
42.	75	4	Mature
43.	50	3	Mature
44.	34	2	Immature
45.	27	1	Immature
46.	61	5	Mature
47.	30	1	Immature
48.	28	1	Immature
49.	47	3	Mature
50.	42	2	Immature
51.	31	1	Immature
52.	34	2	Immature
53.	59	4	Mature
54.	33	2	Immature
55.	65	5	Mature
56.	43	2	Immature
57.	58	4	Mature
58.	50	2	Immature
59.	46	2	Immature
60.	56.5	4	Mature
61.	49	2	Immature
62.	47	2	Immature
63.	62	5	Mature
64.	41	2	Immature
65.	65	5	Mature
66.	59	4	Mature
67.	68	5	Mature
68.	71	5	Mature
69.	46	2	Immature
70.	42	2	Immature
71.	58	2	Immature
72.	57	2	Immature
73.	32	1	Immature
74.	38.5	2	Immature
75.	56	2	Immature
76.	35.4	1	Immature
77.	37	2	Immature
78.	28	1	Immature

79.	65	5	Mature
80.	67	3	Mature
81.	74	5	Mature
82.	61	5	Mature
83.	66	5	Mature
84.	61	3	Mature
85.	36	2	Immature
86.	35	2	Immature
87.	31	2	Immature
88.	57	2	Immature
89.	40	2	Immature
90.	37	2	Immature
91.	32.5	1	Immature
92.	34.5	1	Immature
93.	39	2	Immature
94.	41	2	Immature
95.	42	3	Mature
96.	30	1	Immature
97.	45	2	Immature
98.	74	5	Mature
99.	72	5	Mature
100.	46	3	Mature
101.	60	5	Mature
102.	77	5	Mature
103.	70	5	Mature
104.	30	2	Immature
105.	61	4	Mature
106.	79	4	Mature
107.	36	2	Immature
108.	32	1	Immature
109.	35	2	Immature
110.	39	2	Immature
111.	73	5	Mature
112.	71	5	Mature
113.	63	5	Mature
114.	58.5	4	Mature
115.	60	5	Mature
116.	37	2	Immature
117.	68	3	Mature
118.	43	2	Immature
119.	28	1	Immature
120.	32	2	Immature

121.	64	5	Mature
122.	53	5	Mature
123.	67	4	Mature
124.	63	5	Mature
125.	28	1	Immature
126.	58	2	Immature
127.	44	5	Mature
128.	76	3	Mature
129.	28	1	Immature
130.	40.5	5	Mature
131.	42	4	Mature
132.	41	5	Mature
133.	37	4	Mature
134.	43	5	Mature
135.	38	5	Mature
136.	44	5	Mature
137.	51	4	Mature
138.	47	5	Mature
139.	40	2	Immature
140.	66	4	Mature
141.	39.5	2	Immature
142.	66	5	Mature
143.	55	3	Mature
144.	73	4	Mature
145.	69	5	Mature
146.	33	2	Immature
147.	54	2	Immature
148.	40	5	Mature
149.	46	2	Immature
150.	67.5	5	Mature
151.	43	4	Mature
152.	30	1	Immature
153.	49.2	2	Immature
154.	78	3	Mature
155.	51	2	Immature
156.	27	1	Immature
157.	56	2	Immature
158.	26	1	Immature
159.	28	1	Immature
160.	56	3	Mature
161.	68	3	Mature
162.	65	4	Mature

163.	63	5	Mature
164.	36	2	Immature
165.	51	3	Mature
166.	59	3	Mature
167.	43	2	Immature
168.	66	5	Mature
166.	75	5	Mature
167.	27	1	Immature
168.	49	2	Immature
169.	45	2	Immature
170.	38	2	Immature
171.	68	5	Mature
172.	66	2	Immature
173.	76	4	Mature
174.	65	2	Immature
175.	36	2	Immature
176.	42	2	Immature
177.	35	2	Immature
178.	64	3	Mature
179.	26	1	Immature
180.	23	1	Immature
181.	21.5	1	Immature
182.	60	2	Immature
183.	48	2	Immature
184.	40	2	Immature
185.	36	2	Immature
186.	37	2	Immature
187.	29	1	Immature
188.	42	2	Immature
189.	45	2	Immature
190.	72	5	Mature
191.	34	2	Immature
192.	76	5	Mature
193.	79	4	Mature
194.	28	1	Immature
195.	54	3	Mature
196.	56	4	Mature
197.	31	2	Immature
198.	61	2	Immature
199.	73	5	Mature
200.	78	4	Mature
201.	28	1	Immature

