

Morphological and Molecular Systematics of Freshwater Fish Diversity and Physico-chemical Parameters of Jebba Hydro- electric Power Reservoir, Nigeria

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06/55EK081

B.Sc. (ILORIN) 2010; M.Sc. (IBADAN) 2015

**A Thesis Submitted to the Department of Zoology, Faculty of Life Sciences, University of
Ilorin, Ilorin, Nigeria, in Partial Fulfillment of the Requirements for the Award of the Doctor
of Philosophy (Ph.D.) Degree in Zoology**

January, 2021

CERTIFICATION

We certify that this work was carried out by Mr. Segun Olayinka Oladipo, having met the requirement of the Department of Zoology, and Post Graduate School, University of Ilorin, Ilorin, Nigeria, for the award of the degree of Doctor of Philosophy (Ph.D.) in Zoology.

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DEDICATION

This research work is dedicated to my lovely wife, Mrs. Roseline Adeshike Oladipo and my son, Enoch Olamide Oladipo.

DECLARATION

I, Segun Olayinka Oladipo hereby declare that this thesis entitled “Morphological and Molecular Systematics of Freshwater Fish Diversity and Physico-chemical Parameters in Jebba Hydro-electric Power Reservoir, Nigeria” is a record of my research work. It has neither been presented nor accepted in any previous application for a higher degree. All sources of information have been specifically acknowledged.

In addition, the research work has been ethically approved by the Faculty of Life Sciences Ethical Review Committee.

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ACKNOWLEDGEMENTS

I am grateful to the God Almighty, the Alpha and Omega that helps me through the period of research.

My gratitude goes to my supervisor, Professor M.K. Mustapha for his guidance, patience, mentorship and input through the period of my study and to my co-supervisor, Dr. O.A. Iyiola, for his immersed contribution towards this research.

I am also grateful to Dr. M. L. Nneji and Dr. Charles Adeola for their contributions and opportunity to run my molecular analysis in Kuming Institute of Zoology, China. I also sincerely thank them for their help in teaching me how to carry out the statistical analyses of the molecular data.

My gratitude goes to Prof. J.S. Omotosho, Prof. U.S. Ugbomoiko, Prof. Gladys C. Nze and Prof. A.T. Ande, Dr. O.D. Owolabi, Dr. A.O. Oduola, Dr. Olutomi A. Adeyemi-Ale, Dr. Saratu I. Abdulkareem and other academic staff of the Department of Zoology, University of Ilorin for their input, motivations, encouragements and contributions during the research. To the technical staff of the Department of Zoology, University of Ilorin for their technical assistance, I say thank you.

I sincerely thank the Mainstream Energy Solution Nigeria Limited, Jebba, for the permission to carry out the research at the site. Most importantly, my gratitude goes to Mr. Umar at the Environmental Unit of the company for his support and assistance during water sampling and analysis. To Mr. Sule Muhammed and many fishermen at the up- and down-stream of the Jebba hydro-electric power reservoir, for the assistance during fish sampling, I am grateful.

I am indebted to my employer, Kwara State University, Malete for giving me opportunity to undergo and finish my Ph.D programme in due time and also to recommending me for TETFund grant and staff development. I sincerely thank all my friends, family and colleagues who have contributed, advised and inspired me in one way or the other on the work.

I am grateful to my parents Mr. John Kayode and Mrs. Lydia Omolara Oladipo (JP) for their encouragement and prayers during the study.

Special thanks to my wife, Mrs. Roseline Adeshike Oladipo, who was my interpreter and field assistant during the research work and for her moral, mental and homely support during the study.

Oladipo S.O
January, 2021.

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ABBREVIATIONS

JHPR	Jebba Hydro-electric Power Reservoir
CO1	Cytochrome c oxidase 1
DNA	Deoxyribonucleic acid
FAO	Food and Agriculture Organization
DO	Dissolved oxygen
TS	Total Solids
TSS	Total suspended solids
TDS	Total Dissolved Solids
COD	Chemical Oxygen Demand
BOD	Biological Oxygen Demand
HCL	Hydrochloric acid
EDTA	Ethylenediaminetetraacetic acid
NaCl	Sodium Chloride
TE	TrisEthylenediaminetetraacetic acid
PCR	Polymerase chain reaction
LC	Least concern
NT	Near Threatened.
VU	Vulnerable
EN	Endangered
NE	Not Evaluated
dNTP	Deoxyribonucleotide triphosphate
BSA	Bovine Serum Albu

ABSTRACT

Fishery activities in Jebba Hydro-electric Power Reservoir (JHPR) contribute to socio-economic development of Jebba town and Nigeria. There is paucity of information on fish biodiversity in JHPR, hence, this study aimed at identifying fish species and their ecology. The objectives of the study were to: (i) investigate the physico-chemical parameters in up- and down-streams of JHPR; (ii) identify fish species, abundance and diversity; (iii) determine the relationship between fish diversity and physico-chemical parameters; (iv) determine phylogenetic relationships of the barcoded fish species; and (v) determine intra- and inter-generic diversities of the barcoded fish species.

The study of physico-chemical parameters in relation to fish composition and diversity in JHPR was carried out between January, 2017 and December, 2018. The physico-chemical parameters of water in the reservoir were determined using standard methods. Fishes were collected with the aid of gill and cast nets of different mesh sizes and identified morphologically utilizing morphometric and meristic features; and molecular approach adopting DNA barcoding. Simpson's, Shannon-Wiener and Margalef's indices and relationship between the physico-chemical parameters and fish abundance/diversity in the sites/seasons were statistically analysed with correlation matrix and factor analysis in XLstat at $p \leq 0.05$. The phylogenetic relationships, intra- and inter-specific divergence of the barcoded fish species were determined applying MEGA 5.0.

The findings of the study were that:

- (i) the range for dissolved oxygen (DO), chemical oxygen demand (COD), turbidity and nitrate concentration in up- and down-streams of JHPR was 2.0-5.5mg/L, 20.50-35.67mg/L, 1.2-375NTU and 0.2-3.4mg/L respectively;
- (ii) there was a significant ($p < 0.05$) seasonal variation in turbidity with higher mean value of 175.40 ± 34.49 NTU observed in rainy season;
- (iii) eighty-three fish species belonging to forty-three genera were identified morphologically while 170 nucleotide sequences generated confirmed all the species identification except for *Chromidotillapia guntheri*, *Ctenopoma kingsleayae*, *Malapterurus electricus* and *Dasyatis garouaensis*;
- (iv) fish species distribution in the family Cichlidae and Mochokidae were more abundant in up- and down-streams of JHPR, but diversity indices showed higher species richness (Margalef=9.73) and diversity ($H = 3.95$; $1-D = 0.98$) at the downstream;
- (v) positive correlations (≥ 0.73) between DO, nitrate concentration and fish abundance were obtained for all fish families except Claroteidae, Latiidae, and Tetraodontidae, while turbidity positively correlated (≥ 0.71) with the abundance of Mormyridae, Gymnarcidae, Characidae, Distichodontidae, Bagridae, Malapteruridae, Dasyatidae, Polypteridae and Schilbedae;
- (vi) all the barcoded sequences showed levels of genetic distinctiveness among species in the phylogenetic tree and taxonomical hierarchy; and
- (vii) a range of 0-18.83% and 0.00-0.45% were generated for intra- and inter-generic divergence respectively in the barcoded species.

The study concluded that JHPR harboured high diversity of fish species which was influenced by seasonal variations in turbidity, DO, COD and nitrate concentrations. The study recommended that morphological and molecular methods be used for fish species identification, biodiversity monitoring, ecology and management.

CHAPTER ONE

1.0 Introduction

1.1 Background to the Study

In Nigeria, freshwater ecosystems such as rivers, streams, natural and man-made reservoirs are known to serve different purposes in industries, homes, power generation and agriculture. They are also blessed with variety of fish resources contributing to the socio-economic development of the people and Nigeria as a Nation (Bolorunduro, 2003). Water is an important and essential compound in fish life. The integrity of fish life is a function of water availability, quantity and quality because without water, they cannot exist. River Niger, a tropical freshwater ecosystem, and the other freshwater bodies in Nigeria house a well diverse fish fauna that are of economic importance with many species awaiting discovery, description and delination (Kottelat and Whitten, 1996; Olaosebikan and Raji, 1998; Mustapha, 2010; Iyiola *et al.*, 2018, Oladipo *et al.*, 2018).

The increase in human population in Nigeria has brought about high demand for water and fish resources. This gives an indication that, aquatic environment is not only a resource that supply water for human use and animal existence but also serves as a resource that needed adequate attention and management to ensure sustainability of the resource for future purposes (Mustapha, 2009; Oladipo *et al.*, 2018). The supply, quantity and aquatic life have been on pressure and risk which necessitate conservation and better management of the freshwater resources to provide water for living and provision of protein through fish production (Mustapha, 2009).

The up- and down-stream of Jebba reservoir contributes to the socio-economic development of the inhabitants and Nigeria through fishery resources (Olaosebikan and Raji, 1998; Owolabi, 2005). In the recent time, human activities arising from dam construction and overfishing have caused drastic decline in the fish catch from reservoirs which are threat to the fish community and its

associated habitat (Kolawole *et al.*, 2008). Despite this, there is little comprehensive information on the diversity, ecological requirements and conservation status of the fish species in most area known to accommodate diverse fish species. There is no gainsay that some species might have been lost or yet undocumented. This could be attributed to longtime effects of dam construction, insufficient fish surveys of the reservoir and the use of traditional morphology in species identification which is a common taxonomical tool in Nigeria as recorded by many fish scientists (Ita *et al.*, 1993; Olaosebikan and Raji, 1998; Idodo-Umeh, 2003). The use of morphology alone in fish taxonomy has often led to misidentification of species especially the cryptic ones, thus, leading to challenges in species conservation (Nwani *et al.*, 2011; Iyiola *et al.*, 2018). Recently, DNA barcoding, involving mitochondrial Cytochrome c oxidase subunit I (CO1), has been widely recommended as an alternative tool in complimenting morphological species identification and in unravelling cryptic (hidden) diversity (Hebert *et al.*, 2003; Bucklin *et al.*, 2010; Nwani *et al.*, 2011; Iyiola *et al.*, 2018).

Assessment and monitoring of water resources are fundamental methods for good management, and diversity monitoring of any reservoir (Mustapha, 2009). The extent of its importance shows how organizations such as World Health Organization (WHO), Wildlife foundation and others prefer water resources assessment to know detailed information on the quality of the water as well as the fauna resources that are present (WHO, 1997). Therefore, given the increased rate of human activities in up- and down-stream of Jebba reservoir, with antecedent effects on the aquatic ecosystem, there is a need to create a comprehensive inventory of fish diversity using molecular approach to complement the morphological method to identify the fish species collected from this area. In addition, information on the ecology of fish community through water quality, influenced by seasons and locations were necessitated to examine the dam effect on up- and down-stream of the reservoir.

1.2 Justification and Significance of the Study

Jebba town is a location that serves as a route of Nigerian main river - River Niger. Various fishing activities are carried out in the reservoir apart from Hydro-electric Power machine for electricity generation. The fishing activities are carried out both at the reservoir region as well as downstream for fish production and as source of income. It has been established that both Lakes Kainji and Jebba had considerable diversity of fish species than other lakes in Nigeria with about 101 species and 52 species respectively (Ita *et al.*, 1993), although most of the diversity study carried out was done in Kainji with little work in Jebba.

In Nigeria, most of the ecological monitoring in fishery has been based on physio-chemical parameters, fish population and diversity using morphological identification. There were challenges in carrying out morphological identification of some fish species due to their close relationship, necessitating the need of taxonomic expertise to carry out meristic, appearance, colours, positions of organs and landmarks for identification which many times are of great challenge (Nwani *et al.*, 2011; Iyiola *et al.*, 2018).

In the face of alteration in the diversity of aquatic life, there is the need to bring about proper and sustainable harvest in the use of freshwater fishes. Determination and assessment of the actual status of area taxonomic units is essential for the fish conservation programme and development to ensure sustainability in food availability, tourism, aquaculture and continuity in scientific investigations, hence, identification to know the catch abundance and diversity of individual species provide recognition of the basic link between systematic and fisheries management (Hajibabaei *et al.*, 2007). Species identification is fundamental to biology in which without taxonomy, report of empirical findings and accessibility to information on target organisms may prove difficult (Amanda and Luciane, 2010).

Diversity study is an important tool used to know the current status of species and helps in ensuring future sustainability of resources. Fisheries activities in up and down-stream of Jebba reservoir involve harvest of varieties of species ranging from fry to mature size which might be altered by the hydro-electric dam. Construction of dams is to improve the standard of living by conserving water at upper stream, which drastically alters the water flow of the rivers to the lower stream. This affects the physio-chemical characteristics, sediment and biotic community, thus disrupting the ecology of the water system (Koshy and Nayar, 1999; Kolawole *et al.*, 2008). Similarly, the spatio-temporal pattern of water discharge which is useful in fish assemblages in river system will be altered by irregular fluctuation and may lead to population decline, evolution of species and genetic restructuring (Poff and Allan, 1995; Meldgaard *et al.*, 2003; Aliko *et al.*, 2010). This necessitate the needs to determine the present status of fish catch abundance, richness and diversity, for management of fish resources in up and down-stream of Jebba reservoir. It is also to determine the abundance and diversity of fishes in up- and down-stream of the reservoir, since it has been reported that distance, overexploitation and habitat alteration affect diversity (Barlow and Munsey, 1976).

Due to the challenge encounter during morphological identification, new tools and methods have been in place on order to have a correct diversity status. This help in proper confirmation of identity of the fish species. Worldwide, molecular identification of fishes have been carried out effectively using mitochondrial DNA sequences of animals CO1 gene to create a unique “barcode but its use is limited in Nigeria (Hebert *et al.*, 2003; Nwani *et al.*, 2011; Iyiola *et al.*, 2018). So therefore DNA barcode can be of great help in confirmation of the identity of the fish species encountered and help in determining the proper diversity of the group of fish community present in up and down-stream of Jebba reservoir. The species identification that is complicated, difficult or

impossible by the presence of numerous siblings of a species or groups using morphological characters can be differentiated using CO1 gene “barcode and thus creating a database for future Nigeria fish identification using molecular systematic (Bucklin *et al.*, 2010).

Similarly, there has not been information on the fish diversity using morphological and molecular identification in up- and down-stream of Jebba Hydro-electric Power Reservoir (JHPR). There is paucity information based on the use of DNA barcode to create a database for Nigerian freshwater fish species. In this work, inventory of fish diversity using molecular approach to complement the morphology method to identify the fish species collected from this area were investigated. In addition, information on the ecology of fish community through its water quality as influenced by seasons and locations were determined.

Findings from this research will benefit Nigeria as a whole, because it will serve as a guide that will give detailed information on fish species for multi-faceted purposes of identification, taxonomy, species-species relationship, diversity and ecology of fish species for creating improved conservation strategies in River Niger, Jebba since there is little information on baseline information concerning diversity of fish species in up- and down-stream of JHPR, Nigeria using molecular identification. This research would also assist in managing fisheries for long-term sustainability, and improve the ecosystem research and conservation by making the information available to fisheries researchers, non-fisheries taxonomists and policy makers.

1.3 Aim and Objectives of the study

This study investigates physico-chemical parameters and its relationship with the catch abundance, distribution and diversity of fish species in up- and down-stream of JHPR employing morphological and DNA barcode for the fish species identification.

Specific objectives

The following objectives were used to achieve the aim:-

- (i) investigate the physico-chemical parameters in up- and down-streams of JHPR;
- (ii) identifies fish species, its abundance and diversity using morphology and DNA barcoding approach in up- and down-streams of JHPR;
- (iii) determines the relationship between fish diversity and the physico-chemical parameters in up- and down-streams of JHPR;
- (iv) determine the phylogenetic relationships of the barcoded fish species; and
- (v) determine the intra- and inter-generic diversity of the barcoded fish species.

CHAPTER TWO

2.0 Review of Related Literature

2.1 Freshwater Ecosystem

The world freshwater ecosystem make up of about 0.01% of world water (Gleick, 1996) supporting 6% of all animal species described (Hawksworth and Kalin-Arroyo, 1995). Freshwater ecosystems are known to harbour 43% of total fish species that gives about 11,952 species in inland waters, lakes and river belonging to 33 orders (Nelson, 2006). Freshwater ecosystems faced challenges of being endangered in respect to it biodiversity as the treat is grouped into some interacting category (Sala *et al.*, 2000). These includes degradation of habitat, water pollution, overexploitation and flow modification superimposed by environmental modifications such as changes runoff patterns and precipitation (Galloway *et al.*, 2004; Dudgeon *et al.*, 2006)

The Habitat degradation often times result from river excavation bringing direct or indirect effect. The overexploitation, pollution and flow modification occur in a rapid increase mainly from human needs. The resultant influence of the threats brings population reduction of the freshwater fish's diversity bringing about 84% of the freshwater species to be endangered (IUCN 1996). The habitat alteration, overfishing, and pollution contribute 54%, 29% and 26% respectively of freshwater fish extinction in the world (Harrison and Stiassny, 1999). Globally, freshwater species extinction due to human activities is about 20,000 which continue to increase everyday (Strayer 2006; IUCN 2007).

The conservation of freshwater biodiversity is a field that emerges after conservation ecology as a discipline with a goal to reduce loss of irreplaceable biodiversity (Strayer andDudgeon, 2010). The process includes the assessment of the present biodiversity and identifies the important

composition for the genetic, species and ecosystem diversity. The population often requires evolving and adapting to variability in environment through genetic diversity. This can be measured through allele, proteins, nuclear DNA, mitochondrial DNA and chromosomes. The number of species in an ecosystem and their relative abundance brings about the species richness, composition, evenness, the species interaction, spatial- temporal differences and abiotic with biotic interaction (Glowka *et al.*, 1994; Chapin *et al.*, 2000).

2.2 Hydropower

Hydropower is the main contributor to electricity production in the world, including Nigeria. The damming of rivers and its activities brings significant changes to physical parameters, alterations to water and habitat quality in downstream ecosystem (Ligonet *et al.*, 1995). Numerous studies have checked out the impacts of hydroelectric dam operation on river ecosystems, but general trends in fish populations response to river regulation remain difficult as these responses may be species-specific (Korman and Campana, 2009; Poff and Zimmerman, 2010; Finch *et al.*, 2015). Therefore, simple overarching environmental flow restrictions may not be broadly effective and there is a need for long-term, large-scale studies aimed at identifying processes and relationships between physical alterations and biological responses (Arthington *et al.*, 2006; Mims and Olden, 2013; Olden *et al.*, 2014). The hydrologic and thermal indices can be used to calculate and investigate fish diversity, health indicators such as condition, growth and survival in order to determine mechanisms between hydroelectric dam physical changes and fish responses. These fish health indicators are better calculated for species that are morphologically diversified with a range of behavioural characteristics and habitat preferences in order to have a total understanding of the effects of river regulation on the fish community.

A physical conditions gradient exists along the river length while fish and other are adapted to this gradient. The introduction of the barrier by hydroelectric dams alters the gradient creating impacts in the downstream biotic component (Vannote *et al.*, 1980; Ward and Stanford, 1983). A hydroelectric operation brings about large daily fluctuations in discharge to meet the electricity demand and alter the natural flow and thermal regimes component such frequency, timing, duration, magnitude and rate of change (Morrison and Smokorowski, 2000; Olden and Naiman, 2010). This brings serious implication on the ecology and biology of fish survival, growth, traits and population variation (Quinn and Kwak, 2003; Alexandre *et al.*, 2014; Finch *et al.*, 2015).

Apart from hydroelectric dam alteration to downstream fish fauna, food availability was also being tampered to increase invertebrate abundance and drift (Murchie and Smokorowski, 2004; Patterson and Smokorowski, 2011; Jones, 2013; Bond *et al.*, 2015). The changes to food availability, fish behavior and habitat all have the ways to influence fish life characteristics and population (Bøhn and Amundsen, 2001). Barrier creation to passage of fish movement due to dam creation similarly reduces fish ability to access thermal refuges in different part of river system (Schilt, 2007; Hillyard and Keeley, 2012). The dam brings about water temperature differences at various time intervals. Water temperatures increases at the downstream through warm water discharge from surface water while cool water was made available when receiving water from a deeper depth (Petts, 1986; Lessard and Hayes, 2003). This fluctuation results in negative impacts on time of spawning, larval development and growth rate (Saltveit, 1990; Zhong and Power, 1996; Clarkson and Childs, 2000). However, dam management for desired water temperature may also benefit specific fish species at the downstream and could be used to mitigate water temperature increases as a result of climate change (Isaak *et al.*, 2012; MacDonald *et al.*, 2012; Robson *et al.*, 2013; Rheinheimer and Viers 2014).

2.3 Jebba Hydro-electric Power Reservoir

Improvement in standard of living as a result of population increase call for developmental project on freshwater ecosystem to maximize water resource use in Nigeria. One of the developmental projects on freshwater ecosystem is the creation of reservoirs which serves for different purposes such as irrigation, domestic usages, industrial usage, generation of power supply and others. The essence and need of a reservoir most often determines the location and size and these eventually determines its resultant effect on the ecosystem (Poff and Hart, 2002).

In Nigeria, several reservoirs in different categories and size ranging from small, medium and large sizes have been constructed which is equivalent to about ten percent (10%) of the country's potential freshwater ecosystem (Oyebande, 1995). Majority of the reservoirs are majorly constructed for the purpose of water supply to the communities, industries, for irrigation while just few were dedicated for fisheries, recreation and hydro-electric power generation (Salami, 2007).

Niger River is the main freshwater system in Nigeria with several tributaries. The constructions of HEP plants have been embarked on this river before its main tributary, River Benue joined at Lokoja. The Jebba reservoir was the first man-made lake in Nigeria, created in August 1983 as part of a hydroelectric project scheme for improving electric supply in Nigeria to supplement Kaiji Lake basin capacity (Adelakun *et al.*, 2017). It extends from Jebba to southern Kainji dam. Its main tributaries include the Awun, Eku, Moshi and Oli rivers. Apart from generation of hydroelectric power from Jebba reservoir, it brings opportunities to fisheries industry for increase in fish catch potential of upstream of the dam estimated at 909 – 1818 tons/annum (fresh weight) (Salami, 2007).

The dam was constructed to improve the populace standard of living, but this conserve the water at upper stream and drastically alter the water flow of the rivers to the lower stream that may

affect physico-chemical characteristics, sediment of the rivers and biotic community which in turn disrupt the ecology of the water system (Koshy and Nayar, 1999; Kolawole *et al.*, 2008). This can also lead to habitat fragmentation and destabilized aquatic habitats in respect to productive station for fish, livestock, and wildlife. The spatio-temporal pattern of water discharge changes which is useful in fish assemblages in river system will be affected by irregular fluctuation leading to rapid rate of population decline, evolution of species and genetic restructuring (Poff and Allan, 1995; Meldgaard *et al.*, 2003; Aliko *et al.*, 2010). These modifications in the environment bring about a call for comprehensive diversity assessments to provide recent data of species distributions in up- and down-stream area of the reservoir.

2.4 Nigerian Freshwater Ecosystem and Fish Diversity Assessment

The quality assessment of the water resources with the use of different methods had been described by different authors in Nigeria and all over the world. The nature and ecology of the river makes it an ideal setting for biodiversity studies (Khedkar *et al.*, 2014). Any conservation strategy needs indigenous animal species knowledge and their environmental interactions. The fish fauna assessments concentrate on fish diversity, abundance and ecology studies that generate basic reports in Nigerian freshwater fish assessment through morphological identification. Ever since, river Niger being reported to have considerable number of freshwater fish species, tremendous increase in fish diversity in Nigeria has been reported (Welman 1964; Banks *et al.*, 1965; Read *et al.*, 1967; Akinyemi *et al.*, 1986; Ita *et al.*, 1983, 1985, Olaosebikan and Raji, 1998 and Idodo-Umeh, 2003).

Prior to the establishment of the Kainji and Jebba reservoir basins, about 139 and 51 species of fish were identified respectively and described while many more have been discovered over time (Banks *et al.*, 1965; Ita, 1987). In late sixty's, about 160 species have been reported in Nigerian Northern freshwater ecosystem (Reed *et al.* 1967). Ever since then, numerous studies have been

undertaking in river Niger in Kainji and other Nigeria freshwater bodies leading to the description of many species. The nation has rich and diverse ichthyofaunal resources that consist of about 268 species of freshwater fishes (Ita, 1993; Idodo-Umeh, 1987; 2003; Olaosebikan and Raji, 1998; Froese and Pauly, 2017).

2.5 Nigerian Freshwater Fish Production and Challenges

In Nigeria, demand on freshwater fishes is on the high side every other day, and the intense human intervention and the resultant consequence is endangering fish species abundance and diversity (Raja *et al.*, 2014). Nigeria has been on the list of higher aquaculture producers in Africa which contributes about 2% of National Gross Domestic Product (GDP) (Ekunwe and Emokaro, 2009; Oyase and Jemerigbe, 2016). Protein is an essential nutrient to the body and 40% of the animal protein intakes are gotten from fish in Nigeria. The artisanant fishery provide a substantial proportion of employment, especially in the rural areas which serves as a principal source of livelihood for over three million people which contribute highest production output (Adedeji and Okocha, 2011).

The number of people involved in fishing has brought about continuous and indiscriminate harvest of this inland water fishes in Nigeria without proper management. This generally bring decline of fish yield and fisheries production over time (Odo *et al.*, 2009). Fishery ecology research is an important study area that got attention, due to fish population declining throughout the world. Diversity, distribution and composition studies of freshwater fishes are useful keys to analyse different factors that may influence the nature of the fish abundance and diversity in the water bodies (Mady-Goma, 2016).

For efficacy in fisheries management planning, detailed knowledge of the form and function of the river system and responses of the fish species is required (Welcomme and Halls, 2001). The

poor management of fisheries resources and environmental changes that is observed in inland waters can be assessed in many ways (Jamu and Ayinla, 2003). In the case of the fauna component, one of the methods used is to determine the species richness, diversity and relative abundance to carry out the ecological risk assessment in aquatic ecosystems. Determining the precise status of local taxonomic units is important for the creation of programs to preserve fish for food, aquaculture, tourism, disease control and scientific research purposes hence, identification to know the diversity and abundance of individual species provide recognition of the fundamental link between systematics and fisheries management (Hajibabaei *et al.*, 2007). This species identification is fundamental to biology in which without taxonomy, report of empirical findings and accessibility to information on target organisms may prove difficult (Amanda and Luciane, 2010). The habitat degradation that has continued at high accelerated rate makes the maintenance of species richness and biodiversity become a central point of conservation biology. The significant task in biological research and conservation efforts lies in species identification, thus, rapid, reliable and reproducible tests to identify fish species are needed in many areas (Rasmussen and Morrissey, 2009; Wang *et al.*, 2016).

2.6 Some Commercially Important Freshwater Fish Families in Nigeria

2.6.1 Family Mochokidae

Mochokids belong to category of scaleless and tenacious fishes called catfishes (Vigliotta, 2008). They are nocturnal, scavengers and able to adapt to various habitat life including shallow water. They belong to order Siluriformes and class Actinopterygii (ray-finned fishes). They are one of the most diversified groups of catfishes in Nigeria (Olaosebikan and Raji, 1998; Idodo-Umeh, 2003). The earlier classification of this group of species found in Nigeria was made up of three genera, *Mochocus*, *Synodontis* and *Chinoglanis* (Reed *et al.*, 1967; Holden and Reed, 1972; Araoye,

1999), which was later separated into genus *Mochocus*, *Branchysynodontis*, *Hemisynodontis* which are monospecific; genus *Chiloglanis* and *Synodontis* with the highest number of species (Idodo-Ummeh, 2003; Olaosebikan and Raji, 2013) after taxonomy revision.

Genus *Synodontis*, popularly known as up-side down catfish is the largest group of catfishes in the order Siluriformes (Friel and Vigliotta, 2006). They occur throughout tropical region of Africa and high abundance occurrence in River Niger and Benue of Nigeria contributing significantly to economic growth through subsistence fishing (Ezenwaji *et al.*, 2005; Iyaji, 2011). They include small to medium sized of about 26 species recorded in River Niger and most of the Nigerian inland waters (Imevbore and Okpo, 1975; Olatunde, 1989; Araoye, 2001; Araoye and Owolabi 2005; Adedeji and Araoye, 2006; Idodo-Ummeh, 2003; Olaosebikan and Raji, 2013), 110 species reported in African (Willoughby, 1976; Blache *et al.*, 1964) with about eighteen genera and over two hundred species have been reported worldwide (Welcomme, 1976).

Their body description is unique having the head enclosed in a heavy bony case; well-developed barbels of three pairs, two mandibular pairs branched and serrated spine form from the first ray of the dorsal fin and pectoral fin. The adipose fin lacks supporting bony rays forming the second dorsal fin. The medium size range with affordable price to the average income earners and local people living close to the riverine makes it a highly important in the fishery industry (Araoye, 1999).

The relatedness in the morphology of the species of this group and due to species-rich general makes the identification and taxonomy of the *Synodontis* more complex (Skelton and White, 1990). The species morphology characteristics such as colour pattern, maxillary barbels, mandibular barbels and humeral processes that were used for identification overlap and complicate the

identification (Bruwer *et al.*, 200) and this often times makes colour patterns having more preference over other taxonomic characteristics (Jubb, 1967)

Their abundance has been reported to be as a result of their diverse feeding habit (Araoye, 1999; Mustapha, 2010). The diet comprises of food varieties present in their habitat such as phytoplankton, zooplankton, green algae, worms, crustaceans, detritus, and seeds and decaying vegetable matter, hence they are benthopelagic freshwater fish (Reed, 1967). They are also more abundant when there is a low predation and good spawning ground for their breeding (Mustapha, 2010).

2.6.2 Family Cichlidae

Cichlids are group of fish that are mainly indigenous to fresh waters of tropics and were associated with lowland (Stauffer *et al.*, 2006). They are common group of fish readily available in the society for common man as a source of protein and are being used by many researchers for study of feeding specialisations, diverse and unique mating systems (Stauffer *et al.*, 2006; Mustapha, 2010). The unique morphological feature of Cichlids is the laterally compressed shape and body covered with cycloid scales. They were also characterised by the presence of one nostril on each side of the head with two incomplete lateral lines.

There are about 10 genera of cichlids that have been reported in Nigerian freshwater ecosystem, namely *Gobiocichia*, *Tylochromis*, *Astatotilapia*, *Pelvicachromis*, *Thysochromis*, *Chromidotilapia*, *Hemichromis*, *Tilapia*, *Oreochromis* and *Sarotherodon* (Ita, 1978; Idodo-Umeh, 1987; Olaosebikan and Raji, 1998; Idodo-Umeh, 2003). The dominance of this group in Nigerian freshwater especially the reservoirs have been reported by many authors (Reynolds, 1973; Ita, 1978; Ita and Balogun, 1982; Omotosho, 1993; Omotosho, 1997; Balogun, 1986, 2005; Mustapha, 2009).

Mustapha, (2009; 2010) have also reported their feeding, adaptation to their environment and reproductive success as contributing to their species richness and diversity.

They have omnivores habit, known to feed on phytoplankton; aquatic plants; periphyton; invertebrates like copepods, aquatic insects and shrimps; benthic fauna such as chironomids larvae; detritus; bacterial films; other fish and fish eggs (Konings, 1995; Albertson *et al.* 1999; Idodo-Umeh, 2003; FAO 2012). They can also actively pick up rock to scrape and eat the algae on it. They naturally flourish in a tropical ecosystem but can adapt very wide temperature as low as 8°C but mature early between 20-31°C. Occurrences were found to be round the year both in rainy and dry season (Idodo-Umeh, 2003).

Breeding habit involved mouth brooding, creating a spawning nest by male and female lay eggs into the nest when the water temperature increases above 24°C. The laid eggs will be taken up by the female in the mouth for about 21 to 40 days and the fry were released when they are large and able to feed (FAO 2012).

2.6.3 Family Centropomidae

Centropomidae is being represented by only one species in Nigeria called *Lates niloticus*. It was originally described by Linnaeus (1758) as *Perca nilotica* but Cuvier and Valenciennes, (1828) changed the name into *Lates niloticus*. It is popularly known as Niger perch and makes a major commercial important in Nigeria lakes (Olaosebikan and Raji, 1998; Idodo-Umeh, 2003).

It has been reported that, this species of fish is one of the largest freshwater fishes, length growing up to 200cm and weight of about 42kg have been recorded in Nigerian freshwater (Idodo-Umeh, 1987; Froese and Pauly, 2010). They mainly have deep body, somewhat compressed,

small scales and ctenoid. The adults mainly inhabit deep water, while juveniles are found in shallow water (Froese and Pauly 2007).

Lates niloticus is a predatory fish that is indigenous and spread across all parts of Africa, above the equator (Froese and Pauly, 2017). Due to perch-like predatory characteristics, feed on fish especially clupeids and Alestes (Reed *et al.*, 1967; Froese and Pauly; 2017). Smaller fish can feed on large crustaceans and insects, while juveniles are planktivorous (Bailey 1994). *L. niloticus* may become the dominant fish species and other species declined or disappeared completely (Ogutu-Ohwayo, 1990; 1993; Kaufman, 1992; Witte *et al.*, 1992) hence, listed among the 100 "World's Worst" invaders (ISSG, 2009).

L. niloticus have been associated with low dissolved oxygen levels and high temperature (Schofield and Chapman, 2000; Wanink *et al.*, 2001; Chapman *et al.*, 2002). *L. niloticus* migrate upwards and dwelled above oxycline level (Wanink *et al.*, 2001; Goudswaard *et al.*, 2006). As a result of its highly commercial value species, makes it suffering from overexploitation in much of its native range, and to some extent caused by the pollution. Little work has been done this species in Nigeria, which makes the rate of decline to be unknown and uncertain (Azeroualet *et al.*, 2010).

2.6.4 Family Citharinidae

In Nigeria freshwater, Citharinidae is made up of three general *Citharidum*, *Citharinops* and *Citharinus* (Olaosebikan and Raji, 1998; Idodo-Umeh, 2003). They are major exploitable fish species in the Nigerian freshwater system commonly found in considerably large ecosystem. They are highly priced because of the flesh quality and often in smoked-dried form because they die-off immediately, when removed from their habitat. Deep and flattened bodies call for their popular name

'moon fish. They feed chiefly on insect larvae, aquatic plants and plankton (Olaosebikan and Raji, 1998; Idodo-Umeh, 2003).

Citharidum and *Citharinops* are occasionally and very rare group with rapid decrease in there population in which without intervention can lead to extinction. *Citharinus* are represented by two species *Citharinus citharus* and *Citharinus latus* found inriver Niger but *C. citharus* is very common among all. They are also common in swamps and rivers throughout Africa (Idodo-Umeh, 2003).

2.6.5 Family Characidae

The group comprises the moderate to large-sized species, having body elongated and covered with cycloid scales. They have scaleless head with small adipose fin. The dorsal fin start in front of level of pelvic fin insertion. The eye almost covered entirely by an adipose eyelid (Idodo-Umeh, 2003). The genera *Hydrocynus*, *Alestes*, *Bryconaethiops*, *Micralestes*, *Rhabdalestes*, *Arnoldichthys* and *Brycinus* have been reported to present in Nigeria freshwater (Oladipo *et al.*, 2018; Olaosebikan and Raji, 1998; Idodo-Umeh, 2003).

Murray and Stewart (2002) describe genera *Alestes*, *Hydrocynus* and *Bryconaethiops* to represent a monophyletic groups, whereas, Paugy (1986) distinguished three groups within the *Brycinus*. The *Hydrocynus* groups were commonly called the tiger fishes. They are active piscivores, known for their voracity. Body elongated, suited to their piscivores feeding habits, actively pursuing their prey. The *Alestidae*, have a brilliant silvery colour pattern , with the scale marked by a dark spot parallel bands visible above lateral line varying with species.

2.6.6 Family Mormyridae

The family Mormyridae comprised of weakly electric fish found in the African freshwaters. This group of fish is commonly found in almost every body of freshwater in Africa (Hopkins, 1986). They have habitat range of being bottom dwellers to top feeders, capable to withstand deoxygenated swamps (Hopkins, 1986) and mostly containing suspended particles (Moyle and Cech, 2000).

Eleven genres have been reported in the Nigerian freshwater, namely *Mormyrus*, *Hippopotamyrus*, *Hyperopisus*, *Campylomormyrus*, *Marcusenius*, *Mormyrops*, *Petrocephalus*, *Pollimyrus*, *Gnathonemus*, *Isichthys* and *Brienomyrus* (Olaosebikan and Raji, 1998). The electrogenic and electrosensory characteristics of Mormyrids make them to produce weak electric discharges by a highly specialized organ in the tail (Hopkins, 1986; Hopkins, 1981). This is use for communication; location of objects, prey, obstacles, and boundaries; and courtship (Crawford and Huang, 1999).

2.6.7 Family Cyprinidae

The general features of the cyprinid fishes of Nigeria have been described many researchers (Idodo-Umeh, 2003; Olaosebikan and Bankole, 1998; Itta, 1993). This group of fishes has a single dorsal fin without adipose fin which has either one or two spinyrays for support. The pelvic fins are situated mid-body and well behind the pectoralfins. All the body scales are large cycloid with scaleless head. Mouth protractile without a tooth in jaw but the fifth gill-arch is modified into pharyngeal bones which are found situatedventrally in the throat, behind the gill cover.

The family Cyprinidae is one of the largest families of fishes with about 1700 species in 220 genera having awide geographic distribution all over the world (Howes, 1991). About 33 species in 6 genera have been reported to present in Nigerian freshwater ecosystem, dominated by species in

the genus *Labeo* and *Barboides* (Olaosebikan and Raji, 1998; Idodo-Umeh, 2003). They commonly found in the middle and lower sections of rivers as well as in the stagnant waters of many lakes and reservoirs. Their morphological and physiological diversity allowed them to present in a wide variety of habitats (Howes, 1991). They feed on varieties of food such as algae, chironomid larvae, mud, odonata nymphs, insects, sand grains and ostracods (Idodo-Umeh, 1987).

2.6.8 Family Bagridae

Bagridae is a large family of catfishes, morphologically diverse. Ever since the establishment of the group, its content and classification have been profoundly changed through the work of various ichthyologists (DePinna, 1998; Ng, 2003). Mo (1991), describe all fishes previously grouped together to Bagridae are phylogenetically distinct with the exception of the genus *Bagrus* as a result of an anatomical and systematic revision based on a phylogenetic cladogram. Other species were grouped into different family of Austroglanididae and Claroteidae.

Bagrus fishes were identified by presence of a retractortemporalis muscle, large heavily ossified post-temporal with a posterior process and a well-developed fossa with a posterolateral exit, dorsomedian surface of the 'post-temporal' thickened and bearing a prominent posterior surface for attachment of the epaxial muscle, and vomer with large crescentic head and lateral tips often extending beyond lateralethmoidal facets (De Pinna, 1998; Ng, 2003). The genus *Bagrus* is characterized by moderately elongated body, scaleless, having first rays of dorsal and pectoral fins with bony spines. A large adipose fin, originate close to the end of the dorsal fin ray. Pelvic fins is well-developed and having a single simple ray and five branched rays. Anal fin with 3-5 simple rays and 8-10 branched rays and the caudal fin is deeply forked (Risch, 1992; Idodo-Umeh, 2003). A single genus present in Africa, *Bagrus*, and three species are represent in Nigerian freshwater

namely, *Bagrus bajad*, *Bagrus filamentosus* and *Bagrus docmac* (Olaosebikan and Raji, 1998; Idodo-Umeh, 2003). They are of economic importance due to their marketable size, good taste, quality flesh and acceptability by common people (Boulenger, 1907; Idodo-Umeh, 2003).

2.6.9 Family Gymnarchidae

Gymnarchidae is represented by only one member, *Gymnarchus niloticus* in the order Osteoglossiformes (Reed *et al.*, 1967). They reproduced during the rainy season and decrease in water conductivity triggered sexual maturation (Elsayed and Mohammad, 2012). Characterized with caudal fins and the dorsal extend almost the entire length of the back. They have long eel-like body that grows to a length of 1.5m and a weight of 15kg.

The head is long with two small eyes and a rounded snout that projects slightly beyond the lower jaw. The mouth is wide and terminal, and is equipped with strong teeth both at the upper jaw and the lower jaw. The teeth are compressed, pointed, truncated and finely serrated on the sides. The fish has a large tongue hence called bony tongue fish and the gill openings are connected by a strong fold of skin (Hagedorn 1984).

Gymnarchus niloticus is mainly a freshwater species found in rivers, lakes and their floodplains. It is majorly found in rivers Benue, Imo and their floodplains, as well as Lake Chad, Kainji and Jebba Lake in Nigeria (Reed *et al.*, 1967 and Sagua 1983). During dry season, they remain deep in the rivers but move into the shallow and grassy floodplains during the rainy season to build nest with the grasses found there (Camouzc *et al.*, 1993). The feeding behavior shows that *G. niloticus* are carnivore. They feed on small fishes like *Synodontis* and *Alestes* (Reed *et al.*, 1967). *Gymnarchus niloticus* is rated as a highly efficient predator especially with the possession of an electric organ located in its tail from which it emits electric signals to locate its prey in muddy

waters and at night (Ewer and Hall, 1978). It is an excellent sporting fish and of commercially important that supports small-scale subsistence fisheries in Nigeria (Holden and Reed, 1972; Arawomo, 2004; Olopade and Taiwo, 2013).

2.6.10 Family Ariidae

The Ariidae family are mostly marine fishes belongs to the order Siluriformes, but some enter into fresh or brackish water. Worldwide, the family has a total of 21 genera and 150 species in tropical regions with 3 identified species in the Nigeria freshwater (Teugels, 2003; Valinassab, 2013). They are known to produce sounds using spring apparatus.

In term of feeding behavior, they have a wide feeding spectrum, vary for deferent life stages. The diet mostly constituted of fish, detritus, zooplanktons and invertebrates (Espírito and Isaac 1999). The reproduction occurs during the rainy season when the temperature is high, when there is a major uptake from rivers (Mazzoni *et al.*, 2000, Fávaro *et al.*, 2005). This group is important to freshwater fisheries for having species with high economic value due to taste and flesh quality.

2.6.11 Family Malapteruridae

This group of fish were generally refers to as the African electric catfishes. They are endemic totropical Africa rivers (Leveque *et al.*, 1991) having three species presently recognized as *Malapterurus electricus*, *M. minjiriya*, *M. microstoma* to be common in West African (Teugels, 1996), having *M. electricus* dominating the common commercial catches (Holden and Reed, 1972). *M. electricus* known to be widely distributed in Nigeria freshwater but *M. minjiriya* have only been reported in upper and lower Niger in their distribution.

Electric catfish lack dorsal fins. They possess three pairs of barbels, lacking the nasal pair, with swim bladder elongating to posterior chambers. They are nocturnal, benthopelagic and potamodromous fish species in their distribution. *M. electricus* commonly found in swamps and occasionally in rivers around the reed beds flanking the flowing water (Sagua, 1975). The Malapteruridae have well-developed electrogenic organs, although electroreceptive systems are common in catfishes but this feature is unique (Sagua, 1979). The electrogenic organ is derived from anterior body musculature and lines the body cavity that function both in defensive and offensive predatory behavior and feed primarily on other fish, incapacitating their prey with electric discharges (Belbenoit *et al.*, 1979).

2.6.12 Family Tetraodontidae

The family Tetraodontidae is commonly called toad fish and Puffers fish. They include over 100 species, of which more than 25 species are found in West Africa (Fagundes *et al.*, 2016; Sujatha and Padmavathi, 2015). Puffer fish have a modified jaws constituted by two upper and lower plates to give a powerful bite. They lack pelvic fin and typical scales. They commonly inhabit coastal waters, estuary and fresh-water (Figueiredo and Menezes 2000). The family has torpedo-shaped bodies, scaleless soft skin that is sometimes imbedded with small spines and fused teeth that form a beak.

Another unique characteristic of this family is presences of highly lethal toxin, called tetrodotoxin, present in the skin, flesh and internal organs of the fish. *Tetraodon fahaka* and *Tetraodon pustulatus* were the only two species reported in Nigeria (Olaosebikan and Raji, 1998; Idodo-Umeh, 2003; Fagundes *et al.*, 2016). Puffers fishes are highly commercially valuable and regarded as food, despite the presence of specific toxin that causes death of gastronomers every year (Fiedler, 1991). Similarly, increasing in demand of tetraodontids in the aquarium trade has also been

reported. Although, basic ecological knowledge of the natural populations usually scarce (Sujatha and Padmavathi, 2015).

2.7 Diversity Assessment and Species Identification

Taxonomy, an important area in diversity assessment involves the discovering, describing, naming, and identifying species (Moritiz and Cicero, 2004; Prendini, 2005; Meier *et al.*, 2006; Carvalho *et al.*, 2008; Amanda and Luciane, 2010). The result of lack of specialists in several taxonomic groups brings debates on the correct identification of species (Godfray, 2002, Mallet and Willmott 2003).

2.7.1 Morphological Species Identification and its Challenges

In Nigeria, the morphological identification using morphometric and meristic method in species identification is common. Many researchers have collated the species that were been recorded in Nigeria to make identification guide for easy identification by individuals and fish were described based on their unique features possessed (Olaosebikan and Raji, 1998; Idodo-Umeh, 2003). The morphometric measurement and meristic count which is the simplest and direct way in identifying fish stocks have been used to access the function and the fish species response to habitat and environmental change (Turan *et al.*, 2004; Olufeagba *et al.*, 2015). It has been noted that divergence and morphological change tend to occur if there is isolation, environmental change and when fish were exposed to environment bringing new evolutionary and developmental forces which decide their body shapes (Mohamed, 1990; Goncalves *et al.* 1996; Froese and Pauly, 1998; Mwanja *et al.* 2011) nor through hybridization or environmental factors at early stages of development (Nei, 1987; Currens *et al.*, 1989; Mohamed, 2010).

Diversification can occur through genetic variation and phenotypic variation process (Ackerley, 2003). Phenotypic variations in species have a wide view of study including intraspecific, interspecific and individuals in a given population determined by species response to the events (Rundell and Price, 2009; Mobley *et al.*, 2011; Olufeagba *et al.*, 2015). Likewise interaction of underlying genetic basis is also a major factor in morphological variation (Hodgins-Davis and Townsend, 2009; McGuigan *et al.*, 2010). Hence variation is part of event that occurs during speciation (Langerhans *et al.*, 2007) and there is need to understand pattern of the variation in a natural population of disturbed environment (Mobley *et al.*, 2011).

There is need to understand the mechanism and relationship of underlying genetic variation role and morphological changes in population diversification with their importance (Scheiner, 1993; Pfennig *et al.*, 2010) which can be done intraspecifically or interspecifically (Ruzzante *et al.*, 2003; Parson *et al.*, 2011). Examination of divergence in more than one species with potential constrain evaluation gives the understanding of causes and pattern of diversification (Hendry *et al.*, 2001; Johnson and Belk, 2001; Jennions and Telford, 2002).

Tackling the issues of divergence and morphological change in species, there are some challenges using morphological methods. Firstly, the Nigerian freshwater ichthyofaunas known to be of high diversity may bring about wrong identification of these species resulting from little knowledge of identification and inability to ascertain the species which has undergo preservation or decay. This has also results to fading away of provision of names for organisms and determination of the phylogenetic (evolutionary history) relationships because of its complexity and few or no expert is left.

Another challenge of morphological identification of species also seen in cryptic species that was often overlooked. The similarities between closely related species which make it difficult to discriminate from each other (Hebert *et al.*, 2003; Rasmussen, 2009). Some group of species from same lineage might also look different due the adaptability of a fish to changes in its environment in different habitats, and this makes morphological identification difficult to standardize (Anna, 2015). Other related issue includes gender and life stages of the species (Hebert *et al.*, 2003) that lead to difficulties in recognition of specimens and inability to easily track divergence. All these creates a problem for conservation plan as a result of habitat variation and difficulties in understanding the differences in identification of species, hence cannot be protected effectively (Swartz *et al.*, 2008).

Although, inaccuracies of species identifications have not been reported, but good percentage of identifications may still be erroneous as a result of evolution and changes in genetic make-up which call for improving methods for species identification (Ward *et al.*, 2009). The time frame, number of samples and lack of interest in taxonomy to study biodiversity have also brought about taxonomic crisis seen in recent years. This situation, together with upper reason justifies the use of new technologies of molecular identification of species and population structure studies in fisheries including the use of DNA, to revitalize taxonomy (Nwakanna *et al.*, 2015).

2.7.2 Molecular Characterization in Species Identification and Diversity Study

Understanding the underlying principles, processes and logical evolution of biodiversity is a fundamental goal of molecular systematics. Despite morphological studies serve as a good tool in tracing some physical traits and is required in taxonomy, it may not reveal the lineage that diverge many years ago especially where the environmental stability are characterized long time ago (Colborn *et al.*, 2001).