202.	24	1	Immature
203.	23	1	Immature
204.	27	1	Immature
205.	26	1	Immature
206.	35	2	Immature
207.	39	2	Immature
208.	56	3	Mature
209.	39	1	Immature
210.	43	2	Immature
211.	44	2	Immature
212.	64	4	Mature
213.	39	2	Immature
214.	36	3	Mature
215.	33	2	Immature
216.	31	2	Immature
217.	25	1	Immature
218.	32	1	Immature
219.	44	2	Immature
220.	44	5	Mature
221.	37	1	Immature
222.	44	2	Immature
223.	33	1	Immature
224.	66	5	Mature
225.	59	4	Mature
226.	72	5	Mature
227.	49	2	Immature
228.	61	4	Mature
229.	30	1	Immature
230.	41	2	Immature
231.	39	2	Immature
232.	75	4	Mature
233.	37	2	Immature
234.	30	2	Immature
235.	77	4	Mature
236.	47	2	Immature
237.	53	3	Mature
238.	69	5	Mature
239.	36	5	Mature
240.	38.5	2	Immature
241.	34	2	Immature
242.	30	1	Immature
243.	60	4	Mature

244.	63	5	Mature
245.	38	2	Immature
246.	28	1	Immature
247.	62	5	Mature
248.	60	5	Mature
249.	46	3	Mature

Appendix XXX: Length, gonad maturity stages and maturity status of *Clarias gariepinus* male fish samples of the Lake Baringo (LBA) population. Fish samples were collected for 5 months, from September 2016 to January 2017. All the fish with gonads in maturity stage 3

Serial Number	Length of Fish (Cm)	Maturity stage	Maturity status
1	56	4	Mature
2	49	3	Mature
3	41.5	3	Mature
4	78.5	2	Immature
5	54	4	Mature
6	74	4	Mature
7	67.5	3	Mature
8	37	1	Immature
9	54	2	Immature
10.	44.5	2	Immature
11.	44	2	Immature
12.	45	2	Immature
13.	67.5	3	Mature
14.	65	5	Mature
15.	65.5	2	Immature
16.	54	2	Immature
17.	62	5	Mature
18.	58.5	5	Mature
19.	63	2	Immature
20.	56	2	Immature
21.	62.5	4	Mature
22.	67	3	Mature
23.	71	2	Immature
24.	53	4	Mature
25.	69	2	Immature
26.	75.5	5	Mature
27.	66.5	5	Mature
28.	60	3	Mature
29.	37	1	Immature
30.	35.5	1	Immature
31.	71	2	Immature
32.	69	5	Mature
33.	57	4	Mature
34.	56	3	Mature
35.	58.5	2	Immature
36.	62	2	Immature

37.	31	1	Immature
38.	44.5	2	Immature
39.	60	5	Mature
40.	49	2	Immature
41.	61	3	Mature
42.	46	4	Mature
43.	51	4	Mature
44.	57	2	Immature
45.	33.5	1	Immature
46.	63	4	Mature
47.	65	1	Immature
48.	77.5	5	Mature
49.	46	2	Immature
50.	58	2	Immature
51.	50	2	Immature
52.	49	3	Mature
53.	31	1	Immature
54.	36	1	Immature
55.	31	5	Mature
56.	30	2	Immature
57.	37.5	2	Immature
58.	62	2	Immature
59.	72	4	Mature
60.	53	3	Mature
61.	34	2	Immature
62.	80	5	Mature
63.	46	2	Immature
64.	59.5	3	Mature
65.	76.5	2	Immature
66.	61	4	Mature
67.	53	1	Immature
68.	75	4	Mature
69.	47	1	Immature
70.	39	2	Immature
71.	43	2	Immature
72.	43	1	Immature
73.	34	2	Immature
74.	35	1	Immature
75.	29	1	Immature
76.	37	3	Mature
77.	60	3	Mature
78.	40	2	Immature