A wide variety of molecular based methods have been used for investigating diversity in fishes (Rasmussen *et al.*, 2009; Pereira *et al.*, 2013). These includes protein-based analyses, random amplified polymorphic DNA (RAPD) analysis (Calvo, 2001), nuclear DNA and Mitochondrial DNA (*mtDNA*) which includes sequences of COI, 16S rRNA (16S) and cytochrome b (Cyt B) genes amongst the common used genetic markers for fish species identification, genetic divergence and evolution (Iyiola *et al.*, 2018). Several types have been assessed for the molecular identification of fish species in Africa, however, they are not comparable for the purposes of species identification due to lack of standardization (Waters and Cambray, 1997; Wishart *et al.*, 2006; Swartz *et al.*, 2008). Likewise, sequencing the whole genome of an organism is time consuming and expensive. This has led to finding a new direct, simple way for species identification by DNA barcode using COI gene of mitochondrion DNA (Ward *et al.*, 2009).

Despite the accomplishment of underlying change in the genetic code in any heritable morphological divergence, tracking those changes within entire genome can be tasking, hence, markers such as mtDNA control region and microsatellites which may accumulate mutations in the absence of morphological divergence, have become a workhorse in studies of closely related taxa. For instance, using mtDNA as a common marker, because of its haploid nature and lack of recombination, that facilitate rapid lineage sorting (Avice, 2004). There may be also instances that molecular studies may fail to reveal all relevant biodiversity (Simons *et al.*, 2001).

Mitochondrial genes have been discovered to be promising markers for fish species identification (Kochzius, 2009) when compared to protein base analyses and nuclear genes as a result of its several characteristics features. Mitochondrial DNA (*mtDNA*) poses high number of copy in each cell with the size of 15-20kb, which makes DNA easily extracted using various methods (Hubert, 2008). There is also limited recombination in *mtDNA* because it is maternally

inherited in most animals (Gissi *et al.*, 2008) and rapid mutation rate with small effective population that make it a tool for studying phylogeny of taxa (Moore 1995; Mindell *et al.*, 1996). Additionally, the evolution rate of *mtDNA* genes is rapid and brings about differences between closely related species to discriminate among species and conserved to be less variable within species (Hebert *et al.*, 2003; Hebert *et al.*, 2004). Likewise, require a much shorter nucleotide sequence compared with nuclear DNA in order to differentiate species. The priming site is also reliable in amplification and genes convey sufficient phylogenetic information due to large number of mitochondrial gene copies in every cell compared to nuclear genes that only exists in one copy (Dawnay *et al.*, 2007; Galtier *et al.*, 2009) and this is helpful when dealing with small or damaged samples (Anna, 2015).

For the purpose of designing and develop a universal primers pairs for large scale taxonomical applications, the barcode sequence must be flanked by regions that are well conserved among species (Kress and Erickson 2008). A short 648 base-pair region in the cytochrome c oxidase 1 (*COI*) qualifies to serve as a practical and standardized DNA barcode for all animals (CBOL, 2009) in accordance with the above qualities.

DNA barcode has been suggested as a universal tool used to identify biological diversity including freshwater fishes in Nigeria (Nwakanna *et al.*, 2015; Nwani *et al.*, 2011). The barcode of biological species is ongoing all over the world aiming to standardize process for species identification by creating a DNA barcode reference library for all species through 'The International Barcode of Life project (iBOL)' (CBOL, 2009). The Fish Barcode of Life campaign (FISH-BOL) is a group with the goal to collate fish barcodes in a database that will serve as a standardized reference library for fish species (FISH-BOL, 2009). Hebert *et al.*, (2004) reported that, DNA barcode uses the 5' region of the mitochondrial cytochrome C oxidase subunit I (*COI*) as a target gene. In order for DNA barcoding to work, sequence variation must be high enough between species in such a way

that they can be distinguished from each other and this are being done using the methodology widely applicable throughout phylogenetically distant animal group (Lahaye *et al.*, 2007).

DNA barcode has been accepted globally and broadly applicable species identification tool, particularly for fish as coordinated by the Fish Barcode of Life campaign (FISH-BOL; www.fishbol.org) (Ward *et al.*, 2009; Nwani *et al.*, 2011). DNA barcode has successfully been used for both species identification and discovery of new species in previous studies, involving Lepidoptera (Hebert *et al.*, 2004a; Hajibabaei *et al.*, 2006; Wilson, 2010), fish parasites (Locke *et al.*, 2010), birds (Hebert *et al.*, 2004b). In fish identification using DNA barcode, there have been reports that give useful results and relevant information among their cryptic species within a number of systematic clade in fish (Ward *et al.*, 2005; Nwani *et al.*, 2011; Iyiola *et al.*, 2018; Nneji *et al.*, 2020). This method of species identification based on DNA barcodes has been previously assessed and successful for many freshwater fish species, for example in Canada (Hubert *et al.*, 2008), Mexico and Guatemala (Valdez-Moreno *et al.*, 2009), Brazil (Carvalho *et al.*, 2011; Pereira *et al.* 2010) and South-East Nigeria (Nwani *et al.*, 2011).

Ever since barcode system has been established, more than 23,000 fish species have been recorded in the Barcode of Life Data Systems (BOLD) database. The database provides detailed information of COI sequenced species, the origin and location of voucher specimens (Ratnasingham and Hebert 2007). Other morphological, ecological, natural history and geographic variation were also used for complimentary (Ward *et al.*, 2005; Ferri *et al.*, 2009). Barcoding may also be a reliable approach in the case of processed fish as morphological information is no longer visible and available.

There are gaps of information pertaining to the identification of fish based on morphological identification and molecular identification in Nigeria. These challenges call for concern because

many species are threatened due to poor management of freshwater bodies and lack of good conservation policy and awareness (Olaosebikan and Bankole, 2005). There is a need to discover the true species identity and diversity of the Nigeria freshwater ecosystem using molecular marker to complement morphological identification and assessment to ensure proper management before the loss rate exceeds its limits. The use of molecular methods to support species identification have been established since each organism carries unique genetic setup of DNA (Ward *et al.*, 2005) and this help in comparing and analyzing relationships between DNA sequences. Proper conservation plans and long-term management of fisheries resources are based on proper monitoring of diversity and evolution, a good understanding of the molecular systematics and divergence of fish will be a tool for conservation in fishery sector based on its effective solid knowledge of the diversity and existing evolutionary units of the freshwater fishes (DeSalle and Amato, 2004).

CHAPTER THREE

3.0 Materials and Methods

3.1 Description of the Study Area

River Niger in Jebba serves as landmark in separating Niger and Kwara States. It falls within the Guinea savanna region of Nigeria. The area is characterized mainly by two seasons: dry (November to March) and rainy (April to October) seasons (Adelakun *et al.*, 2017). The area is characterized by a total annual rainfall ranging between 1270 mm - 1524 mm, with highest rainfall observed in the month of August. Monthly temperature is highest (about 30°C) in March and lowest (about 25°C) in August (Adelakun *et al.*, 2017). The River gives high fish production potentials currently supporting a high number of fisher men mainly artisanal that uses manually operated wooden (dugout) canoes and multi-gears to harvest fish. Human activities in and around the river include fishing, bathing, washing, sand dredging, human transportation to farms with local and motorized canoes. At the Northern area of the river in Jebba is a hydro-electric power dam that serves the purpose of generating power to large populace in Nigeria.

Jebba reservoir was created in 1983 on River Niger at Jebba North, downstream of Kainji dam. It lies within the middle belt of Nigeria between the coordinates 4°34'12'' - 4° 43'48''E and latitude 9°10' - 9°55'N. The reservoir basin has a length of 134 km, width of 24.1 km, mean and depth of 11 m and 60 m respectively, surface area of 1270 km², a volume of 13×10^9 m³, and catchment's area of 1.6×10^6 km² (Ita *et al.*, 1984; Obot, 1989). It has its source mainly from Kainji reservoir with other six major rivers which empty into it which are Oli, Wuruma, Moshi, Awuru on the western side and Kontangora and Eku on the Eastern part as described by Adesina *et al* (2007). The lake experiences two major floods events per year, namely the white and black floods. The white flood is a result of rain from Nigeria that enters from mid-august with peak flow of 4000-

6000m³s⁻¹ from September to October. Hence name white flood is characterised by high turbidity. The rainfall at the upper area of the Niger River in Guinea, Mali and Burkinafaso that enters the Jeba Lake in November leads to black flooding with a peak flow of about 2000 m³s⁻¹. This is distinguished by its strong clarity of water.

The study was carried out in both up- and down-stream of the dam with three (3) stations per region (Fig. 1) that covers the section notable for fishing activities. The upstream sampling stations of the dam location are about 8.7 km distance apart from the downstream stations. The downstream of Jebba reservoir flows towards Jebba south which receives water from the dam outlet and some other rivers downstream. The fisheries at the upper and downstream of Jebba reservoir are mainly artisanal. The main type of gears used are gillnets and cast nets while others include fishing traps, longlines, atalla lift-nets, and seine nets.

3.2 Sampling and Sampling Stations

Sampling followed ethical approval number UERC/ASN/2017/991 from the University's Ethical Review Committee (UERC), University of Ilorin, Nigeria. The study was carried out in up- and down-stream of JPHR located on River Niger, North-central, Nigeria. The study was structured to involve field sampling and laboratory analysis. It involved sampling of water and fish done early morning hours (06:00-09:00 am), once in a month for the period of 24 months covering two seasons at the reservoir basin and the downstream of the reservoir. Triplicate surface water samples were collected monthly in the mornings at each sampling points. Three purposive stations each where fishing activities take place were sampled and designated in each zone of the river section. Three sampling points were chosen at the upstream, located at the upper region of the dam and downstream of the dam. The sampling sites were of about 50m in breadth and the distance between each station was about 8.7 kilometers. Water samples were taken randomly in three replicates in the sampling

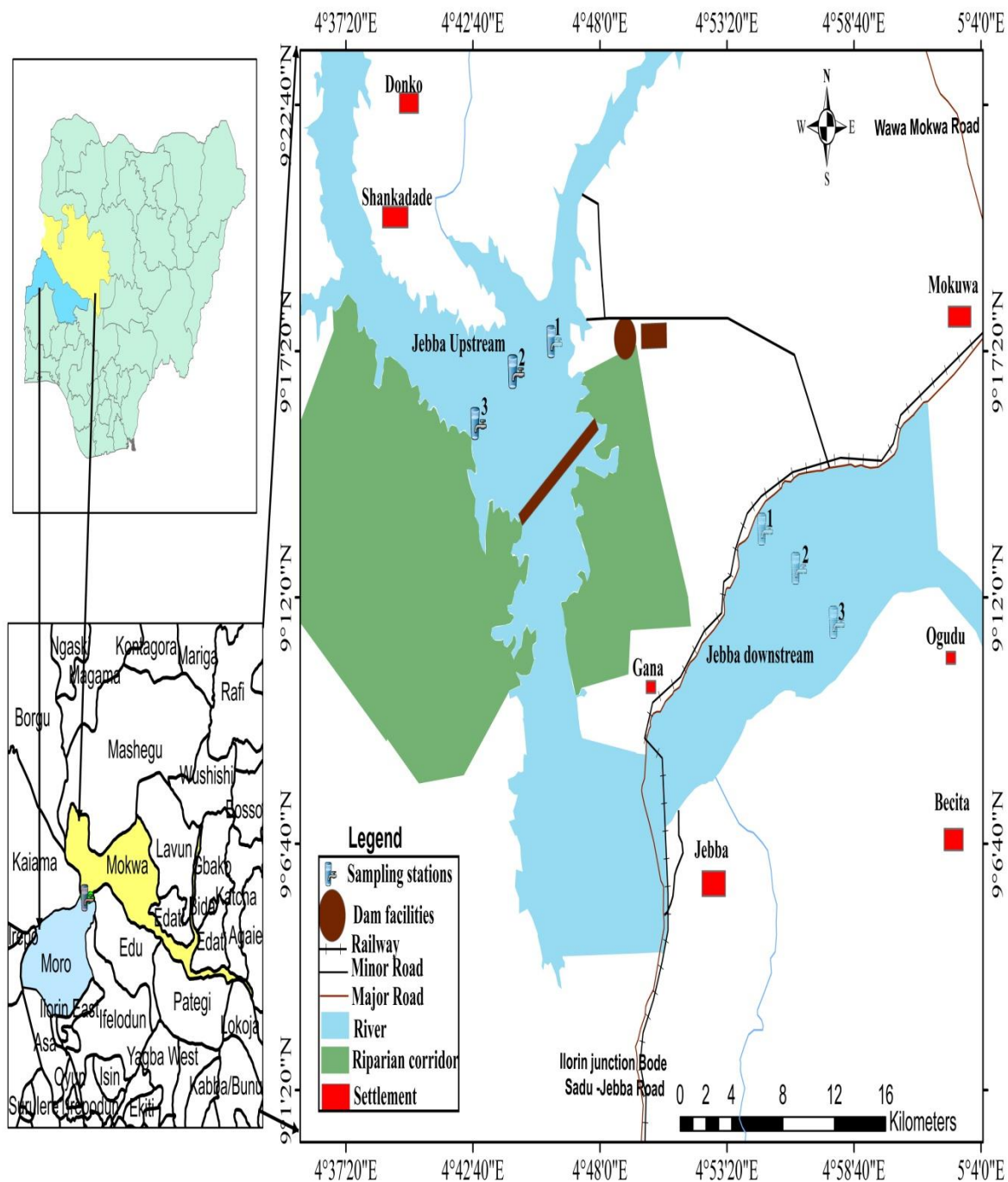


Figure 3.1: Map of Up- and Down-Stream of JHPR showing the Sampling Points

sites to determine various physico-chemical parameters.

The physical parameter and some chemical factors measurement like temperature, dissolved oxygen pH, electrical conductivity and total dissolved solids were taken in the field. Water samples were collected for the determination of the other chemical factors from 10cm depth in a sample bottles from the sampling stations of the river and taken to the laboratory for immediate analysis after collection. Analyses of the chemical parameters were done at the environmental and water quality laboratory of Mainstream Energy Nigeria Limited and at the Department of Biosciences & Biotechnology, Kwara State University, Malete.

3.3 Methodology

3.3.1 Water Temperature, pH, Electrical Conductivity and Total Dissolved Solids

Water temperature, pH, electrical conductivity and total dissolved solids were measured insitu on the water surface using Hanna portable pH/ EC/ TDS/ Temperature combined waterproof tester model HI 98129 dipped in the water for about 1-2minutes then the readings were recorded. Electrical conductivity was measured in $\mu\text{S}/\text{cm}$, temperature in degree Celsius ($^{\circ}\text{C}$) while total dissolved solids values measured in mg/l .

3.3.2 Dissolved oxygen

The dissolved oxygen of the water sample was measured via Azide modified Winkler method in which reagents H1-9373A-0, H1-93732B-0 and H1- 93732C-0 were added. A capped 60ml glass bottle that has already been filled with unreacted water sample gotten from the sampling site was uncapped and 5 drops of reagent H1-93732A-0 and 5 drops reagent of H1-93732B-0 were added simultaneously and more samples were added to completely fill the bottle to avoid trapping of the air bubbles inside the bottle. The bottle was capped and inverted several times until an orange-

yellow filtrate and flocculent precipitate appeared. It was then allowed to settle for two minutes after which 10 drops of HI 93732C-0 was added to completely dissolve the flocculent and the solution became limpid. A 10ml cuvette containing the unreacted sample was placed into the holder of Hanna multiparameter photometer, the lid was closed and zero key was pressed to prepare the machine for measurement. Another 10ml cuvette containing the reacted sample was inserted into the lid and read button was pressed to display the reading for dissolved oxygen.

3.3.3 Nitrite

Exactly 6ml of sample was taken into the cuvette with the help of pipette. The cuvette was placed into the holder of Hanna multiparameter photometer, the lid was closed and zero key was pressed to prepare the instrument for measurement. The cuvette was then removed and reagent HI 93728-0 was added and immediately shaken for exactly 10 seconds while taking care not to induce air bubbles. The cuvette was reinserted into the instrument, taking care not to shake it. The timer button was pressed to display the countdown prior to the measurement. The instrument displays the results in mg/L.

3.3.4 Phosphate high range (PO_4^{3-})

A cuvette was filled with 10ml of unreacted sample and the cuvette was inserted into the holder of Hanna multiparameter photometer, zero button was pressed to prepare the instrument for measurement. The cuvette was then removed from the holder and 10 drops of HI 93717A-0 molybdate reagent and one packet of HI 93717B-0 phosphate reagent B was added to the cuvette. The cuvette was reinserted into the instrument and timer button was pressed to display the countdown prior to the measurement. The result was displayed in mg/L.

The BOD, COD, TSS, TS, Sulphate, Chloride, Potassium, Calcium, Sodium and Magnesium also determined using Hanna multiparameter bench photometer for laboratories model HI 83200.

3.3.5 Total hardness

Total hardness was determined using titration method described in APHA (2005). 25ml of water sample transferred into a flask and diluted with 50ml distilled water. 1ml of borate buffer reagent and calmagite indicator tablet were added to the sample giving red colour and was titrated with EDTA until the red colour changed to blue. The total hardness was calculated: Number of ml of EDTA used $\times$ 20 = the amount of total hardness (mg/l) in the sample.

3.3.6 Calcium hardness

Calcium hardness of the water was measured using the Burette titration method. 50ml of the water sample diluted with 100ml distilled water. Then 2ml of 0.1M sodium hydroxide solution added to buffer sample and murexide indicator added to give pink colour. The sample then titrated with EDTA until the colour changed to blue (APHA 2005).

Calcium hardness was calculated as: No of ml of EDTA used $\times$ 0.1 = the amount of calcium hardness (mg/l) in the sample.

3.3.7 Magnesium hardness

The value was been derived by subtracting the calcium hardness value from the total hardness value (Lind, 1979).

Total hardness (mg/l) – calcium hardness (mg/l) = magnesium hardness (mg/l).

3.4 Fish Sample Collection and Morphological Identification

The samplings were carried out according to the procedures approved by the Department of Zoology, Faculty of Life Science and the University's Ethical Review Committee (UERC),

University of Ilorin, Nigeria with ethical approval number UERC/ASN/2017/991. Field trips was conducted between January, 2017 and December, 2018 to collect randomly across the selected points of upper and down-stream of Jebba reservoir in the morning hours between 06.00 and 09.00 a.m. Three locations each in upper and down-stream of Jebba reservoir were selected in order to maximize high diversity of specimens sampled amongst the most common species in the area. The sampling was conducted once a month during the collection. Fish sampling was done with the support of local fishermen using hook and line, cast and gill nets following the recommendation that reliable sampling should involve a combination of two or more gears (Gullard, 1980), which were set at the surface and bottom habitats as described by Araoye (1999). Uniform fishing efforts were used at each sampling station. Fish caught were collected into iced cooler and transported to the laboratory for further analysis and were sorted, classify into different family and identified into species level using morphological parameters as described by Idodo-Umeh (2003) and Olaosebikan & Raji (1998).

Representative sample specimens of the species encountered were collected in up and downstream, photographed and the tissue samples (tail fin) of the fish were collected and preserved in 95% ethanol for molecular characterization. Fixed voucher specimens were done with 4% formalin. Mitochondrial COI gene sequence data for the fishes were extracted and sequenced in collaboration with the State Key Laboratory, Chinese Academy of Sciences, China.

3.5 DNA Digestion and Extraction

3.5.1 Digestion

20mg each of the fin tissue were placed in an Eppendorf tube and cut into pieces with sterilized scissors (sterilized with a lamp and clean with alcohol and cotton wool). A buffer

containing 300mM Tris-HCL, 200Mm EDTA, 50mM NaCl, pH8.0 with 200g/ml of proteinase K was added to digest protein. Liquids mix together completely and incubate 8-12hours at 65°C.

3.5.2 Extraction

The phenol of same volume as those liquid was added, vortex, then centrifuge at 7000 rpm for 10minutes. The supernatant is pipette into new tube and phenol/Chloroform/isoamyl alcohol was added in ratio 25:24:1 as same volume as supernatant and vortex together. Centrifuge at 8000 rpm for 10mins and pipette the supernatant into new tube. Same volume of chloroform/isoamyl alcohol (24:1) was added as supernatant and the centrifuged at 8000 rpm for 10mins. The supernatant was pipette into new tube and isopropyl alcohol is added as the same volume as supernatant to precipitate DNA. The tube is put into fridge overnight at -20°C after which it was centrifuge at 10,000 rpm for 10mins and the supernatant removed and throws away. The extract DNA is wash in 70% ethanol, centrifuge at 10,000rpm for 10mins and supernatant is removed. The latter step is repeated and DNA is dissolved in 50 TE (pH=8.0) and store at -20°C.

3.5.3 Checking Extracted DNA Quantity Using Nanodrop

The total DNA is diluted times ten using dd H₂O. The Nanodrop is opened, wipe the sample pedestal and sample arm with a tissue to remove any leftover DNA. 2µl of dd H₂O was added on the measurement pedestal and close. The 'Measure' button was press and click blank on the desktop to ensure there is no contaminant. The apparatus arm of the sample is closed and slightly compresses the droplet and press 'Blank'. Water is wiped away from the sample and 2µL of the diluted DNA was added, sample identity was ensured and the apparatus closed to compress the droplet to measure. This was done for every sample and re-blank about every 15 samples. The result was export and 1 µL H₂O was added on the pedestal and measure twice to clean the system.

3.6 Amplification - Polymerase Chain Reaction (PCR)

3.6.1 Preparation Test Gel and Extraction Gel

1.5g of Agarose powder and 90ml of buffer with 10ml H₂O were mix together in a conical flask and warm. A gradual cooling was done through shaking in water in two directions and divide into two parts. To extract the gel, 1.5g of Agarose powder and 90ml of buffer with 10ml H₂O was used following the above procedure using bigger comb. The equipment for the PCR equipment was sterilized using UV cupboard for 10mins after which it opens for the smell to go. The concentrated 2μL of Primer is diluted in 18μL of H₂O to give 20 μL of diluted primer.

3.6.2 Materials Needed for PCR reaction

H₂O- 17.5 x (no of sample + Negative control)

Buffer- 2.8 x (no of sample + Negative control)

BSA- 1.2 x (no of sample + Negative control)

dNTP- 0.6 x (no of sample + Negative control)

Primer- 0.6 (forward) x (no of sample + Negative control)

0.6 (backward) x (no of sample + Negative control)

Taq- 0.15 x (no of sample + Negative control)Total: =24.05

The two primers is centrifuge before use with microtubes. The mixture is shakes on the thermoclyne for about 1 min and the mixture is centrifuge for about 30sec. 24 μL is put in each tubes and 1μL of the DNA template is added into each of the tubes with the PCR materials, code and centrifuge at 2000RPM. Then it was placed in PCR machine and run by setting the temperature, time, no cycle, “10” and saving the setting and then placing the sample in and run)

3.6.3 Check for PCR Result

The PCR result was check running the electrophoresis using Agarose gel. 2 μ L of the DNA template PCR result is mix with the loading buffer. 2 μ L of the DNA marker is also put on the last well of each gel at 250 bp DNA ladder and run at 150 V for about 15 mins and the result is visualize using “Genesnap” and observe each band.

3.6.4 Purification of PCR Product

The brightness/thickness of the bands is compare with the thickness of the DNA marker and dilutes the PCR product.

Dilution of PCR product (as observed in the gel)

1. Result less bright as DNA marker: Code 1- PCR product 9 μ L + 0 μ L H₂O
2. Result brightness is as high as marker: Code 2- PCR product 6 μ L + 3 μ L H₂O
3. Result too much brighter than marker: Code 3- PCR product 3 μ L + 6 μ L H₂O

The already coded micro tubes are arranged according to the dilution power coded on the same roll. The enzymes EXO1 and SAP are used cut and recover pure double stranded DNA. They hydrolyze Single-stranded DNA and dNTP.

0.3 μ L SAP + 0.15 μ L EXO1 + 0.55 μ L H₂O form the enzyme mixture. 1 μ L of the enzymes mixture above is added to 3 μ L of the dilution Code 1,2,3 PCR product above. The end mixture is centrifuge before using and thermolyne to mix it for about one minute. Then 3 μ L of the mixture is put in each tube, cover and put in the PCR machine programme at 37°C for 30mins or 80°C for 20mins. The end results now keep in the fridge until it carries out for the sequence reaction.