79.	76	5	Mature
80.	30-	1	Immature
81.	28.5	1	Immature
82.	60.5	4	Mature
83.	43	3	Mature
84.	37	2	Immature
85.	55	4	Mature
86.	83	5	Mature
87.	54	3	Mature
88.	56	2	Immature
89.	79	4	Mature
90.	43	2	Immature
91.	55	4	Mature
92.	53	4	Mature
93.	43	4	Mature
94.	66	4	Mature
95.	78	5	Mature
96.	76	5	Mature
97.	52	2	Immature
98.	79	4	Mature
99.	83	5	Mature
100.	74	2	Immature
101.	79	4	Mature
102.	80	4	Mature
103.	56	4	Mature
104.	35	1	Immature
105.	65	3	Mature
106.	45	2	Immature
107.	56	2	Immature
108.	49	5	Mature
109.	54	3	Mature
110.	67	4	Mature
111.	32	1	Immature
112.	50	3	Mature
113.	74	3	Mature
114.	65	3	Mature
115.	75	5	Mature
116.	39	4	Mature
117.	49	3	Mature
118.	41	4	Mature
119.	52	2	Immature
120.	50	2	Immature

121.	46	1	Immature
122.	45	2	Immature
123.	45	2	Immature
124.	84	3	Mature
125.	47	2	Immature
126.	41	1	Immature
127.	37.5	2	Immature
128.	64	4	Mature
129.	44	4	Mature
130.	41	2	Immature
131.	35.5	1	Immature
132.	64	3	Immature
133.	64	2	Immature
134.	59	2	Immature
135.	46	5	Mature
136.	58	4	Mature
137.	64	5	Mature
138.	65	4	Mature
139.	58	4	Mature
140.	74	4	Mature
141.	75	4	Mature
142.	77	4	Mature
143.	60	3	Mature
144.	50	3	Mature
145.	38	4	Mature
146.	72	3	Mature
147.	68	3	Mature
148.	85	5	Mature
149.	83	3	Mature
150.	70	3	Mature
151.	84	3	Mature
152.	78	3	Mature
153.	40	3	Mature
154.	62	3	Mature
155.	62	4	Mature
156.	49	3	Mature
157.	34	2	Immature
158.	80	5	Mature
159.	65	4	Mature
160.	68	4	Mature
161.	68	4	Mature
162.	73	5	Mature

163.	83	5	Mature
164.	82	5	Mature
165.	88	5	Mature
166.	72	4	Mature
167.	95	5	Mature
168.	41	4	Mature
166.	100	5	Mature
167.	94	5	Mature
168.	87	4	Mature
169.	93	4	Mature
170.	95	5	Mature
171.	96	5	Mature
172.	87	5	Mature
173.	63	5	Mature
174.	82.6	5	Mature
175.	45	4	Mature
176.	58	2	Immature
177.	66	4	Mature
178.	72.5	5	Mature
179.	56	4	Mature
180.	48	4	Mature
181.	49	5	Mature
182.	46	4	Mature
183.	43	4	Mature
184.	59	4	Mature
185.	44	4	Mature
186.	72.5	3	Mature
187.	70.5	3	Mature
188.	86	3	Mature
189.	48.5	2	Immature
190.	46	3	Mature
191.	44	3	Mature
192.	55.5	4	Mature
193.	56.5	3	Mature
194.	70	3	Mature
195.	71	3	Mature
196.	76.5	5	Mature
197.	76	5	Mature
198.	32	1	Immature
199.	49	1	Immature
200.	67.5	3	Mature
201.	84	4	Mature