3.7 DNA Sequence Reaction

3.7.1 Procedure

3 μ L of the Kit (H₂O) and 3 μ L of (0.5x) primer are added into the bottom of each well together with 1 μ L of the recovery DNA template on the other side of the well. Centrifuge at

200rpm for 1mins. Then cover it with clean cover from the Oven and run the sequence reaction (PCR) for 2-3hours.

3.7.2 Purification of the Sequence Product

To purify the product, it was centrifuge for 1min. 35 μ L (75% of Isopropyl Alcohol) in each tube was added, cover back and shake for 1min at volume 4 and keep in the fridge or cupboard at room temperature for 30mins. It is then centrifuge at 3,800 rpm for 30 mins. The steps also repeated with 70 μ L of 75% of Isopropyl Alcohol. After which the Isopropyl Alcohol is drained with piles of tissue paper, keep drying and add 75 μ L of water to each well. Centrifuge at 2000rpm for 1mins (without cover) and cover it after centrifuge. Keep out of light for about about 6-8hours, and then send for sequencing.

3.8 Statistical Analysis

3.8.1 Fish Species Abundance and Diversity Assessment

Fish species abundance was assessed using the following criteria: = 10 percent = dominant, 1– 9 percent = subdominant, < 1 percent (but caught more than once) = Occasional, < 1 percent (caught only once) = Rare adopting the formula by Benech *et al.* (1983). The fish richness and diversity were determined using Margalef's index (d) for species richness, Simpson's index (D) & Shannon-Wiener index (H) for general diversity and Evenness index (E) which is the ratio of H and $H_{\max}$ in seasons and locations using PAST(Kreb, 1978; Odum, 1995; Hammer, 2001).

Data analysis was carried out to find mean $\pm$ standard error (SD) of the physico-chemical value and fish abundance per season using SPSS version 20. Percentages were also used for fish abundance for each sampling season. Factor analysis was used to test the relationship between the physico-chemical parameters and fish abundance in site and season using XLStart and PAST

software. Significant difference between up- and down-stream; dry and rainy season was tested using T-test. Significant differences level were considered at $p < 0.05$.

3.8.2 DNA Data Analyses

The nucleotide sequences were viewed and confirmed by eye using SeqManTMII (DNASTAR Lasergene 7) and aligned in MEGA 5.0 using ClustalW (Tamura *et al.*, 2011) with default parameters.

The sequences were translated into amino acids to check for premature stop codons and to confirm that the open reading frame was maintained in the protein-coding loci. All amplified FASTA sequences were submitted to a BLAST search in GenBank (<https://blast.ncbi.nlm.nih.gov/Blast.cgi>) to examine the identity and taxonomic designations of best-match sequences. All the related COI sequences in the Genbank were downloaded and neighbor-joining (NJ) tree were drawn for each of the species identified morphologically as implemented in MEGA 5.0 based on the Kimura 2 parameter distance (K2P) (Kimura, 1980).

The identification using criteria by Deichmann *et al.* (2017) and Nneji *et al.* (2019) were followed for NJ trees based on: (1) samples were identified as the identical species if the sequences clustered with such individuals from GenBank; (2) if samples were morphologically identified as the same but in different clades (population divergence), samples were treated as geographic variation of the same species; (3) samples were regarded as different species if they did not match the morphological definition of that species and displayed significant genetic variability as well; and (4) specimens were regarded as different species even when morphologically classified as the same species but in separate groups, sister to other species.

A similarity cut-off of 97% was used for species identification (Hebert *et al.*, 2003). MEGA v. 5.0 was used to create a neighbor-joining (NJ) tree based on the Kimura 2 parameter distance (K2P) (Kimura, 1980) and estimate inter- and intraspecific sequence divergences. Nodal support for NJ tree analysis was estimated using 1000 bootstrap pseudoreplicates

CHAPTER FOUR

4.0 Results

4.1. Physico-Chemical Characteristics of the Water Body

The ranges mean and standard error values of the physico-chemical parameters in up and downstream of Jebba reservoir are presented in Table 4.1a. All the parameters values were within the stipulated limit of Federal Ministry of Environment in Nigeria. The T-test analysis of the water parameters was not significantly ($p>0.05$) different across the locations of the up and down-stream during the period of study. However, COD was significantly ($p<0.05$) different having higher value at the downstream. The DO, hardness, turbidity, nitrate, TS, BOD, chloride, and ions has higher insignificant ($p>0.05$) values at the downstream. Only the TSS and hydrogen carbonate have higher value that are not statistically different at the upstream.

Generally, higher concentration values were recorded during the dry season in calcium hardness, magnesium hardness, TS, Total hardness, BOD, COD, chloride, sodium ion, calcium ion and magnesium ion (Table 4.1b) with other parameters showing higher concentration values during the rainy season. The turbidity, calcium hardness, magnesium hardness, total hardness, TSS, and magnesium showed a significant ($p<0.05$) difference in seasons.

The water temperature showed no significant ($p>0.05$) difference across the locations and seasons for the period of study. The monthly mean changes in the surface water temperature in up- and down-stream of Jebba reservoir is shown in Figure 4.1a. The mean monthly temperature of the upstream was $27.48\pm0.37^{\circ}\text{C}$ and downstream was $27.16\pm0.26^{\circ}\text{C}$ with higher mean temperature toward the inception of rainy season. The temperature range at the up- and down-stream was between $23.85\text{--}32.86^{\circ}\text{C}$ and $23.65\text{--}32.85^{\circ}\text{C}$ respectively.

Table 4.1a: Mean Physico-chemical Parameters in Up and Down Stream of JHPR during the sampling year

Parameters	Upstream Section Range	Mean±S.E	Downstream Section Range	Mean±S.E	FMEnv . Limit
Temperature(°C)	27.40-32.20	27.64±0.39	24.20-29.50	27.11±0.28	<40
pH	7.5-8.51	7.86±0.11	7.03-8.37	7.73±0.09	6-9
Conductivity(µS/cm)	51.0-76.00	58.49±1.44	51.00-65.00	58.38±1.42	NS
TDS(mg/L)	26.00-37.00	29.63±0.71	24.00-35.00	29.82±0.69	2000
DO(mg/L)	2.00-5.40	5.29±0.34	3.06-5.50	5.45±0.32	>2
Turbidity(NTU)	1.70-360	105.7±28.72	1.20-375.00	106.6±28.77	NS
Nitrite(mg/L)	0.20-3.40	1.45±0.18	0.38-3.20	1.53±0.19	20
Phosphate(mg/L)	3.05-5.65	3.87±0.23	2.40-4.99	3.87±0.20	5
Calcium hardness(mg/L)	2.05-7.70	5.88±0.35	0.81-9.10	6.67±0.48	NS
Magnesium hardness(mg/L)	1.62-9.56	7.40±0.47	1.72-11.05	7.89±0.54	NS
TSS(mg/L)	0.22-2.55	1.25±0.17	0.19-2.50	1.22±0.16	30
TS(mg/L)	26.23-30.55	28.88±0.40	25.27-32.20	29.55±0.44	NS
Total hardness(mg/L)	3.73-16.70	13.62±0.80	2.53-20.15	14.85±1.02	NS
BOD(mg/L)	0.20-2.10	1.51±0.13	0.4-2.55	1.69±0.13	30
COD(mg/L)	20.50-29.00	28.15±0.94	25.80-35.67	31.28±0.76*	40
Chloride(mg/L)	19.00-119.00	53.89±6.86	25.10-128.22	56.85±6.85	600
Hydrogen Carbonate(mg/L)	30.00-110.00	59.05±3.57	38.00-92.50	56.19±3.21	NS
Potassium ion(mg/L)	0.80-1.78	1.39±0.07	0.45-1.74	1.43±0.08	NS
Sodium ion(mg/L)	1.00-1.81	1.72±0.15	1.04-1.88	1.79±0.15	NS
Calcium ion(mg/L)	0.82-3.00	1.99±0.12	0.81-3.35	2.35±0.18	200
Magnesium ion(mg/L)	1.22-2.16	2.03±0.11	1.10-2.50	2.17±0.12	200

Legend: TDS: Total dissolved solids; DO: Dissolved oxygen; TSS: Total suspended solute; TS: Total solids; BOD: Biological oxygen demands; COD: Chemical oxygen demands.

Table 4.1b: Mean Seasonal Physico-chemical Parameters in Up and Down Stream of JHPR during the sampling year

Parameters	Dry season		RainySeason		FMEnv · LIMIT
	Range	Mean±S.E	Range	Mean±S.E	
Temperature(°C)	24.40-32.20	29.93±0.40	24.20-29.50	27.83±0.24	<40
pH	7.05-8.51	7.71±0.10	7.3-8.37	7.88±0.10	6-9
Conductivity(µS/cm)	51.0-76.00	57.54±0.87	51.00-65.00	59.33±1.80	NS
TDS(mg/L)	26.00-37.00	28.99±0.45	24.00-35.00	30.46±0.86	2000
DO(mg/L)	2.00-5.40	5.02±0.31	3.06-6.20	5.72±0.34	>2
Turbidity(NTU)	1.70-56	36.76±6.73	1.20-375.00	175.40±34.49***	NS
Nitrite(mg/L)	0.20-3.40	1.35±0.19	0.38-3.20	1.62±0.18	20
Phosphate(mg/L)	2.05-6.65	5.88±0.35	2.40-6.99	6.67±0.48	5
Calcium hardness(mg/L)	2.05-7.70	7.18±0.36	0.81-9.10	5.37±0.41*	NS
Magnesium hardness(mg/L)	1.62-9.56	8.77±0.38	1.72-11.05	6.52±0.51*	NS
TSS(mg/L)	0.22-2.55	0.98±0.16	0.19-2.50	1.48±0.16*	30
TS(mg/L)	26.23-30.55	29.41±0.40	25.27-32.20	29.01±0.44	NS
Total hardness(mg/L)	3.73-16.70	16.51±0.71	2.53-20.15	11.96±0.86***	NS
BOD(mg/L)	0.20-2.10	1.73±0.14	0.4-2.55	1.47±0.10	30
COD(mg/L)	20.50-32.10	29.90±1.13	25.80-35.67	29.54±0.65	40
Chloride(mg/L)	19.00-119.00	64.43±7.71	25.10-128.22	46.31±5.26	600
Hydrogen Carbonate(mg/L)	30.00-110.00	55.08±2.28	38.00-92.50	60.16±4.18	NS
Potassium ion(mg/L)	0.80-1.78	1.35±0.08	0.45-1.74	1.47±0.07	NS
Sodium ion(mg/L)	1.00-2.51	1.97±0.14	1.04-1.58	1.54±0.14	NS
Calcium ion(mg/L)	0.82-3.00	2.31±0.18	0.81-3.35	2.03±0.13	200
Magnesium ion(mg/L)	1.22-3.16	2.42±0.09	1.10-2.50	1.78±0.10****	200

Legend: TDS: Total dissolved solids; DO: Disolved oxygen; TSS: Total suspendent solute; TS: Total solids; BOD: Biological oxygen demands; COD: Chemical oxygen demands.

Highest surface water temperature was recorded in month of March, 2018 at the upstream and lowest in month of January, 2018 at the downstream (Figure 4.1a).

The mean pH variations at the sampling stations showed no significant ($p>0.05$) difference in both locations and seasons (Table 4.1a and b). There were variations in the monthly values recorded with the reservoir showing moderate alkalinity (Figure 4.1b). The mean monthly value at the upstream recorded was 7.80 ± 0.11 and at the downstream was 7.57 ± 0.08 . Higher pH value was recorded during the raining season with the month of June, 2018 having 8.47 and lowest value of 7.11 in the month of May, 2017, both at the upstream with no statistical difference ($p>0.05$) in seasons and locations. The pH was close to neutral during the dry season at both stations but moderately alkaline in rainy season with no value less than 7 recorded in both season and stations.

The mean monthly water conductivity variations range between 51-77 μ S/cm at the upstream and 36.38- 76.67 μ S/cm at the downstream (Table 4.1c). The lowest conductance was recorded in May, 2017 at the downstream and highest in August, 2018 (Figure 4.1c). The total dissolved solids in the sampling stations shows that the lowest and highest TDS was recorded in May, 2017 and August, 2018 (Figure 4.1d). Mean monthly TDS ranges between 25.33mg/L in December, 2018 to 38.33mg/L in August, 2018 at the upstream and 22mg/L in April, 2017- 39.33mg/L in August, 2018 at the downstream. Both conductivity and TDS were not statistically significant ($p>0.05$) among the seasons and locations of the sampling area.

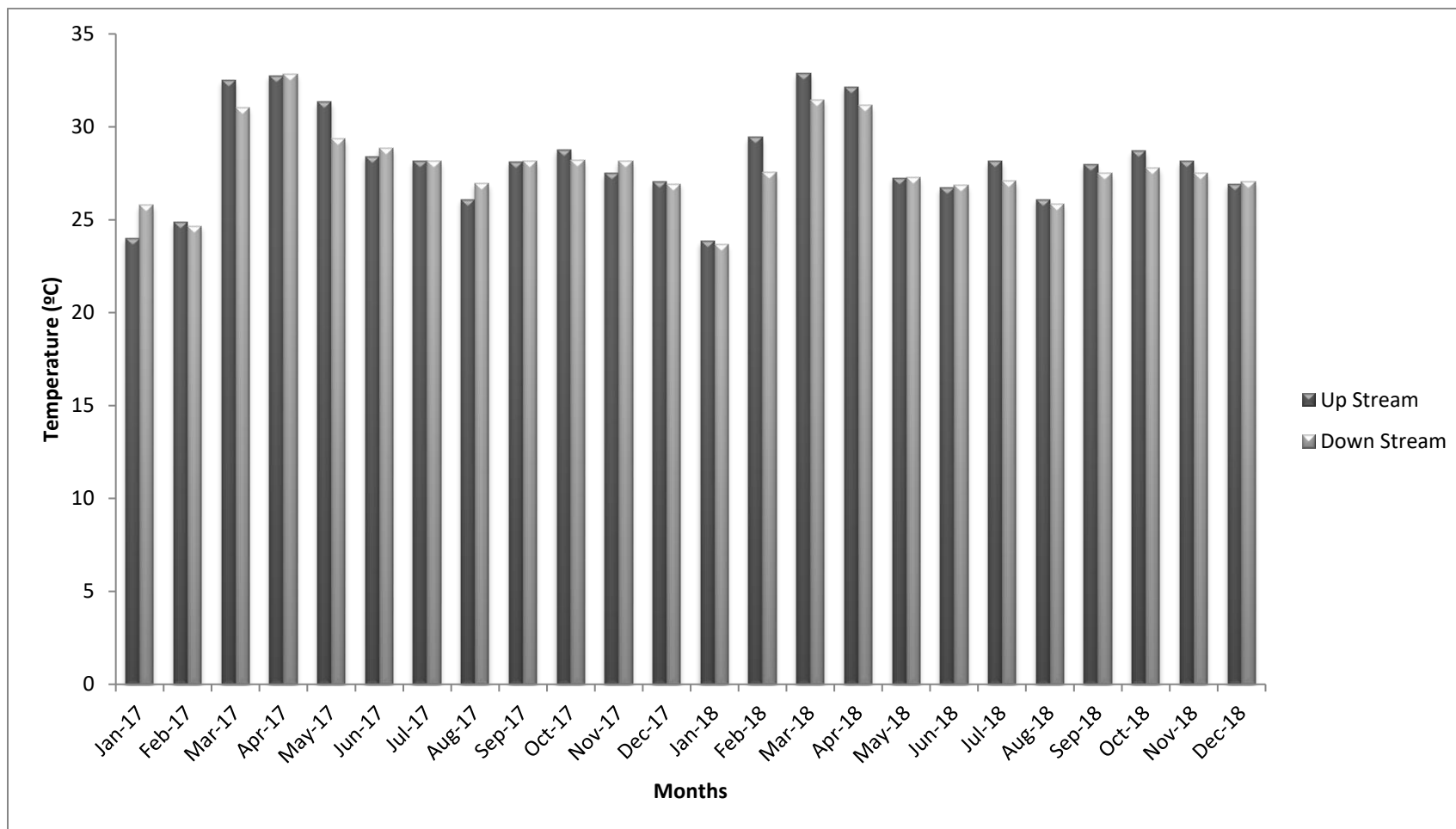


Figure 4.1a: Mean Monthly Variations in the Surface Water Temperature inUp- and Down-stream of JHPR

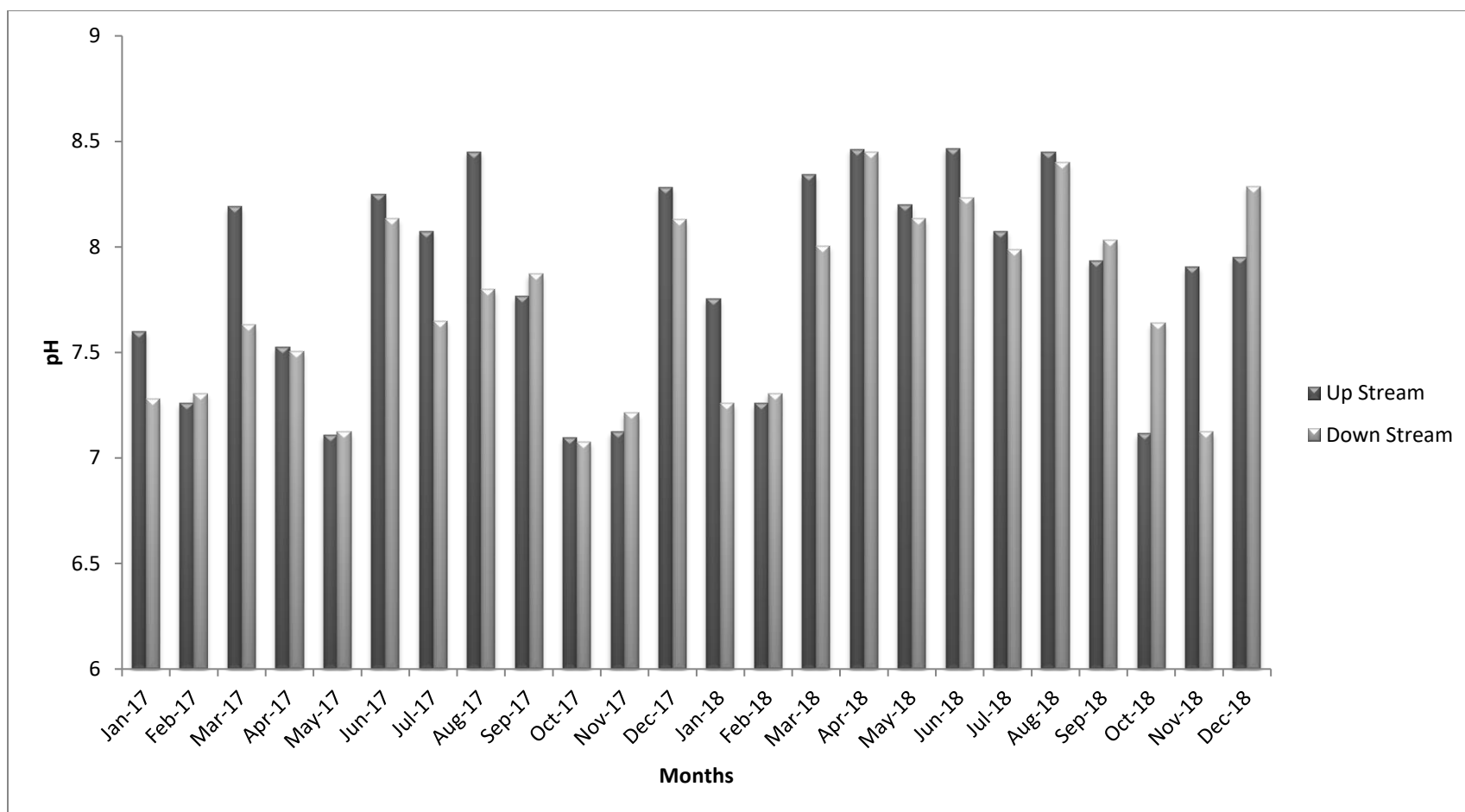


Figure 4.1b: Mean Monthly pH Variations in the Up- and Down-stream of JHPR.

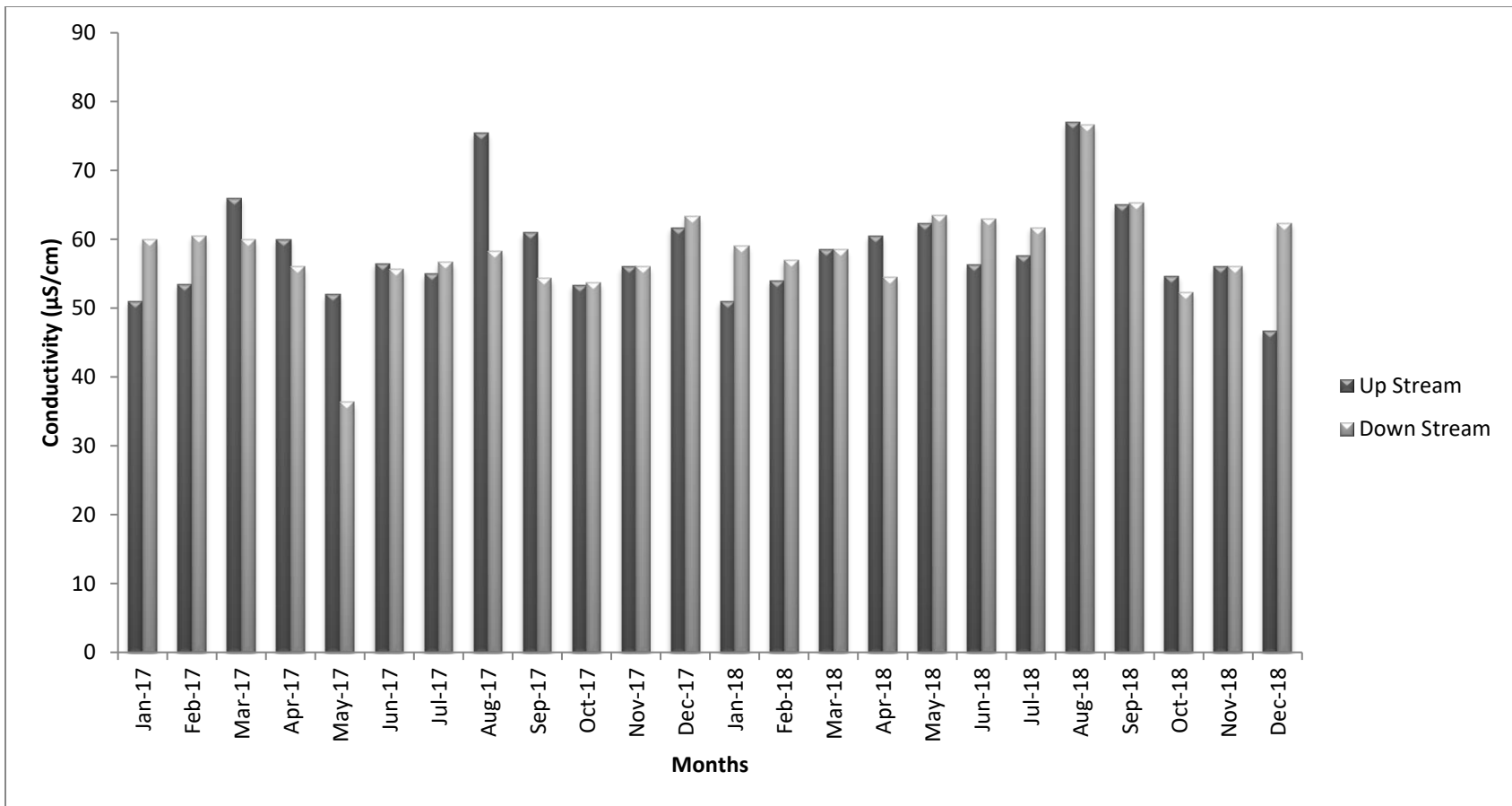


Figure 4.1c: Mean Monthly Variations in the Conductivity in Up- and Down-stream of JHPR.

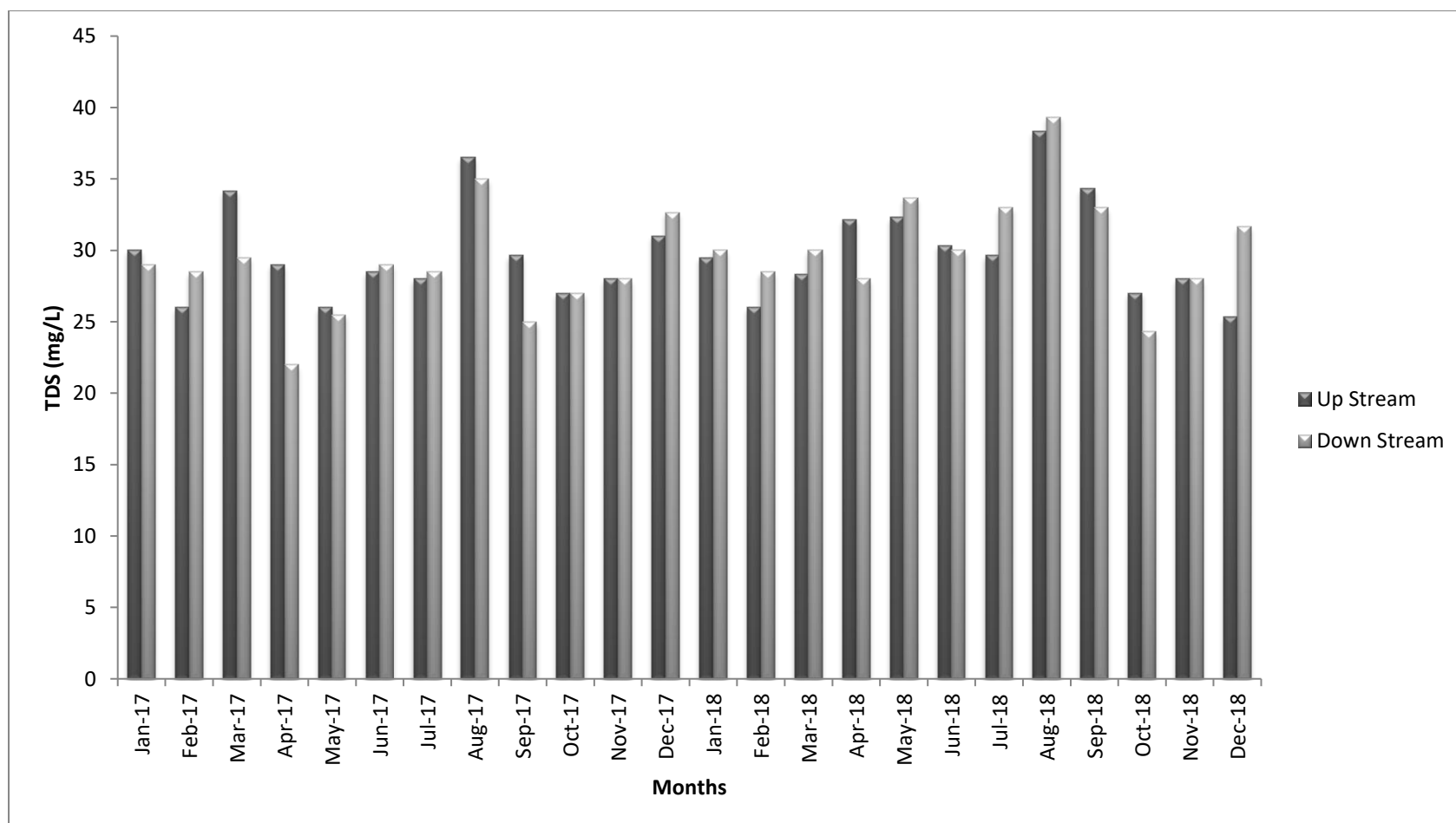


Figure 4.1d: Mean Monthly Variations in the Total Dissolved Solute (TDS) in Up- and Down-stream of JHPR.

Higher value of dissolved oxygen were observed during raining season with no significant ($p>0.05$) difference among the locations and seasons during the period of study. The mean of the dissolved oxygen variation is presented in figure 4.1e. The fluctuation ranges between 3.31mg/L in April, 2017 and 8.13mg/L in August, 2018. The upstream shows a maximum and minimum temperature of 3.31mg/L and 8.03mg/L respectively while the downstream recorded maximum and minimum temperature of 3.65mg/l 8.13mg/L in month of April and June, 2018 respectively.

The turbidity of the water samples were statistically significant ($p<0.05$) among the seasons with high turbidity values towards the end of the raining season. There was no significant ($p>0.05$) differences in the turbidity within the locations with monthly turbidity in up- and down-stream varied between 1.71-359NTU (May, 2017 and August, 2018) and 1.21-371NTU (May 2017 and August, 2017). The highest and lowest turbidity were recorded at the downstream station (Figure 4.1f).

The nitrate concentration ranges between 0.42-3.00mg/L at the upstream and 0.39-3.15mg/L at the downstream with no significant ($p>0.05$) differences in seasons. The nitrate concentration variations observed during the sampling period is presented in Figure 4.1g. The nitrate concentration had its peaks in the month of July and December for raining and dry season respectively. The phosphate had a diurnal fluctuation as shown in Figure 4.1.1h. The phosphate concentration ranges between 1.95-5.75mg/L. At the upstream, the highest and lowest concentration of 1.95mg/L and 5.75mg/L were observed in the month of April and July, 2018 respectively. Whereas at the downstream, October, 2017 had the lowest phosphate concentration of 2.43mg/L while July, 2018 recorded the highest phosphate concentration of 5.75mg/L.

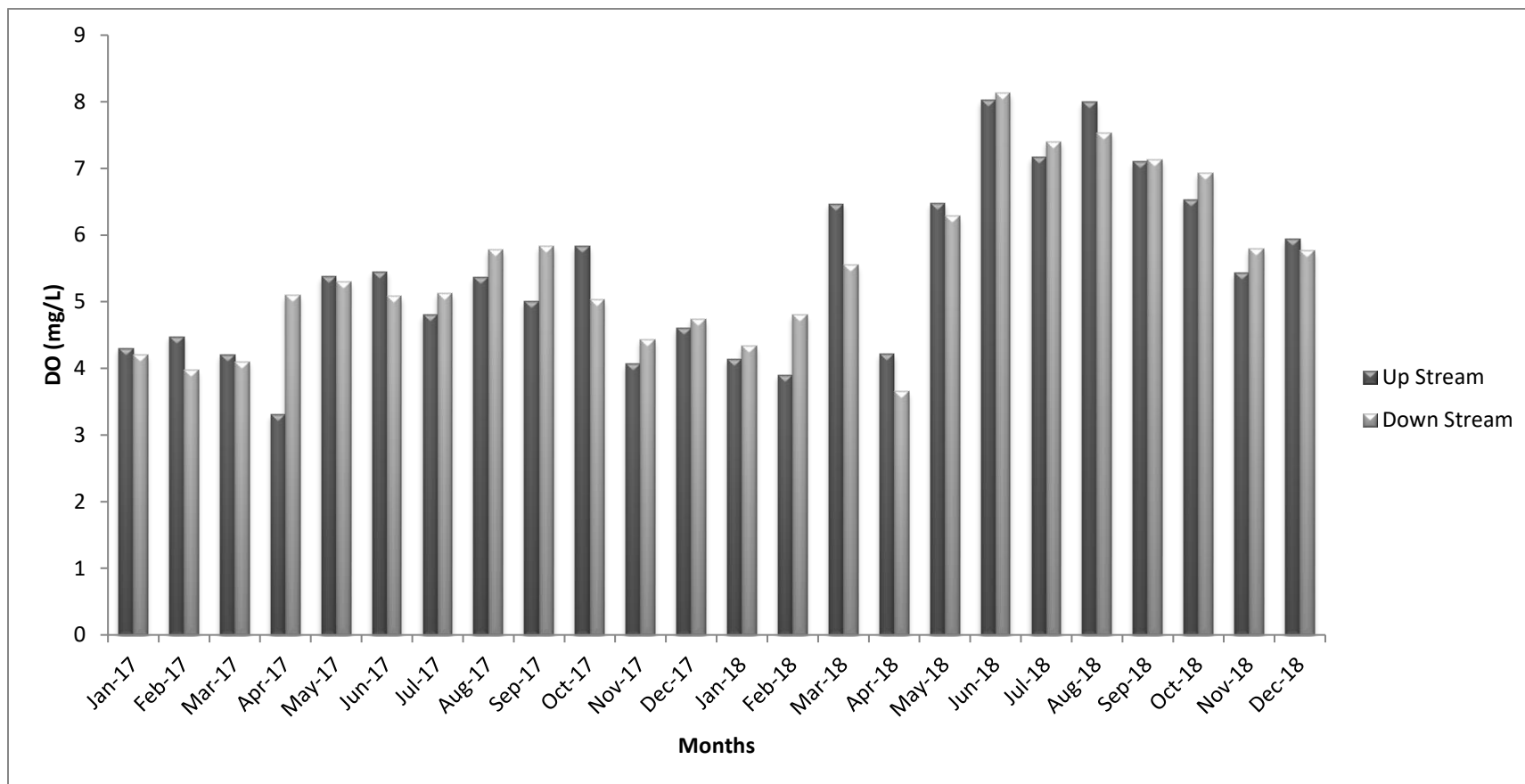


Figure 4.1e: Mean Monthly Variations in the Dissolved Oxygen inUp- and Down-stream of JHPR.

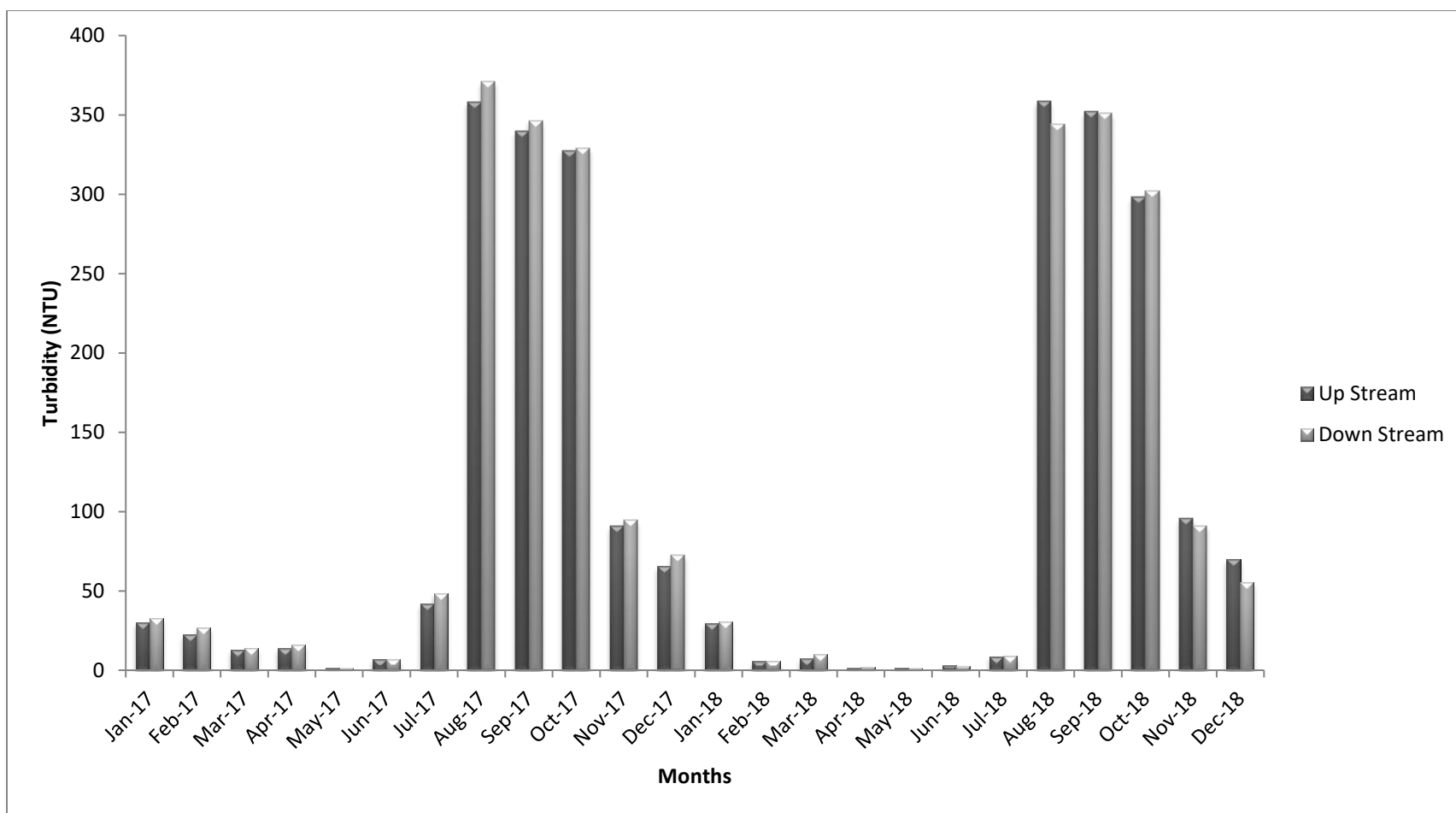


Figure 4.1f: Mean Monthly Variations in the Turbidity inUp- and Down-stream of JHPR.

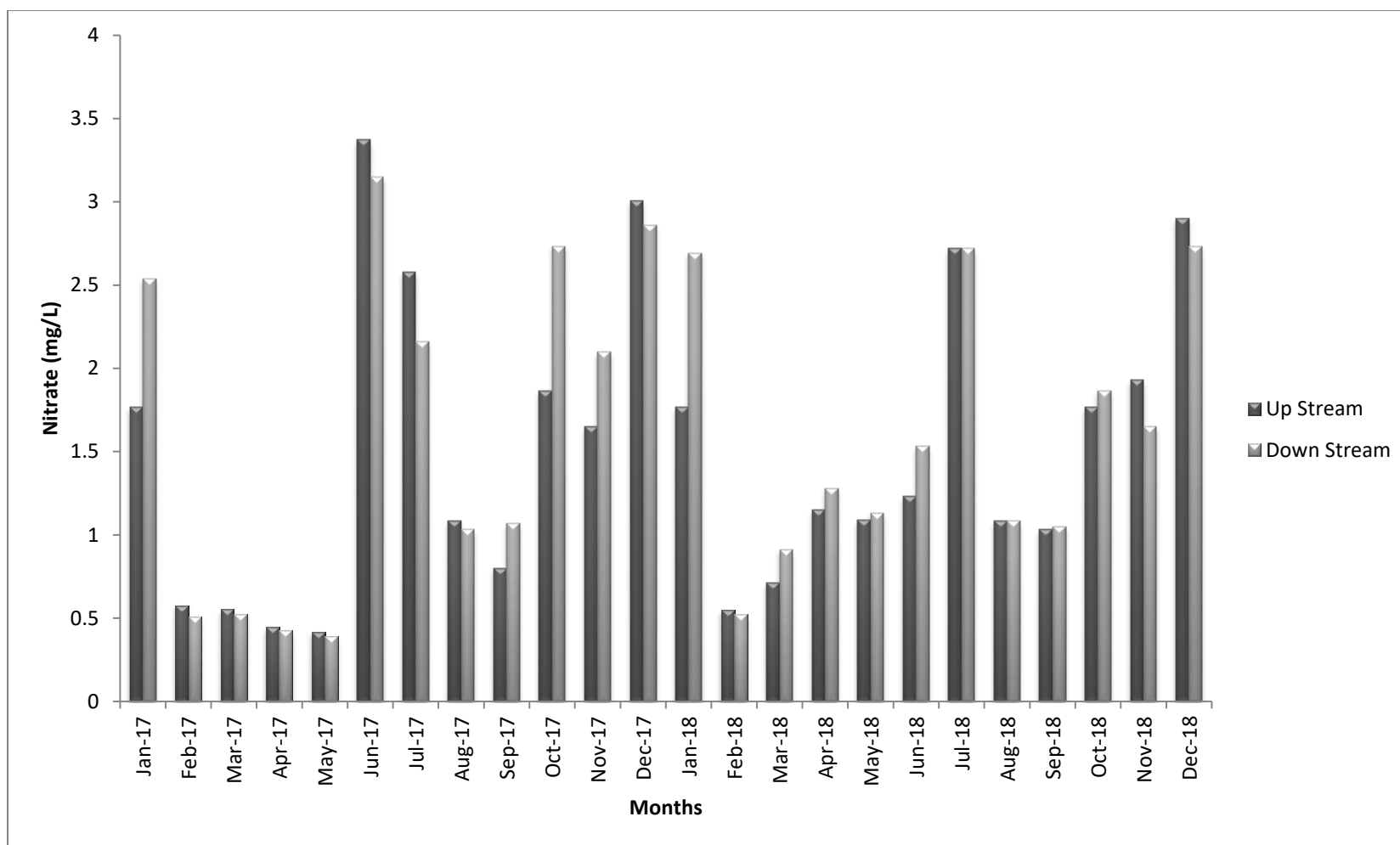


Figure 4.1g: Mean Monthly Variations in the Nitrate concentration in Up- and Down-stream of JHPR.

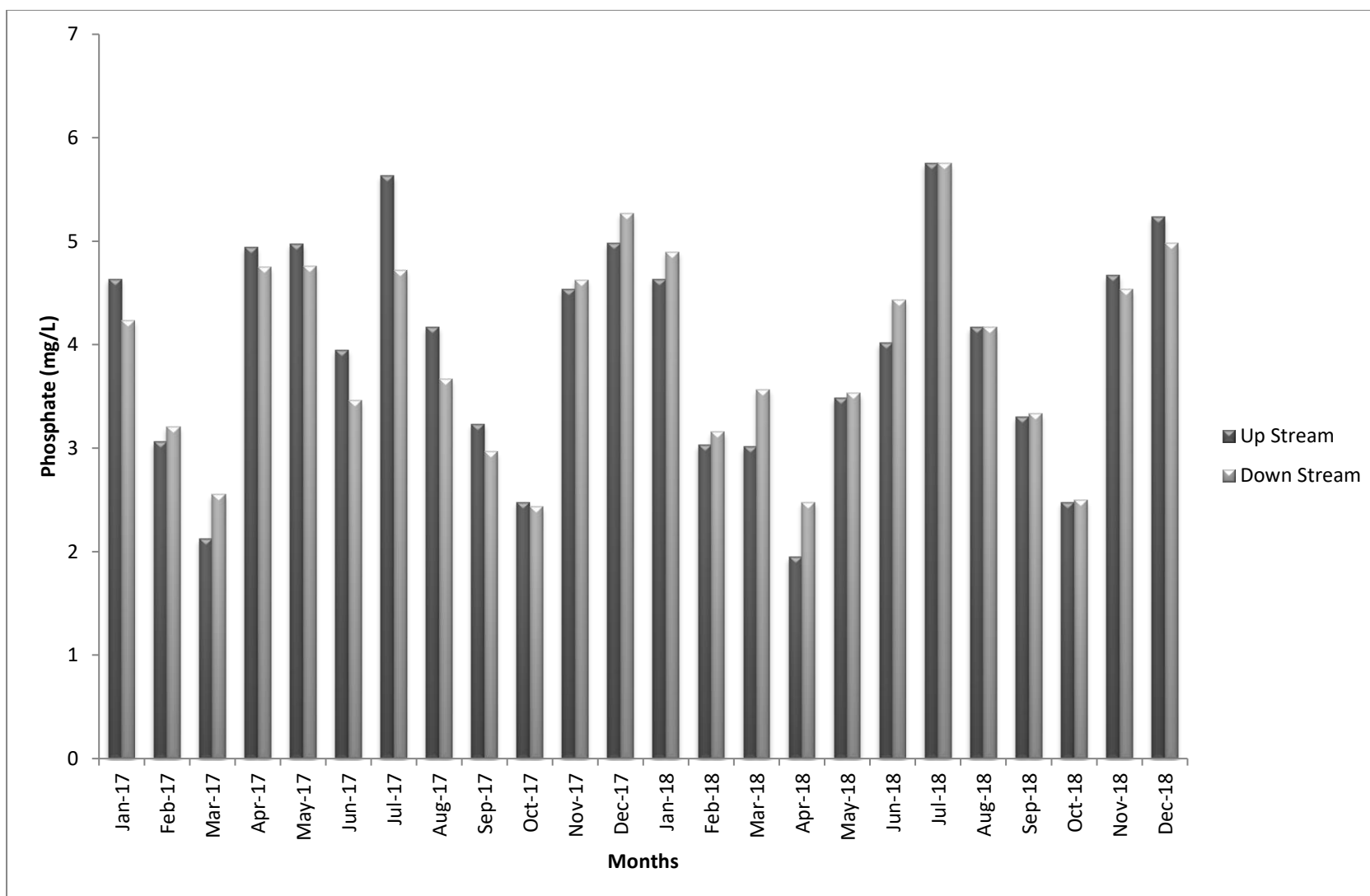


Figure 4.1h: Mean Monthly Variations in the Phosphate Concentrations in Up- and Down-stream of JHPR.

The highest calcium hardness concentration was recorded in the month of March, 2018 and lowest in the month of May, 2017 (Figure 4.1i). The drastic fall and rise was experienced at these periods of time at the downstream. Generally, the downstream has higher calcium hardness concentration than the upstream except in the month of May, 2017 and December, 2018 with a significant ($p<0.05$) difference observed in seasons. The ranges of the concentration recorded were between 0.89-11.075mg/L.

The magnesium hardness were also statistically significant ($p<0.05$) across the locations for the study period. The mean monthly variation of the magnesium hardness of Jebba reservoir ranges between 1.65-12.39mg/L at the upstream and 1.76-13.29mg/L at the downstream in the months of May, 2017 and June, 2018 (Figure 4.1j). The magnesium hardness showed a statistical ($p<0.05$) difference in seasons and there were drastic fall and rise in the ions concentration recorded during the sampling period.

The total hardness follow the pattern of variation as recorded in both calcium and magnesium hardness having a significant ($p<0.05$) difference across the locations and seasons. High concentrations were recorded during the dry season (Figure 4.1k). At the upstream, the lowest (3.73mg/L) and highest (16.70mg/L) concentrations were recorded in May, 2017 and December, 2018 while at the downstream, the lowest (2.53mg/L) and highest (21.48mg/L) concentrations were recorded in the months of May, 2017 and March, 2018 respectively.

The lowest (0.24mg/L) and highest (2.525mg/L) TSS concentration value were recorded in the months of February and July, 2017 at the upstream. At the downstream, the lowest (0.20mg/L) and highest (2.68mg/L) concentration value were obtained in the months of February and July, 2018. A significant ($p<0.05$) difference was also observed in season for the TSS during

the study period with lower concentration in dry season. A fall in concentration value also experience after August break (Figure 4.1l).

The lowest TS concentration value of 25.76mg/L was recorded at the downstream in May, 2017, and highest value of 35.33mg/L recorded at the downstream in December, 2017. The monthly variation in TS as observed in up- and down-stream of the station is shown in figure 4.1m.

The mean monthly mean variation in the biological oxygen demand of the up- and down-stream is shown figure 4.1n. The lowest (0.22mg/L) and highest (2.68mg/L) values were recorded in months of May, 2017 and November, 2018 at the upstream. The lowest value of the biological oxygen demand at the downstream recorded 0.48mg/L in month of May, 2017 and highest value of 2.68mg/L in month of November, 2017.

The mean monthly variation of the chemical oxygen demand of Jebba reservoir ranges between 20.65-38.85mg/L. The lowest and highest mean value were recorded at the upstream in March & January, 2017 respectively while at the downstream the mean range value of 25.93-40mg/L were obtained in October, 2018 and January, 2017 respectively (Figure 4.1o). Generally, a significant ($p < 0.05$) difference was observed in locations having higher value downstreams throughout the sampling periods.