202.	73	2	Immature
203.	65	2	Immature
204.	67	2	Immature
205.	47	2	Immature
206.	60	1	Immature
207.	51	2	Immature
208.	61	2	Immature
209.	61.5	4	Mature
210.	62.5	2	Immature
211.	77	4	Mature
212.	33	1	Immature
213.	32	1	Immature
214.	40	1	Immature
215.	69	3	Mature
216.	58	5	Mature
217.	44	2	Immature
218.	41	2	Immature
219.	42	2	Immature
220.	52	4	Mature
221.	57	3	Immature
222.	56	5	Mature
223.	43	2	Immature
224.	28	1	Immature
225.	40	1	Immature
226.	33	2	Immature
227.	44	2	Immature
228.	53	2	Immature
229.	63	3	Mature
230.	36	2	Immature
231.	43	3	Mature
232.	28	2	Immature
233.	45	3	Mature
234.	35	1	Immature
235.	38	2	Immature
236.	52	4	Mature
237.	60	3	Mature
238.	62	1	Immature
239.	33	1	Immature
240.	41	4	Mature
241.	72	5	Mature
242.	70	5	Mature
243.	38	4	Mature

244.	33	2	Immature
245.	42	2	Immature
246.	32	1	Immature
247.	61	2	Immature
248.	50	2	Immature
249.	45	4	Mature
250.	39	1	Immature
251.	47	4	Mature
252.	45	2	Immature
253.	58	3	Mature
254.	56	2	Immature
255.	68	4	Mature
256.	46	3	Mature
257.	78	4	Mature
258.	56	3	Mature

Appendix XXXI: Length, gonad maturity stages and maturity status of *Clarias gariepinus* **female fish samples of the Lake Baringo (LBA) population. Fish samples were collected for 5 months, from September 2016 to January 2017. All the fish with gonads in maturity stage**

Serial Number	Length of Fish (Cm)	Maturity stage	Maturity status
1	58	5	Mature
2	85.5	5	Mature
3	90.5	5	Mature
4	80	5	Mature
5	72	2	Immature
6	52	2	Immature
7	49.5	2	Immature
8	57.5	5	Mature
9	51.5	2	Immature
10.	72	4	Mature
11.	49	2	Immature
12.	38	2	Immature
13.	52.5	2	Immature
14.	35	1	Immature
15.	67	5	Mature
16.	60	2	Immature
17.	68	5	Mature
18.	46	2	Immature
19.	57	2	Immature
20.	82	4	Mature
21.	52	2	Immature
22.	68.5	5	Mature
23.	77.4	5	Mature
24.	48	4	Mature
25.	49.5	2	Immature
26.	58	3	Mature
27.	44.5	4	Mature
28.	50	2	Immature
29.	50.4	5	Mature
30.	52.5	5	Mature
31.	50.5	2	Immature
32.	50.5	5	Mature
33.	68.5	5	Mature
34.	61	2	Immature
35.	59.5	5	Mature

36.	66	2	Immature
37.	58.5	5	Mature
38.	67	2	Immature
39.	72	4	Mature
40.	67	5	Mature
41.	36	1	Immature
42.	44.5	2	Immature
43.	68	5	Mature
44.	68.5	4	Mature
45.	59	2	Immature
46.	63	5	Mature
47.	53	5	Mature
48.	51	2	Immature
49.	58.5	2	Immature
50.	61	5	Mature
51.	32	1	Immature
52.	31.5	1	Immature
53.	46	2	Immature
54.	75	4	Mature
55.	41	5	Mature
56.	54	5	Mature
57.	62.5	5	Mature
58.	57.5	2	Immature
59.	34	1	Immature
60.	37	1	Immature
61.	45.5	5	Mature
62.	35	1	Immature
63.	57	4	Mature
64.	38	2	Immature
65.	42	2	Immature
66.	50	2	Immature
67.	50.4	2	Immature
68.	33	4	Mature
69.	56	5	Mature
70.	41	2	Immature
71.	37	2	Immature
72.	36	2	Immature
73.	40	4	Mature
74.	76	3	Mature
75.	52	2	Immature
76.	50.5	2	Immature
77.	56	5	Mature