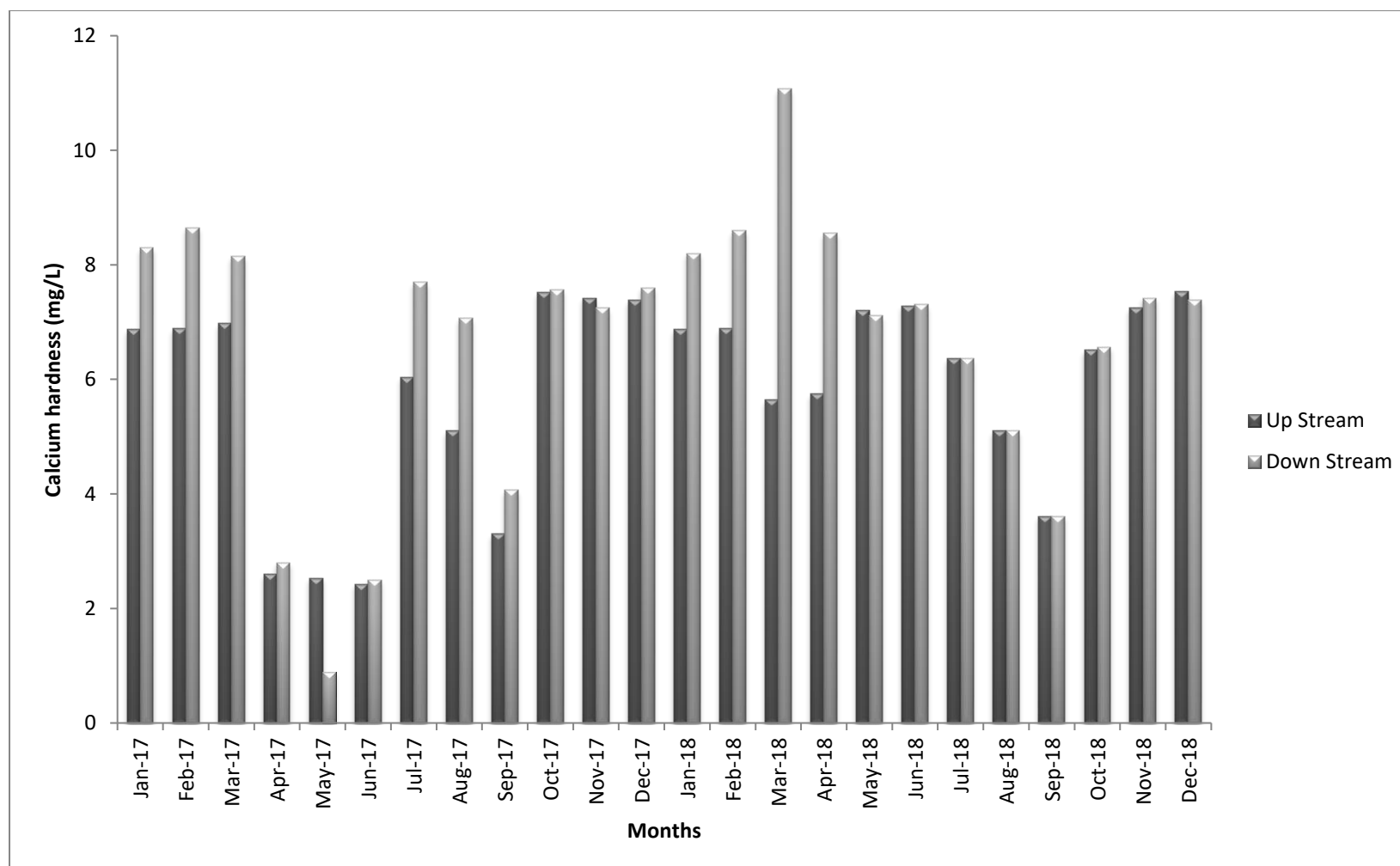


Figure 4.1i: Mean Monthly Variations in the Calcium Hardness inUp- and Down-stream of JHPR

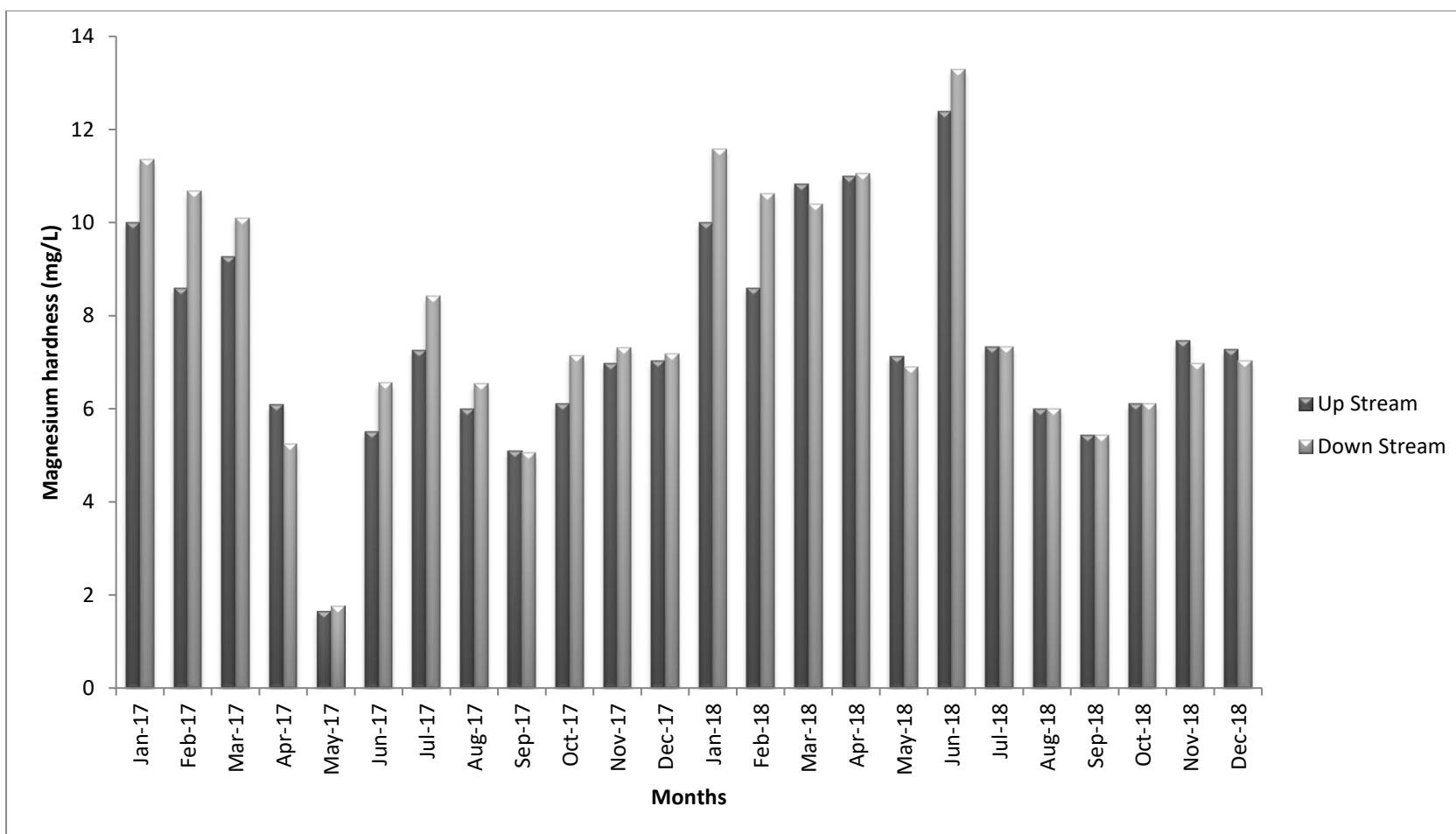


Figure 4.1j: Mean Monthly Variations in the Magnesium Hardness inUp- and Down-stream of JHPR

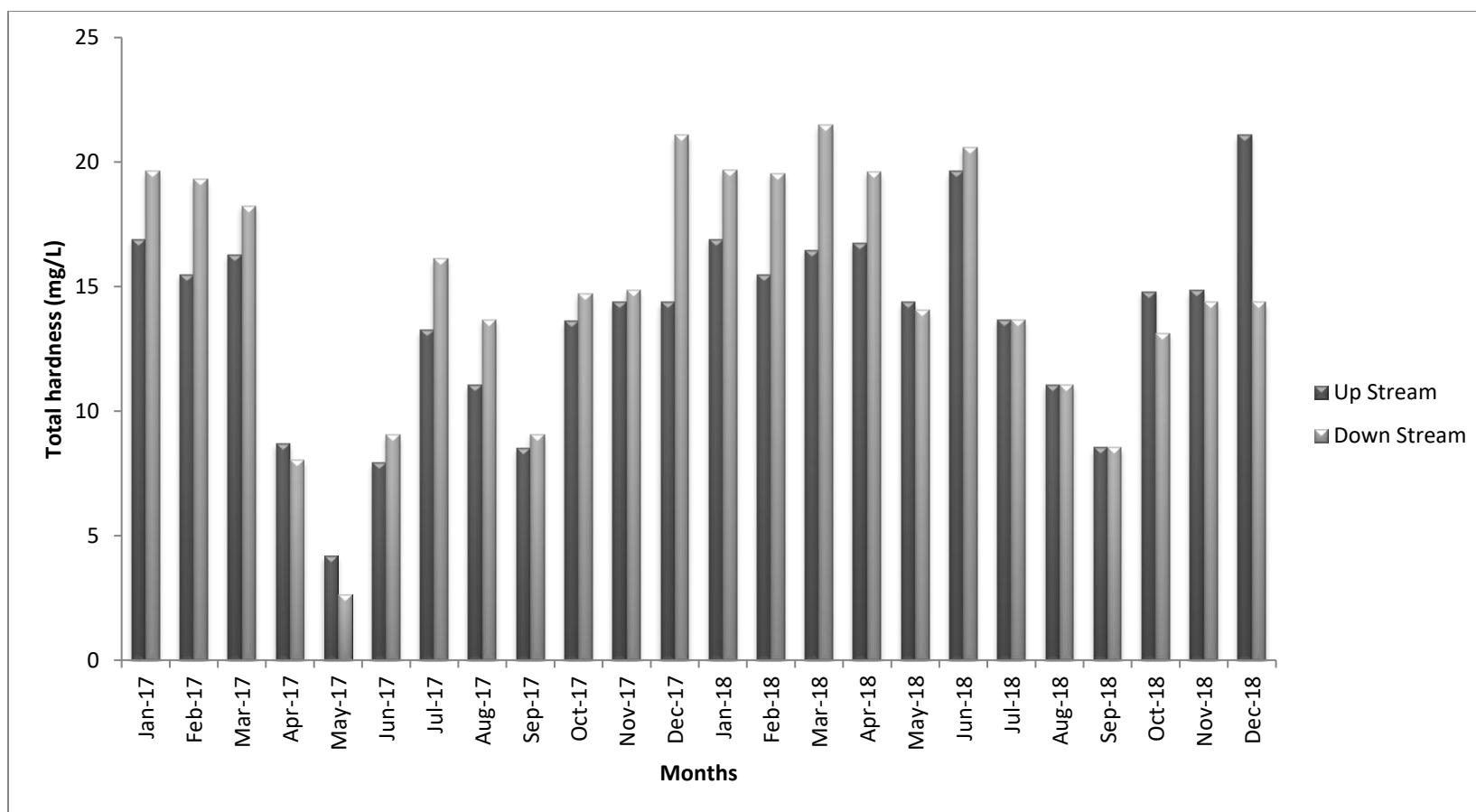


Figure 4.1k: Mean Monthly Variations in the Total Hardness in Up- and Down-stream of JHPR

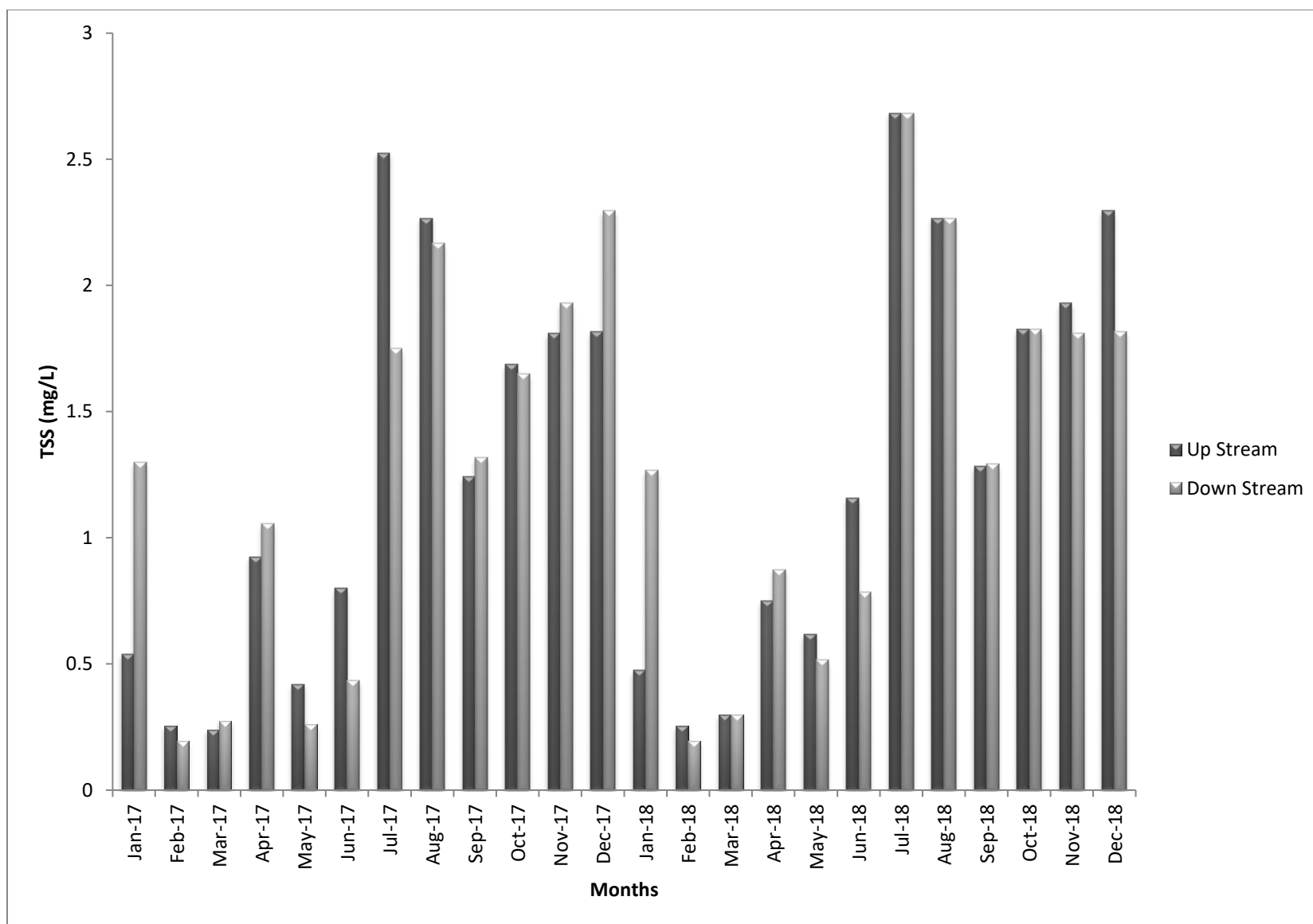


Figure 4.11: Mean Monthly Variations in the TSS in Up- and Down-stream of JHPR

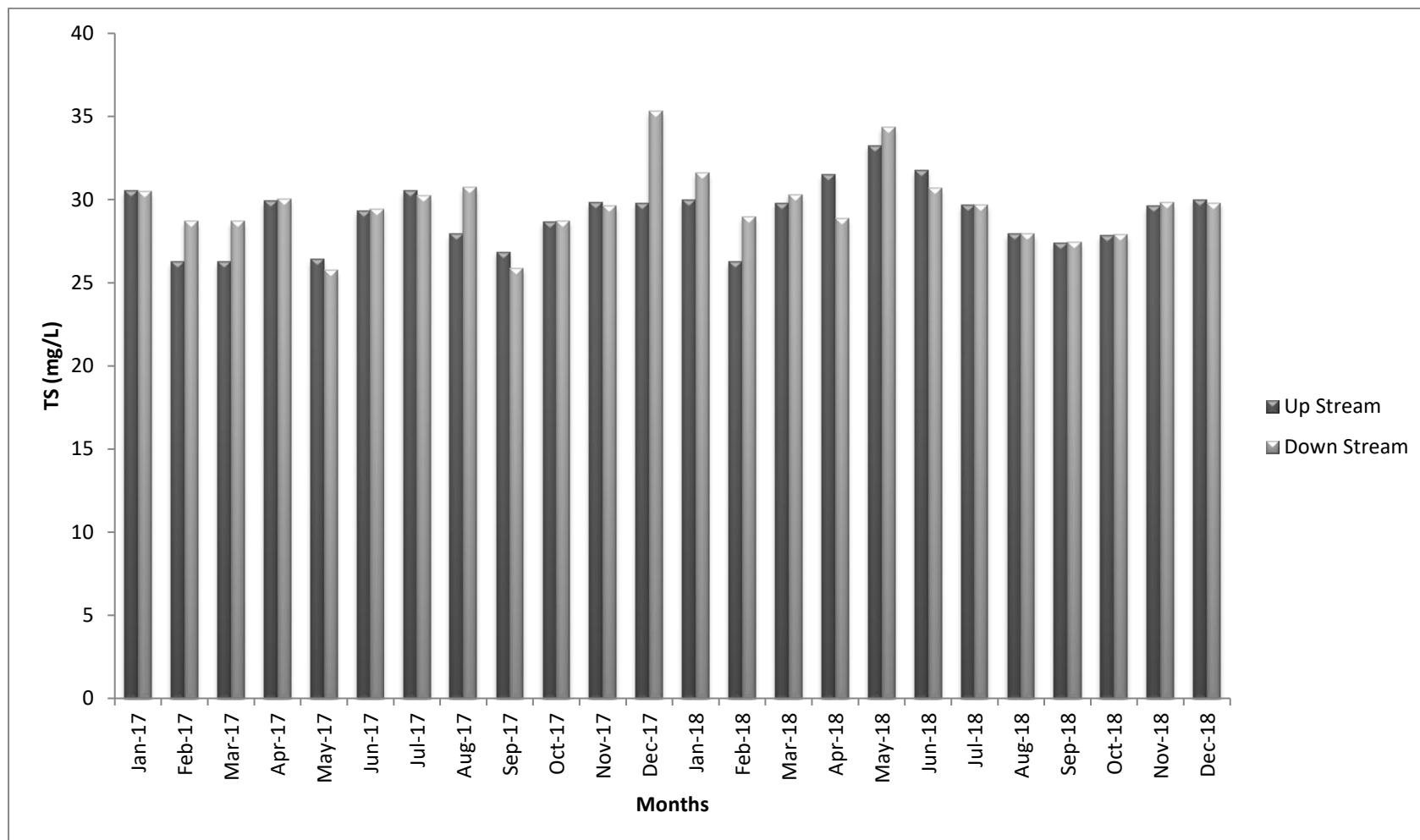


Figure 4.1m: MeanMonthlyVariations in the TS in Up- and Down-stream of JHPR

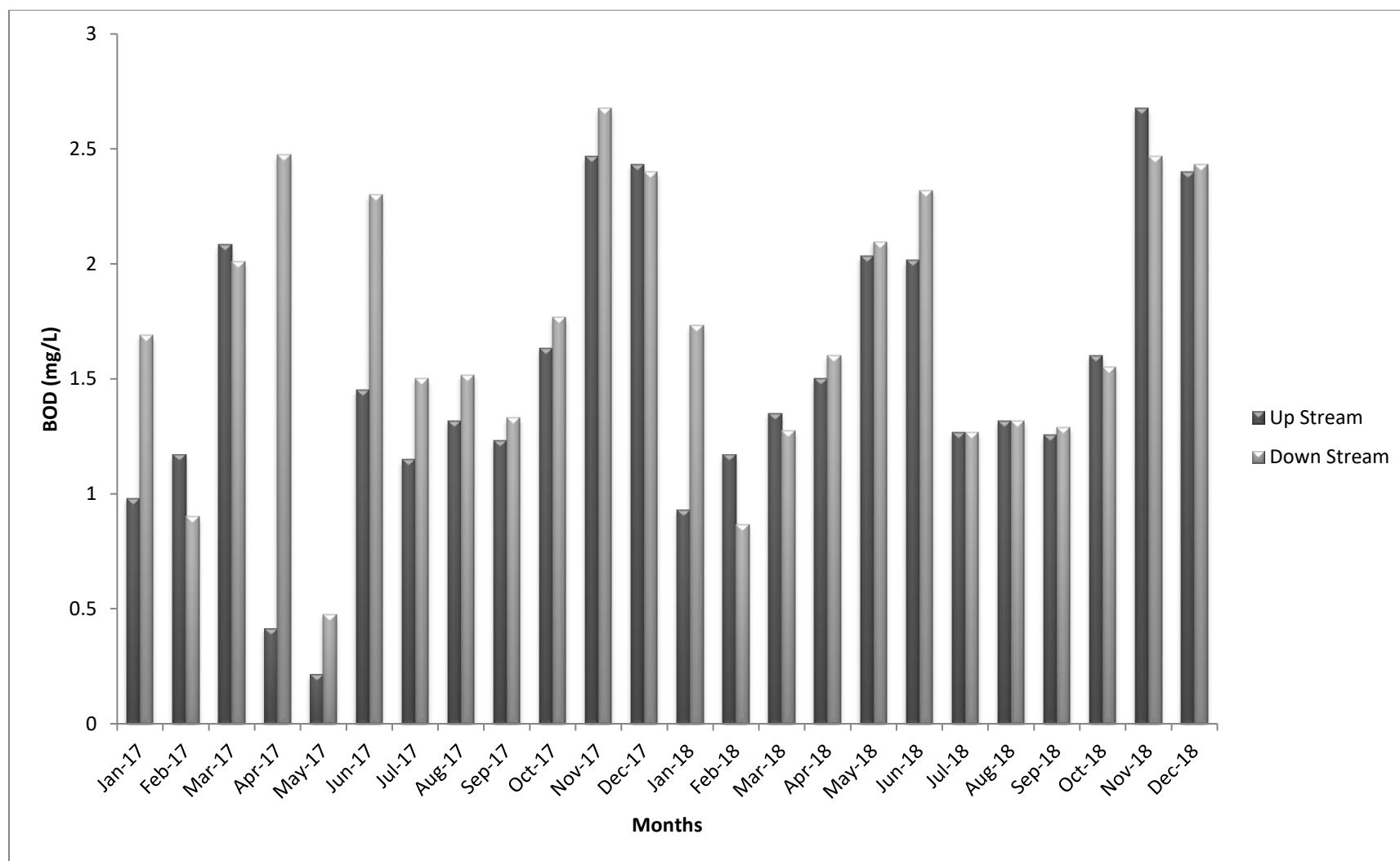


Figure 4.1n: MeanMonthlyVariations in the Biological Oxygen Demand in Up- and Down-stream of JHPR

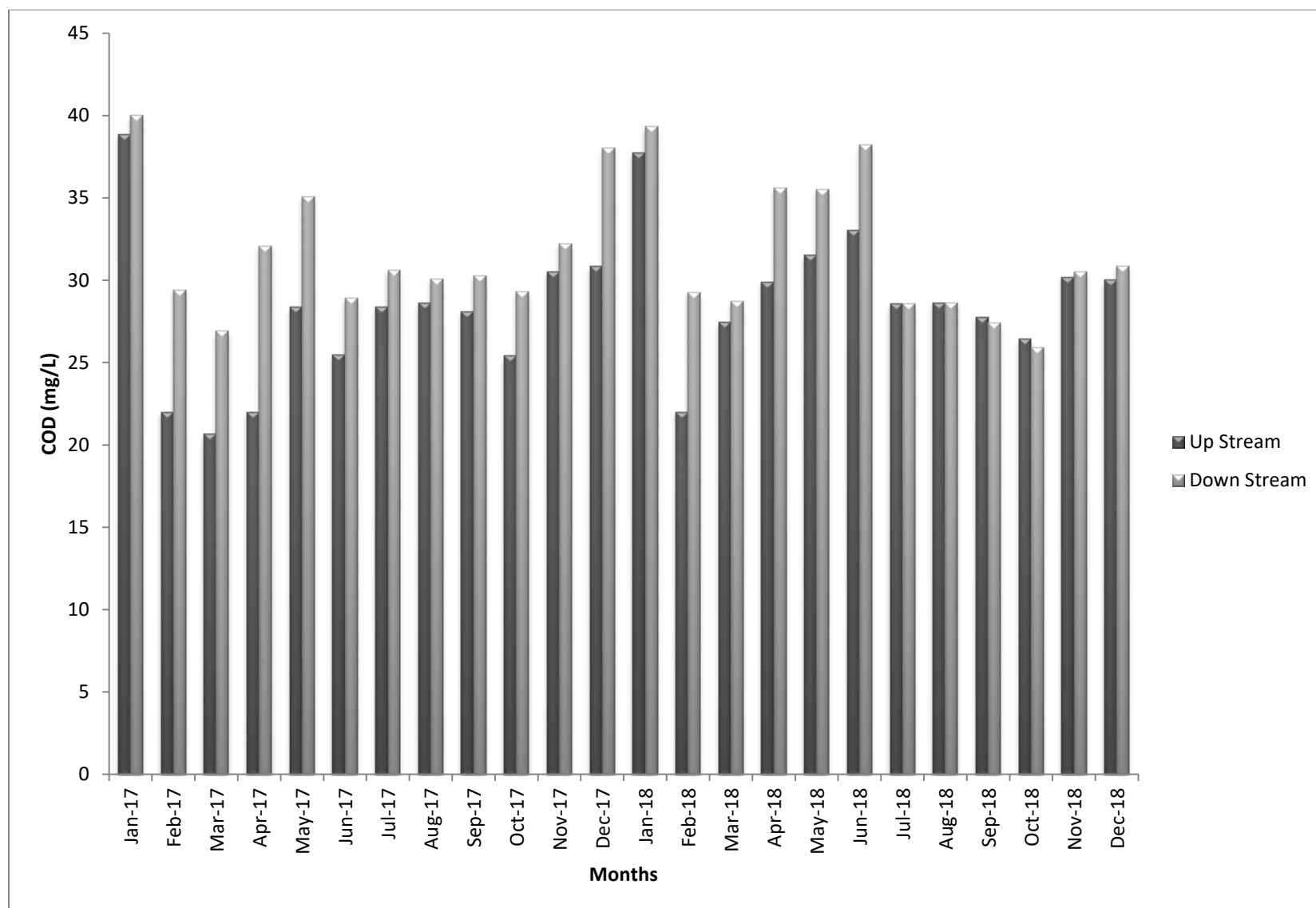


Figure 4.10: Mean Monthly Variations in the Chemical Oxygen Demand inUp- and Down-stream of JHPR

4.2: Species Identification Using DNA Barcode

DNA barcode system of COI gene was used to confirm the identity of fish species from up- and down-stream of Jebba reservoir, Nigeria. One hundred and seventy (170) specimens were collected and were morphologically identified which comprise of 50 species belonging to 33 genera in 23 families. A total number of one hundred and seventy (170) sequences that were generated which comprise of 55 species, 33 genera and 23 families (Table 4.2). The number of sequences per species varied between 1 for rare species to 23 for those species that were abundant in these regions. To ensure simplicity and un-ambiguity, the 170 aligned COI barcodes sequences in all >600 bp average length were obtained with no insertions, deletions, heterozygous sites or stop codons. The information on the COI gene sequence genetic composition data showed the number of variables, conservative and phylogenetically informative sites. The nucleotide composition of the sequence data set analysis revealed as T =28.1%, C=28.9%, A=26.0%, G=17.0%. This support all amplified sequences to be a functional mitochondrial COI sequences and the nucleotide sequences will be deposited in the GenBank for accession number.