78.	32.5	2	Immature
79.	36	1	Immature
80.	35	2	Immature
81.	67	5	Mature
82.	53	2	Immature
83.	43	2	Immature
84.	32	1	Immature
85.	37	1	Immature
86.	33.5	2	Immature
87.	35	2	Immature
88.	33	2	Immature
89.	36.5	2	Immature
90.	76	5	Mature
91.	46	5	Mature
92.	46.5	2	Immature
93.	41	2	Immature
94.	48	2	Immature
95.	45.5	4	Mature
96.	40.5	2	Immature
97.	64	2	Immature
98.	69	2	Immature
99.	57.5	2	Immature
100.	58	2	Immature
101.	39.5	2	Immature
102.	43	1	Immature
103.	36	2	Immature
104.	35	2	Immature
105.	46	1	Immature
106.	38.5	2	Immature
107.	48	3	Mature
108.	41	2	Immature
109.	56	5	Mature
110.	70	4	Mature
111.	50	2	Immature
112.	54	5	Mature
113.	59	2	Immature
114.	62	5	Mature
115.	45	3	Mature
116.	53	5	Mature
117.	48	2	Immature
118.	32.5	1	Immature
119.	53	3	Mature

120.	65	5	Mature
121.	48	4	Mature
122.	29.5	1	Immature
123.	30	1	Immature
124.	75	6	Mature
125.	53	2	Immature
126.	62	3	Mature
127.	62	3	Mature
128.	61.5	5	Mature
129.	63	3	Mature
130.	56	5	Mature
131.	49	2	Immature
132.	58	5	Mature
133.	84	6	Mature
134.	37	2	Immature
135.	55	2	Immature
136.	82	5	Mature
137.	44	2	Immature
138.	70	4	Mature
139.	76	5	Mature
140.	73	5	Mature
141.	51	3	Mature
142.	56	4	Mature
143.	42	2	Immature
144.	42	2	Immature
145.	44.5	2	Immature
146.	46	2	Immature
147.	38	2	Immature
148.	37	2	Immature
149.	67	5	Mature
150.	64	3	Mature
151.	37	2	Immature
152.	38	2	Immature
153.	41	2	Immature
154.	29	1	Immature
155.	79	5	Mature
156.	53	2	Immature
157.	50	3	Mature
158.	53	2	Immature
159.	51	2	Immature
160.	50	4	Mature
161.	36	2	Immature

162.	43	4	Mature
163.	52	2	Immature
164.	35	1	Immature
165.	63	3	Mature
166.	58.5	5	Mature
167.	60	5	Mature
168.	65	5	Mature
166.	59	5	Mature
167.	52	5	Mature
168.	55	5	Mature
169.	63	5	Mature
170.	48	3	Mature
171.	37.5	2	Immature
172.	45	2	Immature
173.	58	3	Mature
174.	69	5	Mature
175.	72	5	Mature
176.	50	3	Mature
177.	40	2	Immature
178.	46	2	Immature
179.	56	5	Mature
180.	60	5	Mature
181.	66	5	Mature
182.	79	5	Mature
183.	78	5	Mature
184.	88.4	5	Mature
185.	49	5	Mature
186.	54	5	Mature
187.	51	5	Mature
188.	50	4	Mature
189.	40	5	Mature
190.	43	4	Mature
191.	51.5	2	Immature
192.	51.5	3	Mature
193.	70	3	Mature
194.	53	2	Immature
195.	42	3	Mature
196.	40	3	Mature
197.	58	3	Mature
198.	74	4	Mature
199.	54	4	Mature
200.	74	5	Mature

201.	42	2	Immature
202.	55	2	Immature
203.	84	6	Mature
204.	48	5	Mature
205.	46	1	Immature
206.	45	5	Mature
207.	58	2	Immature
208.	40	2	Immature
209.	63	3	Mature
210.	56	2	Immature
211.	49	2	Immature
212.	62	5	Mature
213.	58	3	Mature
214.	32	1	Immature
215.	67	3	Mature
216.	47	2	Immature
217.	36	2	Immature
218.	45	2	Immature
219.	37	2	Immature
220.	56	3	Mature
221.	71	4	Mature
222.	74	5	Mature
223.	59	5	Mature
224.	51	2	Immature
225.	46	1	Immature
226.	37	6	Mature
227.	48	2	Immature
228.	47.5	2	Immature
229.	50	2	Immature
230.	62	5	Mature
231.	70	4	Mature
232.	37	2	Immature
233.	30	2	Immature
234.	34	2	Immature
235.	52	4	Mature
236.	60	3	Mature
237.	45	2	Immature
238.	76	3	Mature
239.	30	1	Immature
240.	56	5	Mature
241.	47	1	Immature
242.	40	3	Mature

243.	46	2	Immature
244.	58	3	Mature
245.	60	4	Mature
246.	46	2	Immature
247.	44	2	Immature
248.	84	5	Mature
249.	67	5	Mature
250.	56	2	Immature
251.	44	3	Mature
252.	38	2	Immature
253.	74	3	Mature
254.	44	2	Immature
253.	35	1	Immature
254.	60	3	Mature
255.	52	3	Mature
256.	72	4	Mature
257.	38	2	Immature
258.	35	1	Immature
259.	51	3	Mature
260.	50	5	Mature
261.	32	1	Immature
262.	63	5	Mature

Appendix XXXII: Length, gonad maturity stages and maturity status of *Clarias gariepinus* male fish samples of the Lake Kanyaboli (LKG) population. Fish samples were collected for 5 months, from September 2016 to January 2017. All the fish with gonads in maturity stage

Serial Number	Length of Fish (Cm)	Maturity stage	Maturity status
1	52	4	Mature
2	41	4	Mature
3	37	1	Immature
4	54	4	Mature
5	43.5	4	Mature
6	57	4	Mature
7	39	3	Mature
8	56	3	Mature
9	70	5	Mature
10.	44	2	Immature
11.	40	2	Immature
12.	38	2	Immature
13.	51	4	Mature
14.	34	1	Immature
15.	33	1	Immature
16.	52	4	Mature
17.	76	5	Mature
18.	30	1	Immature
19.	59	4	Mature
20.	33	3	Mature
21.	53	4	Mature
22.	66	3	Mature
23.	82	5	Mature
24.	74	3	Mature
25.	41	2	Immature
26.	27.8	1	Immature
27.	40.2	4	Mature
28.	43.1	3	Mature
29.	32	2	Immature
30.	53	5	Mature
31.	52	4	Mature
32.	41	3	Mature
33.	41	2	Immature
34.	35.6	2	Immature
35.	56.7	5	Mature
36.	46	4	Mature

37.	30	1	Immature
38.	23	1	Immature
39.	66	5	Mature
40.	63	5	Mature
41.	67	4	Mature
42.	45	2	Immature
43.	57	3	Mature
44.	41	2	Immature
45.	42	2	Immature
46.	34	2	Immature
47.	28	1	Immature
48.	70	3	Mature
49.	56	2	Immature
50.	52	4	Mature
51.	47	3	Mature
52.	37	2	Immature
53.	49	5	Mature
54.	44	2	Immature
55.	40	3	Mature
56.	32	1	Immature
57.	31	2	Immature
58.	49	2	Immature
59.	49	3	Mature
60.	36	3	Mature
61.	71	4	Mature
62.	42	3	Mature
63.	82	5	Mature
64.	36	2	Immature
65.	40	2	Immature
66.	39	2	Immature
67.	41	5	Mature
68.	43	4	Mature
69.	31	1	Immature
70.	50.1	4	Mature
71.	38	2	Immature
72.	36	1	Immature
73.	43	4	Mature
74.	29	1	Immature
75.	54	4	Mature
76.	52	4	Mature
77.	45	3	Mature
78.	41	2	Immature