The fish species identification of the individuals' samples collected in up- and down-stream of JJHPR was confirmed using amplified sequences in the GenBank BLAST tools on NCBI database and BOLD system using the similarity cut-off of 97% provided in Table 4.1.2. The total of 155 (91.18%) in NCBI, 125 (73.53%) in BOLD and NJ tree-based analyses of COI sequences were identified to species level and other species that could not identified to species level were thus referred to genera. The total of 139(81.76%) COI sequences in NCBI have similarity corresponding to 48 (87.27%) morphologically identified fish species. In BOLD

Table 4.2: The Morphological Identification and DNA Barcode Approach of the Fish Species in Up- And Down-Stream of JHPR

s/No	Morphological ID	GenBank Identification Species name (Accession no)	No of Samples	Similarity	BOLD Identification Species name	Similarity
1	<i>Auchenoglanis biscutatus</i>	<i>Auchenoglanis biscutatus</i> (JF510501.1)	1	100%	<i>Auchenoglanis biscutatus</i>	100%
2	<i>Auchenoglanis occidentalis</i>	<i>Auchenoglanis occidentalis</i> (MG824558.1)	4	100%	<i>Auchenoglanis occidentalis</i>	100%
3	<i>Bagrus bajad</i>	<i>Bagrus bajad</i> (MG824560.1)	1	100%	<i>Bagrus bajad</i>	100%
4	<i>Bagrus docmac</i>	<i>Bagrus docmac</i> (MG824561.1)	1	100%	<i>Bagrus docmac</i>	95.52%
5	<i>Brienomyrus niger</i>	<i>Brienomyrus niger</i> (JF510502.1)	2	100%	<i>Brienomyrus niger</i>	100%
6	<i>Brycinus nurse</i>	<i>Brycinus nurse</i> (HM882786.1)	1	99%	<i>Brycinus nurse</i>	100%
7	<i>Brycinus</i> sp	<i>Brycinus</i> sp (JF510504.1)	1	99%	<i>Brycinus</i> sp	99.26%
8	<i>Chrysichthys auratus</i>	<i>Chrysichthys cf auratus</i> (MG824569.1)	2	100%	<i>Chrysichthys auratus</i>	
9	<i>Chrysichthys nigrodigitatus</i>	<i>Chrysichthys nigrodigitatus</i> (HG803416.1)	2	100%	N/A	
10	<i>Chrysichthys nigrodigitatus</i>	<i>Chrysichthys</i> sp (MG824574.1)	3	100%	<i>Chrysichthys</i> sp	99.63
11	<i>Tillapia guinensis</i>	<i>Chromidotilapia guntheri</i> (HM882914.1)	1	99.23%	<i>Chromidotilapia guntheri</i>	99.23
12	<i>Citharinus citharus</i>	<i>Citharinus citharus</i> (MG824578.1)	5	100%	<i>Citharinus citharus</i>	100%
13	<i>Clarias gariepinus</i>	<i>Clarias gariepinus</i> (MG824583.1)	9	100%	<i>Clarias gariepinus</i>	100%
14	<i>Clarotes laticeps</i>	<i>Clarotes laticeps</i> (MG824586.1)	6	100%	<i>Clarotes laticeps</i>	100%
15	<i>Ctenopoma kingsleyae</i>	<i>Ctenopoma</i> sp (MK074180.1)	1	92.45%	NA	
16	<i>Distichodius engycephalus</i>	<i>Distichodius engycephalus</i> (HM882993.1)	1	99%	<i>Distichodius engycephalus</i>	99.81%
17	<i>Distichodius rostratus</i>	<i>Distichodius rostratus</i> (MG824590.1)	3	100%	<i>Distichodius rostratus</i>	100%
18	<i>Gymnarchus niloticus</i>	<i>Gymnarchus niloticus</i> (MG824592.1)	1	100%	<i>Gymnarchus niloticus</i>	100%
19	<i>Hemichromis bimaculatus</i>	<i>Hemichromis bimaculatus</i> (MG824594.1)	2	100%	<i>Hemichromis bimaculatus</i>	99.82%
20	<i>Heterotis niloticus</i>	<i>Heterotis niloticus</i> (MG824596.1)	2	100%	<i>Heterotis niloticus</i>	100%
21	<i>Hydrocynus vittatus</i>	<i>Hydrocynus vittatus</i> (MG824598.1)	2	100%	<i>Hydrocynus vittatus</i>	100%
22	<i>Hyperopisus bebe</i>	<i>Hyperopisus bebe</i> (AP011572.1)	1	99%	<i>Brevimyrus niger</i>	100%
23	<i>Labeo coubie</i>	<i>Labeo coubie</i> (JX074182.1)	2	99.85%	<i>Labeo</i> sp	100%
24	<i>Labeo senegalensis</i>	<i>Labeo horie</i> (JX074211.1)	1	99.85%	<i>Labeo senegalensis</i>	100%
25	<i>Labeo senegalensis</i>	<i>Labeo senegalensis</i> (AB238968.1)	14	98.83%	<i>Labeo senegalensis</i>	100%

26	<i>Lates niloticus</i>	<i>Lates niloticus</i> (MG824611.1)	9	99.82%	<i>Lates niloticus</i>	99.83
27	<i>Malapterurus electricus</i>	<i>Malapterurus electricus</i> (HM883006.1)	1	100%	<i>Malapterurus electricus</i>	99.08%
28	<i>Malapterurus electricus</i>	<i>Malapterurus</i> sp (MG824612.1)	1	100%	NA	
29	<i>Marcusenius senegalensis</i>	<i>Marcusenius senegalensis</i> (HM882721.1)	1	99%	<i>Marcusenius senegalensis</i>	99.82%
30	<i>Mormyrops anguilloides</i>	<i>Mormyrops anguilloides</i> (MG824620.1)	4	100%	<i>Mormyrops anguilloides</i>	100%
31	<i>Mormyrus macrophthalmus</i>	<i>Mormyrus macrophthalmus</i> (MG824624.1)	4	100%	<i>Mormyrus macrophthalmus</i>	100%
32	<i>Mormyrus rume</i>	<i>Mormyrus tapirus</i> (HM882745.1)	2	100%	<i>Mormyrus longirostris</i>	100%
33	<i>Oreochromis aureus</i>	<i>Oreochromis aureus</i> (MG824629.1)	3	100%	<i>Sarotherodon galilaeus</i>	100%
34	<i>Oreochromis niloticus</i>	<i>Oreochromis niloticus</i> (MK074533.1)	2	100%	<i>Oreochromis</i> sp.	100%
35	<i>Oreochromis</i> sp	<i>Oreochromis</i> sp (KX781822)	2	100%	<i>Oreochromis aureus</i>	100%
36	<i>Parachana ninsignis</i>	<i>Parachana insignis</i> (MG824634.1)	2	100%	<i>Parachana obscura</i>	100%
37	<i>Parachana obscura</i>	<i>Parachana obscura</i> (MG824636.1)	1	100%	<i>Parachana obscura</i>	100%
38	<i>Polypterus senegalus</i>	<i>Polypterus senegalus</i> (HQ343158.1)	5	99.39%	<i>Polypterus senegalus</i>	99.71%
39	<i>Protopterus annectans</i>	<i>Protopterus</i> sp (MG824637.1)	5	99.09%	<i>Protopterus</i> sp	99.69%
40	<i>Sarotherodon galilaeus</i>	<i>Sarotherodon galilaeus</i> (MG824639.1)	1	100%	<i>Sarotherodon galilaeus</i>	99.82%
41	<i>Schilbe mystus</i>	<i>Schilbe mystus</i> (MG824651.1)	1	100%	<i>Schilbe mystus</i>	98.70%
42	<i>Schilbe spp</i>	<i>Schilbe intermedius</i> (KT193441.1)	1	95%	<i>Schilbe intermedius</i>	98.89%
43	<i>Synodontis clarias</i>	<i>Synodontis clarias</i> (MG824661.1)	3	100%	<i>Synodontis clarias</i>	99.81%
44	<i>Synodontis membranacea</i>	<i>Synodontis membranacea</i> (MG824667.1)	2	100%	<i>Synodontis membranacea</i>	100%
45	<i>Synodontis nigrita</i>	<i>Synodontis nigrita</i> (MG824669.1)	1	100%	<i>Synodontis nigrita</i>	100%
46	<i>Synodontis obesus</i>	<i>Synodontis obesus</i> (MG824671.1)	2	100%	<i>Synodontis obesus</i>	99.26%
47	<i>Synodontis eupterus</i>	<i>Synodontis</i> aff. <i>bastiani</i> (MG824656.1)	23	100%	<i>Synodontis</i> aff. <i>Bastiani</i>	99.82
48	<i>Synodontis violacea</i>	<i>Synodontis violacea</i> (MG824678.1)	5	100%	<i>Synodontis</i> sp	100%
49	<i>Synodontis ocellifer</i>	<i>Synodontis ocellifer</i> (MG824672.1)	1	100%	<i>Synodontis</i> sp	100%
50	<i>Synodontis batensoda</i>	<i>Synodontis batensoda</i> (HF565863.1)	1	100%	<i>Synodontis batensoda</i>	100%
51	<i>Synodontis</i> sp	<i>Synodontis</i> sp (MG824673.1)	1	100%	NA	
52	<i>Tetraodon lineatus</i>	<i>Tetraodon lineatus</i> (MG824681.1)	2	100%	<i>Tetraodon lineatus</i>	100%
53	<i>Tilapia zillii</i>	<i>Coptodon zillii</i> (MG824685.1)	13	100%	<i>Tillapia zilli</i>	100%
54	<i>Xynomystus nigri</i>	<i>Xynomystus nigri</i> (HM882772.1)	1	100%	<i>Xynomystus nigri</i>	100%
55	<i>Dasyatis garouaensis</i>	<i>Dasyatis microps</i> (KJ749656.1)	1	83.11%	NA	

Species identification cut-off of 97% was used for Genbank and BOLD databases. NA: Not Available

system, 117 (68.82%) COI sequences belonging to 39 (70.91%) fish species, show similarity to the morphologically identified individual fishes out of which 8 (4.14%) COI sequences for six (6) individual's fish species sequences were not available in BOLD database.

The DNA barcoding approach showed that individuals morphologically identified as *Auchenoglanis occidentalis* (Cuvier and Valenciennes, 1840), *Bagrus bajad* (Forsk., 1775), *Bagrus docmac* (Forsk., 1775), *Brienomyrus niger* (Günther, 1866), *Citharinus citharus* (Geoffrey, 1809), *Clarias gariepinus* (Burchell, 1822), *Clarotes laticeps* (Ruppel, 1829), *Coptodon zillii* (Gervais, 1848), *Distichodus rostratus* (Gunther, 1864), *Gymnarchus niloticus* (Cuvier, 1829), *Hemichromis bimaculatus* (Gill, 1862), *Heterotis niloticus* (Cuvier, 1829), *Hydrocynus vittatus* (Boulenger, 1898), *Labeo senegalensis* (Cuvier and Valenciennes, 1842), *Lates niloticus* (Linnaeus, 1758), *Malapterurus electricus* (Gmelin, 1789), *Mormyrops anguilloides* (Linnaeus, 1758), *Mormyrus macrophthalmus* (Gunther, 1866), *Parachanna obscura* (Gunther, 1861), *Polypterus senegalus* (Cuvier, 1829), *Sarotherodon galilaeus* (Linnaeus, 1758), *Schilbe mystus* (Linnaeus, 1758), *Synodontis clarias* (Linnaeus, 1758), *Synodontis membranacea* (Geoffrey, 1809), *Synodontis nigrita* (Cuvier and Valenciennes, 1864), *Synodontis obesus* (Boulenger, 1898), *Tetraodon lineatus* (Linnaeus, 1758) and *Xenomystus nigri* (Gunther, 1868) formed clade with individuals of same species from the Genbank, hence, species names were retained valid (Table 4.2)..

Individuals morphologically identified as *Chrysichthys nigrodigitatus* (Lacepede, 1803), *Oreochromis aureus* (Steindachner, 1864), *Synodontis schall* (Bloch and Schneide, 1801), *Ctenopoma kingsleyae* (Günther, 1896), and *Protopterus annectans* (Owen, 1839) clustered with *Chrysichthys* sp, *Sarotherodon galilaeus*, *Synodontis* aff. *bastiani*, *Ctenopoma* sp, *Protopterus* sp respectively hence the name were changed. They were referred to genera level although have

been identified to species level morphologically of which the sample resemble but the sequence were distance from the known species recorded in Nigeria in the Genbank.

Further observed the individuals identified as, *Malapterurus* sp could not be assigned to species-level using both morphology and genetic data and the species morphologically identified as *Dasyatis garouaensis* (Smooth Freshwater Stingray) (Stauch and Blanc, 1962) show a similarity match of 83.10% with *Dasyatis microps* (Smalleye Stingray) from India. Given the unavailability of sequences for *Dasyatis garouaensis*, the species identification could be taken as tentative pending further revision. The sample of the *Malapterurus* sp could not be assigned to species-level clustered with others species in the genus *Malapterurus* but have a sequence distance from the common *Malapterurus electricus* that have been reported in Nigeria. This show the possibility of a species that yet to be described as it matched with only one sequence on the NCBI GenBank that was obtained from the same area having the morphological appearance different from the common *Malapterurus electricus* known in most Nigerian water. Similarly, the species sequences of *Ctenopoma* sp and *Polypterus senegalus* were also being reporting from Nigeria for the first time in this present work which clustered with the sample sequence from the South African.

4.3 Tree-based identification

The NJ tree analyses using K2P distances illustrated the *COI* levels of genetic divergence among intra- and interspecific taxonomical hierarchy (Figures 4.3). From the NJ tree generated from the one hundred and seventy sequences in Mega 5.0, individuals of same species and genus cluster together and the fish species were strongly supported (figure 4.3a).

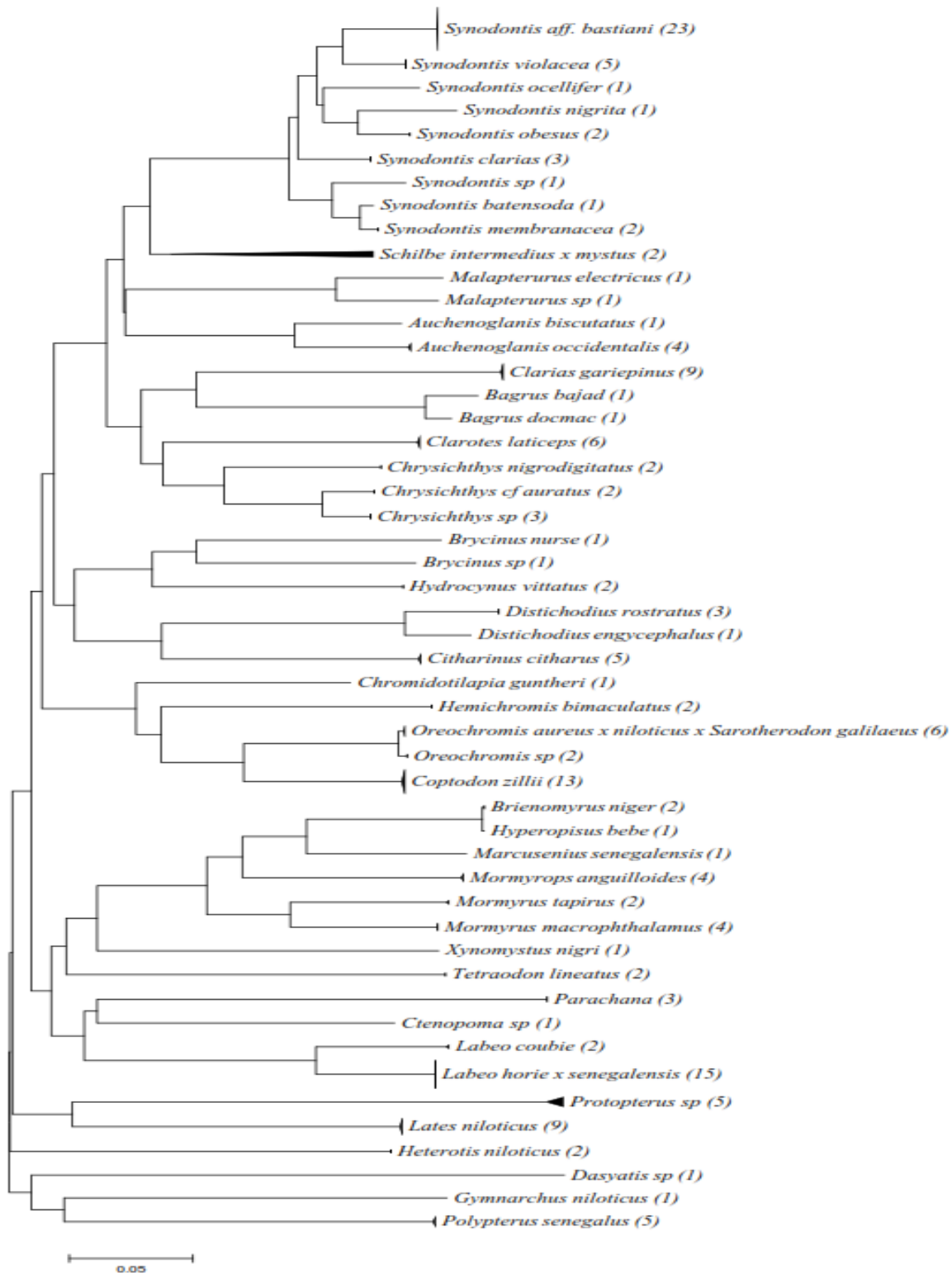


Figure 4.3a: Neighbour-joining tree illustrating the COI barcode sequences (using K2P distance) taxonomical hierarchy levels of selected fish species

Using BOLD system to carry out tree based identification, fish species identified morphologically as *Achenoglanis occidentalis*, *A. bicusulatus*, *B. bayad*, *B. docmark*, *Brycinus nurse*, *B. sp.*, *Bryvimyrus niger*, *Chrysichthys nigrodigitatus*, *C. auratus*, *Citharinus citharus*, *Clarias gariepinus*, *Clarotes laticeps*, *Distichodon engycephalus*, *D. rostratus*, *Gymnarchus niloticus*, *Hemichromis bimaculatus*, *Heterotis niloticus*, *Hydrocynus vittatus*, *Heperopisus bebe*, *Labeo cubie*, *L. senegalensis*, *Lates niloticus*, *Marcusenius senegalensis*, *Mormyrops anguloides*, *Mormyrus macrophthalamus*, *Protopterus sp*, *Schilbe intermedius*, *S. mystus*, *Synodontis schall*, *S. batensoda*, *S. clarias*, *S. nigrata*, *S. obesus*, *S. ocellifer*, *S. violeceus*, *Tetraodon lineatus* and *Tillapia zilli* form same clade with others of same species in either Nigeria or closely African country in the Genbank (Figure 4. 3b-w).

The sequence of *Polypterus senegalus senegalus* in this work presents the first to be generated in Nigeria inland waters that clustered with the sample sequence from the South African. The *Lates niloticus* cluster with sample from Egypt and form a separate clade from Kenya. The NJ tree analysis, the *Oreochromis niloticus* identified morphological clustered with *Sarotherodon galilaeus* in BOLD, hence it was refers to *S. galilaeus* while the morphologically identified *Oreochromis aureus* clustered with both *Oreochromis niloticus* and *Oreochromis aureus*. Similarly, morphological identified speciemen of *Mormyrus rume* form a strong lineage with *M. longirostris* (figure 4. 3n). The *Brycinus sp*, *Synodontis sp*, *Chrysichthys sp*, *Labeo sp*, *Malapterurus sp*, *Oreochromis sp*, *Protopterus sp* and *Schilbe sp*, that were unable to describe to species level formed strongly lineages separated from their closely related sister species in the NJ tree (figure 4.3d, 4.3e, 4.3o, 4.3s and 4.3v).