79.	39.2	2	Immature
80.	46	2	Immature
81.	51	3	Mature
82.	55	4	Mature
83.	52	4	Mature
84.	62	5	Mature
85.	56	4	Mature
86.	55	5	Mature
87.	30	3	Mature
88.	59	4	Mature
89.	33	3	Mature
90.	42	2	Immature
91.	30	1	Immature
92.	60	3	Mature
93.	78	4	Mature
94.	70	5	Mature
95.	33	2	Immature
96.	34	2	Immature
97.	54	3	Mature
98.	48	2	Immature
99.	31	1	Immature
100.	28	2	Immature
101.	32	1	Immature
102.	52	4	Mature
103.	78	5	Mature
104.	43	2	Immature
105.	29	1	Immature
106.	47	4	Mature
107.	88	5	Mature
108.	57	4	Mature
109.	51	4	Mature
110.	59	4	Mature
111.	51	3	Mature
112.	36	2	Immature
113.	56	2	Immature
114.	33	1	Immature
115.	55	4	Mature
116.	49	4	Mature
117.	41	4	Mature
118.	59	4	Mature
119.	33	2	Immature
120.	33	2	Immature

121.	65	5	Mature
122.	60	4	Mature
123.	32	2	Immature
124.	47	4	Mature
125.	51	4	Mature
126.	49	2	Immature
127.	34	2	Immature
128.	35	2	Immature
129.	45	3	Mature
130.	49	2	Immature
131.	30	2	Immature
132.	70	5	Mature
133.	40	2	Immature
134.	38	2	Immature
135.	45	2	Immature
136.	63	4	Mature
137.	28	1	Immature
138.	44	4	Mature
139.	64	4	Mature
140.	65	5	Mature
141.	50	4	Mature
142.	68	3	Mature
143.	34	2	Immature
144.	28	1	Immature
145.	34	1	Immature
146.	54	3	Mature
147.	53	5	Mature
148.	39	1	Immature
149.	34	1	Immature
150.	60	5	Mature
151.	60	5	Mature
152.	59	4	Mature
153.	61	2	Immature
154.	45	4	Mature
155.	49	4	Mature
156.	35	3	Mature
157.	53	4	Mature
158.	53	3	Mature
159.	60	5	Mature
160.	52	4	Mature
161.	53	4	Mature
162.	52	3	Mature

163.	49	4	Mature
164.	44	2	Immature
165.	49	5	Mature
166.	42	4	Mature
167.	48	5	Mature
168.	67	4	Mature
166.	32	1	Immature
167.	48	3	Mature
168.	70	3	Mature
169.	62	4	Mature
170.	65	4	Mature
171.	29	1	Immature
172.	54	3	Mature
173.	67	3	Mature
174.	40	3	Mature

Appendix XXXIII: Length, gonad maturity stages and maturity status of *Clarias gariepinus* female fish samples of the Lake Kanyaboli (LKG) population. Fish samples were collected for 5 months, from September 2016 to January 2017. All the fish with gonads in maturity stage.

Serial Number	Length of Fish (Cm)	Maturity stage	Maturity status
1	59	3	Mature
2	40.1	2	Immature
3	37	2	Immature
4	33	1	Immature
5	28	1	Immature
6	27	1	Immature
7	56	5	Mature
8	28	2	Immature
9	49	2	Immature
10.	61	4	Mature
11.	35	2	Immature
12.	45	3	Mature
13.	63	3	Mature
14.	26	1	Immature
15.	34	1	Immature
16.	39	2	Immature
17.	45	5	Mature
18.	51	4	Mature
19.	54	5	Mature
20.	29	1	Immature
21.	63	5	Mature
22.	31	1	Immature
23.	49	4	Mature
24.	48	3	Mature
25.	57	5	Mature
26.	44	3	Mature
27.	27	1	Immature
28.	67	5	Mature
29.	28	1	Immature
30.	41	3	Mature
31.	64	4	Mature
32.	40	2	Immature
33.	29	1	Immature
34.	60	3	Mature
35.	37	2	Immature
36.	37	2	Immature

37.	37	2	Immature
38.	31	2	Immature
39.	25.6	2	Immature
40.	39.8	4	Mature
41.	37	2	Immature
42.	34	2	Immature
43.	45	5	Mature
44.	43	5	Mature
45.	43	5	Mature
46.	62	5	Mature
47.	54	3	Mature
48.	51	3	Mature
49.	33	2	Immature
50.	21	1	Immature
51.	69	4	Mature
52.	28	2	Immature
53.	26	1	Immature
54.	24	1	Immature
55.	42	2	Immature
56.	60	5	Mature
57.	65	5	Mature
58.	50	5	Mature
59.	40	5	Mature
60.	35	2	Immature
61.	73	4	Mature
62.	27	1	Immature
63.	52	5	Mature
64.	53	5	Mature
65.	35	2	Immature
66.	62	4	Mature
67.	43	3	Mature
68.	48	2	Immature
69.	60	5	Mature
70.	45	5	Mature
71.	55.2	5	Mature
72.	47	5	Mature
73.	49	4	Mature
74.	37	5	Mature
75.	44	5	Mature
76.	41	3	Mature
77.	35	3	Mature
78.	28	1	Immature

79.	53	5	Mature
80.	45	5	Mature
81.	64	4	Mature
82.	50	5	Mature
83.	51	2	Immature
84.	49	3	Mature
85.	42	2	Immature
86.	47	3	Mature
87.	48.5	3	Mature
88.	42	5	Mature
89.	32	1	Immature
90.	40	2	Immature
91.	32	2	Immature
92.	35	1	Immature
93.	23	1	Immature
94.	44	2	Immature
95.	28	2	Immature
96.	56	5	Mature
97.	62	4	Mature
98.	65	5	Mature
99.	59	4	Mature
100.	60	3	Mature
101.	32	2	Immature
102.	57	4	Mature
103.	39	3	Mature
104.	78	5	Mature
105.	49	5	Mature
106.	33	2	Immature
107.	39	5	Mature
108.	52	5	Mature
109.	51	5	Mature
110.	46	3	Mature
111.	44	2	Immature
112.	45	2	Immature
113.	33	1	Immature
114.	47	5	Mature
115.	32	2	Immature
116.	43	2	Immature
117.	42	3	Mature
118.	36	5	Mature
119.	33	2	Immature
120.	54	5	Mature

121.	44	5	Mature
122.	36	2	Immature
123.	33	2	Immature
124.	39	3	Mature
125.	38	3	Mature
126.	60	4	Mature
127.	76	4	Mature
128.	39	3	Mature
129.	56	4	Mature
130.	57	4	Mature
131.	29	1	Immature
132.	57	3	Mature
133.	62	3	Mature
134.	33	1	Immature
135.	70	4	Mature
136.	71	4	Mature
137.	70	4	Mature
138.	42	3	Mature
139.	45	2	Immature
140.	67	5	Mature
141.	48	5	Mature
142.	49	3	Mature
143.	31	2	Immature
144.	33	2	Immature
145.	31	2	Immature
146.	38	5	Mature
147.	48	3	Mature
148.	38	5	Mature
149.	53	5	Mature
150.	44	5	Mature
151.	51	5	Mature
152.	49	5	Mature
153.	47.2	5	Mature
154.	58	5	Mature
155.	43	5	Mature
156.	42	5	Mature
157.	35	2	Immature
158.	47	5	Mature
159.	57	5	Mature
160.	49	5	Mature
161.	47	5	Mature
162.	49	5	Mature

163.	54	5	Mature
164.	60	5	Mature
165.	28	1	Immature
166.	34	1	Immature
167.	56	5	Mature
168.	49	2	Immature
166.	72	5	Mature
167.	45	5	Mature
168.	30	1	Immature
169.	33	1	Immature
170.	38	2	Immature
171.	71	3	Mature
172.	43	2	Immature
173.	56	2	Immature
174.	78	3	Mature
175.	42	3	Mature