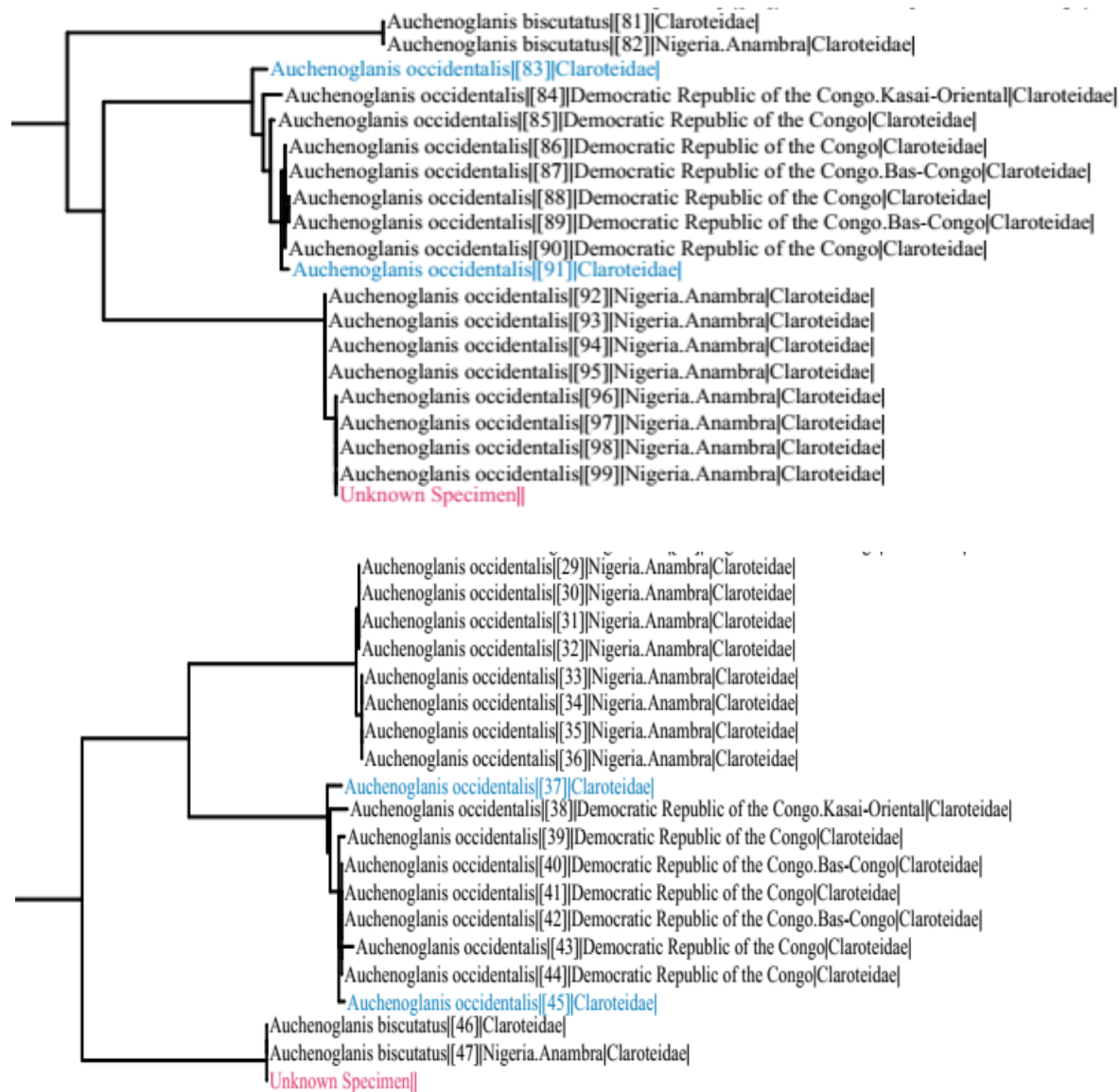


Figure 4.3b: Phylogenetic neighbour-joining tree based on COI barcode using K2P distance generated in BOLD database (www.barcodinglife.org). Unknown specimen shows the *Auchenoglanis occidentalis* and *Auchenoglanis biscutatus* sequence blast in this present study in BOLD

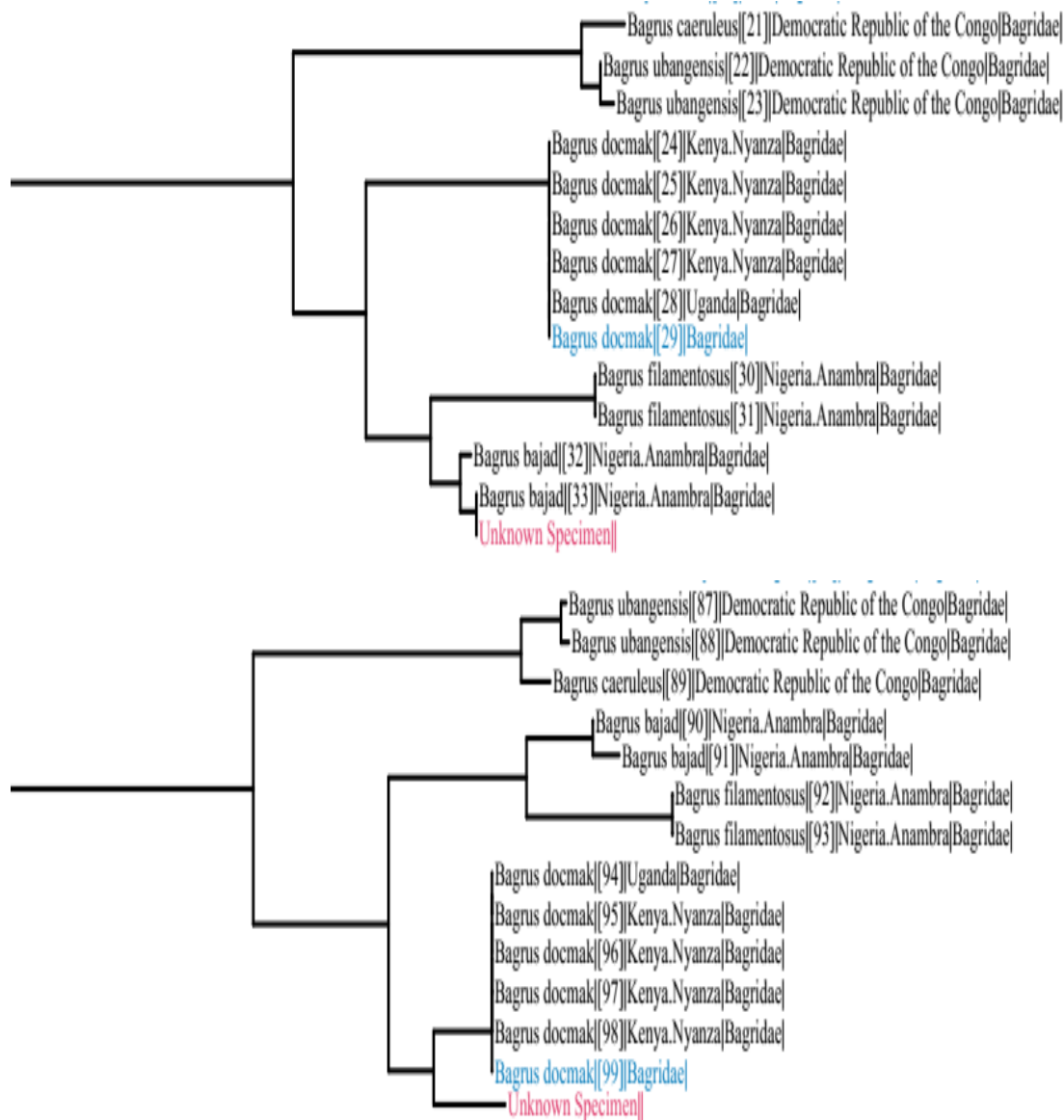


Figure 4.3c: Phylogenetic neighbour-joining tree based on COI barcode using K2P distance generated in BOLD database (www.barcodinglife.org). Unknown specimen shows the *Bagrus bajad* and *Bagrus docmak* sequence blast in this present study in BOLD

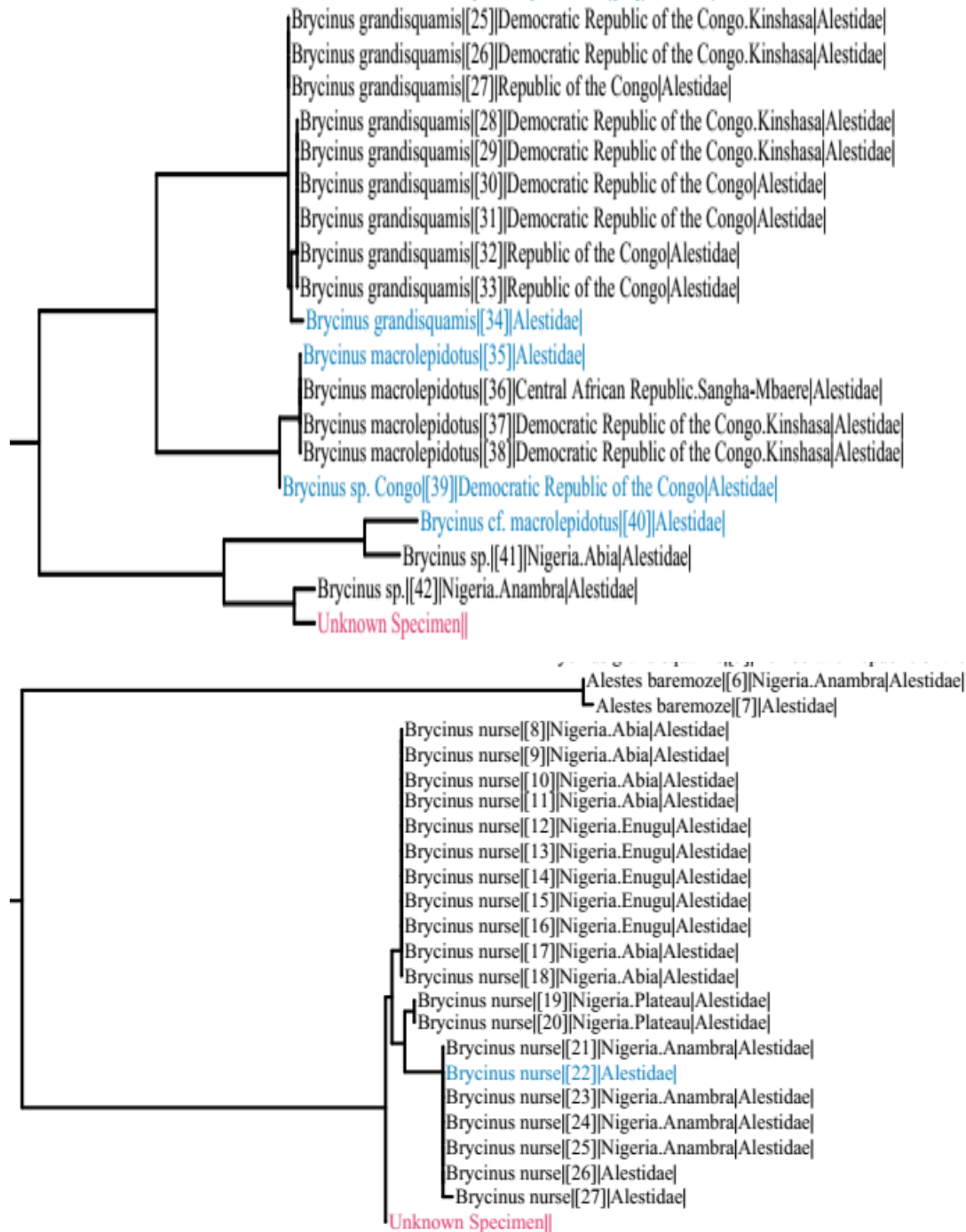


Figure 4.3d: Phylogenetic neighbour-joining tree based on COI barcode using K2P distance generated in BOLD database (www.barcodinglife.org). Unknown specimen shows the *Brycinus sp* and *Brycinus nurse* sequence blast in this present study in BOLD

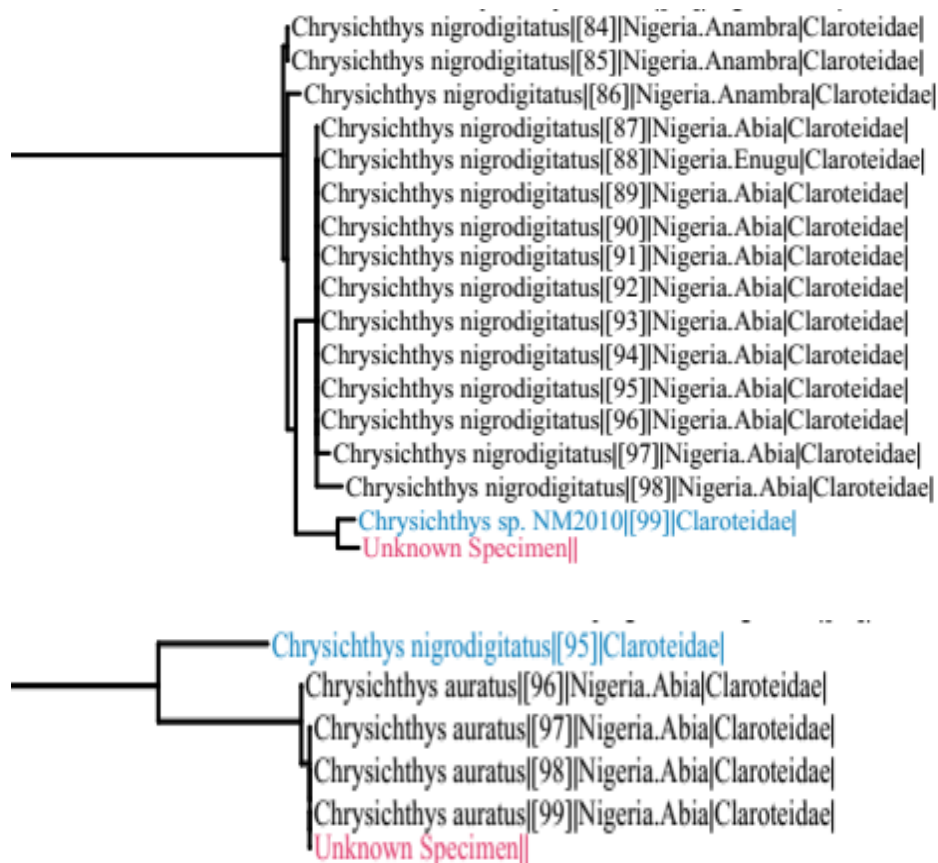


Figure 4.3e: Phylogenetic neighbour-joining tree based on COI barcode using K2P distance generated in BOLD database (www.barcodinglife.org). Unknown specimen shows the *Chrysichthys* sp. and *Chrysichthys auratus* sequence blast in this present study in BOLD

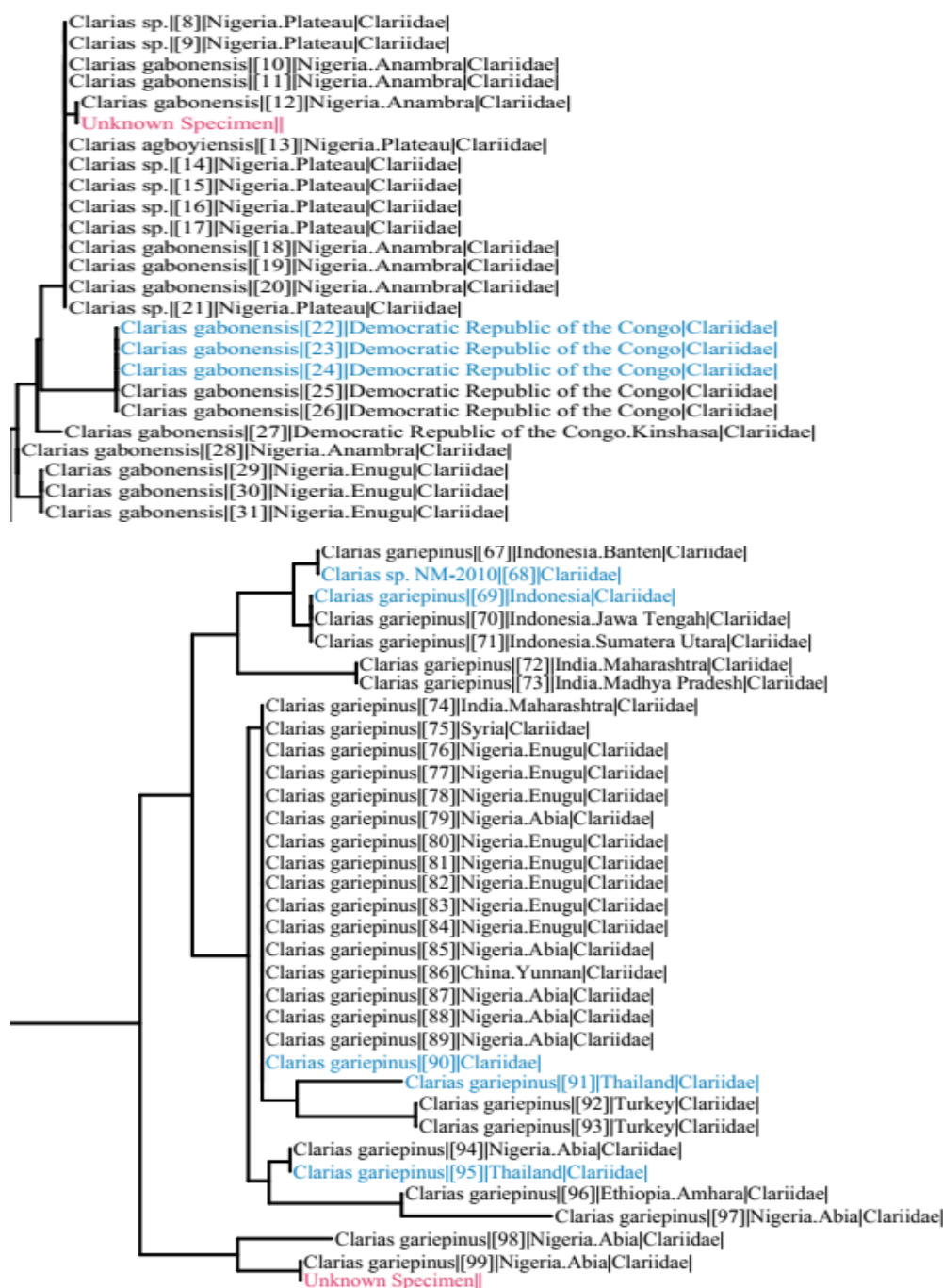


Figure 4.3f: Phylogenetic neighbour-joining tree based on COI barcode using K2P distance generated in BOLD database (www.barcodinglife.org). Unknown specimen shows the *Clarias gabonensis* and *Clarias gariepinus* sequence blast in this present study in BOLD

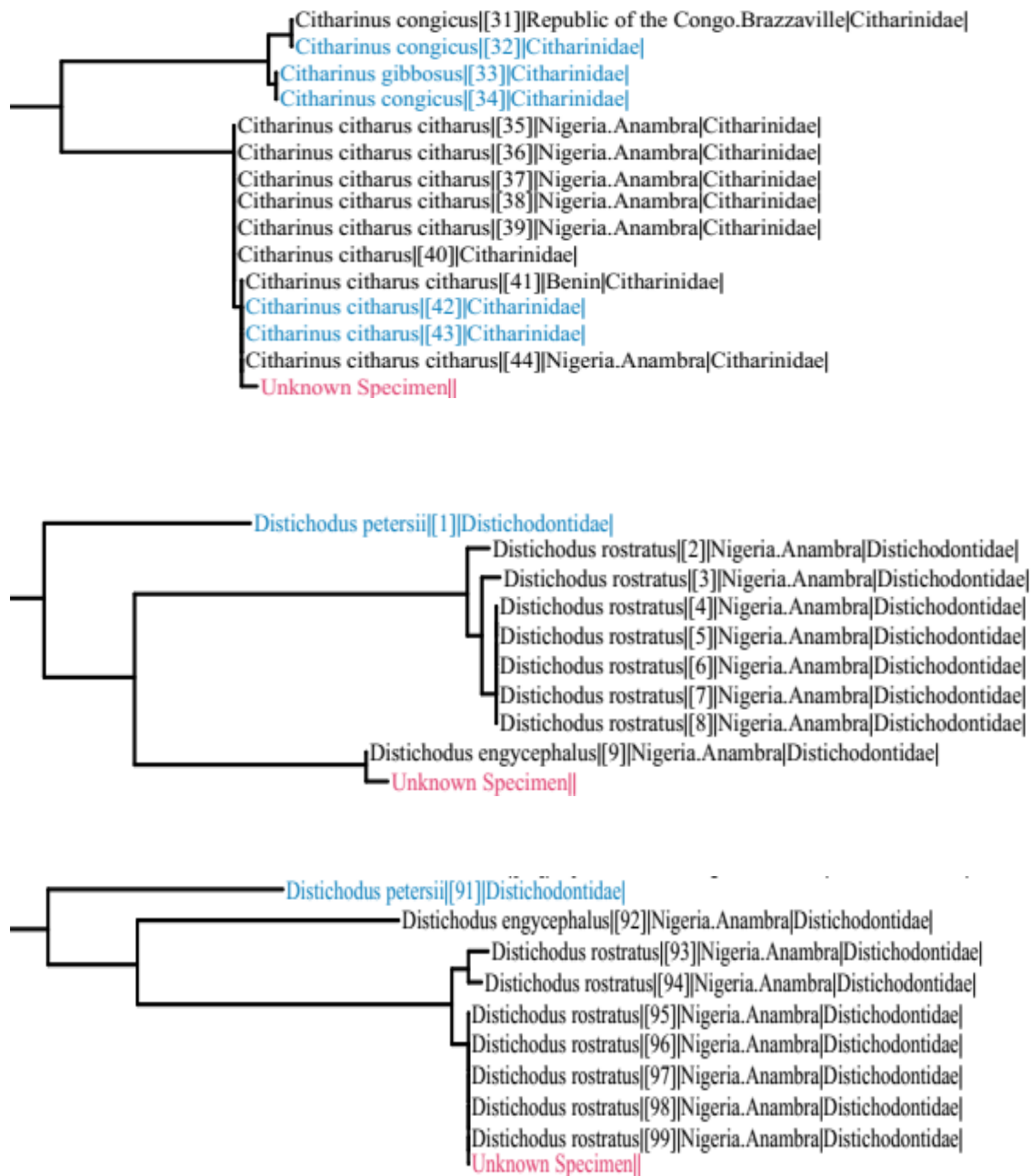


Figure 4.3g: Phylogenetic neighbour-joining tree based on COI barcode using K2P distance generated in BOLD database (www.barcodinglife.org). Unknown specimen shows the *Citharinus citharus*, *Distichodus engycephalus* and *Distichodus rostratus* sequence blast in this present study in BOLD

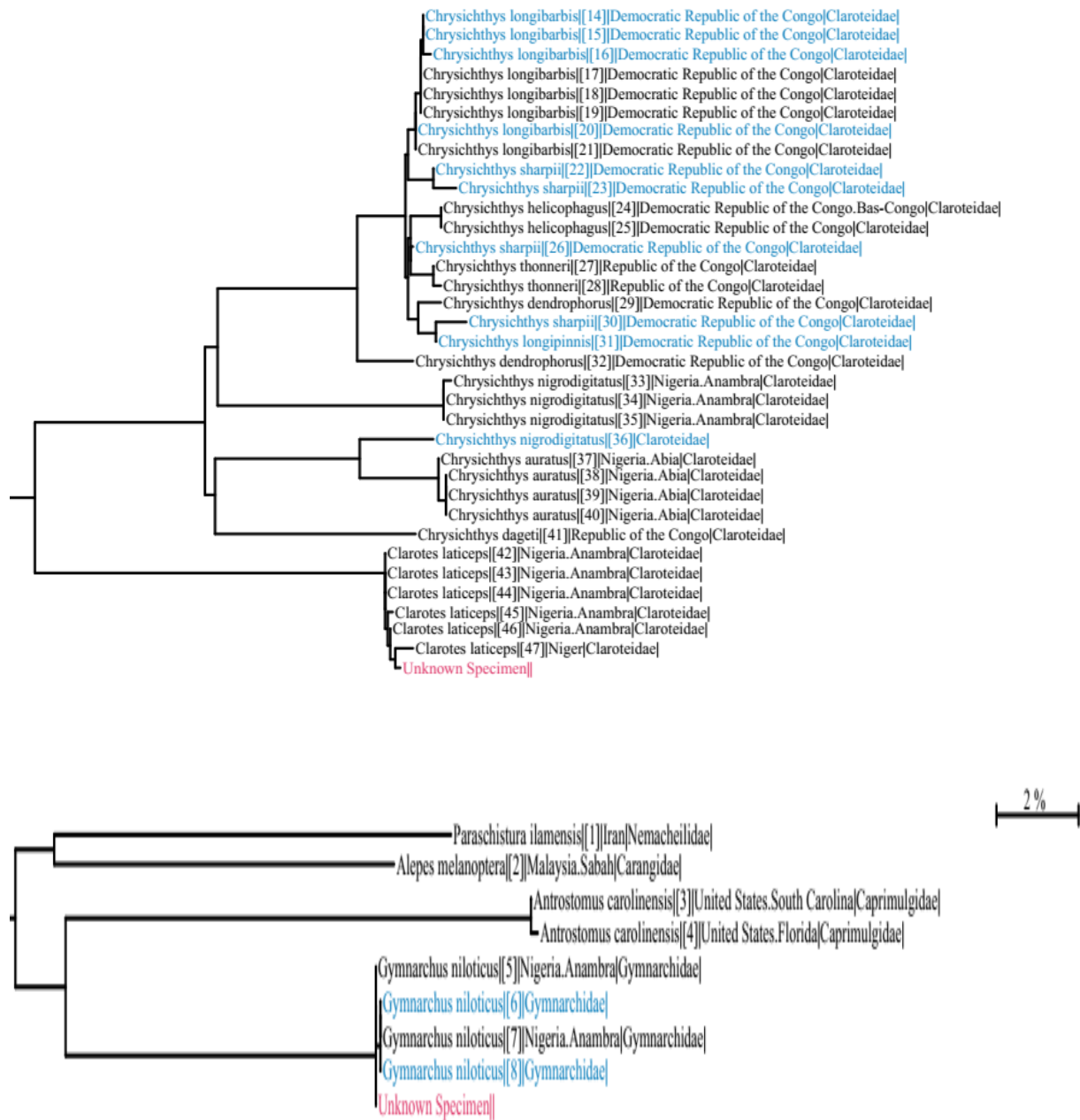


Figure 4.3h: Phylogenetic neighbour-joining tree based on COI barcode using K2P distance generated in BOLD database (www.barcodinglife.org). Unknown specimen shows the *Clarotes laticeps* and *Gymnarchus niloticus* sequence blast in this present study in BOLD

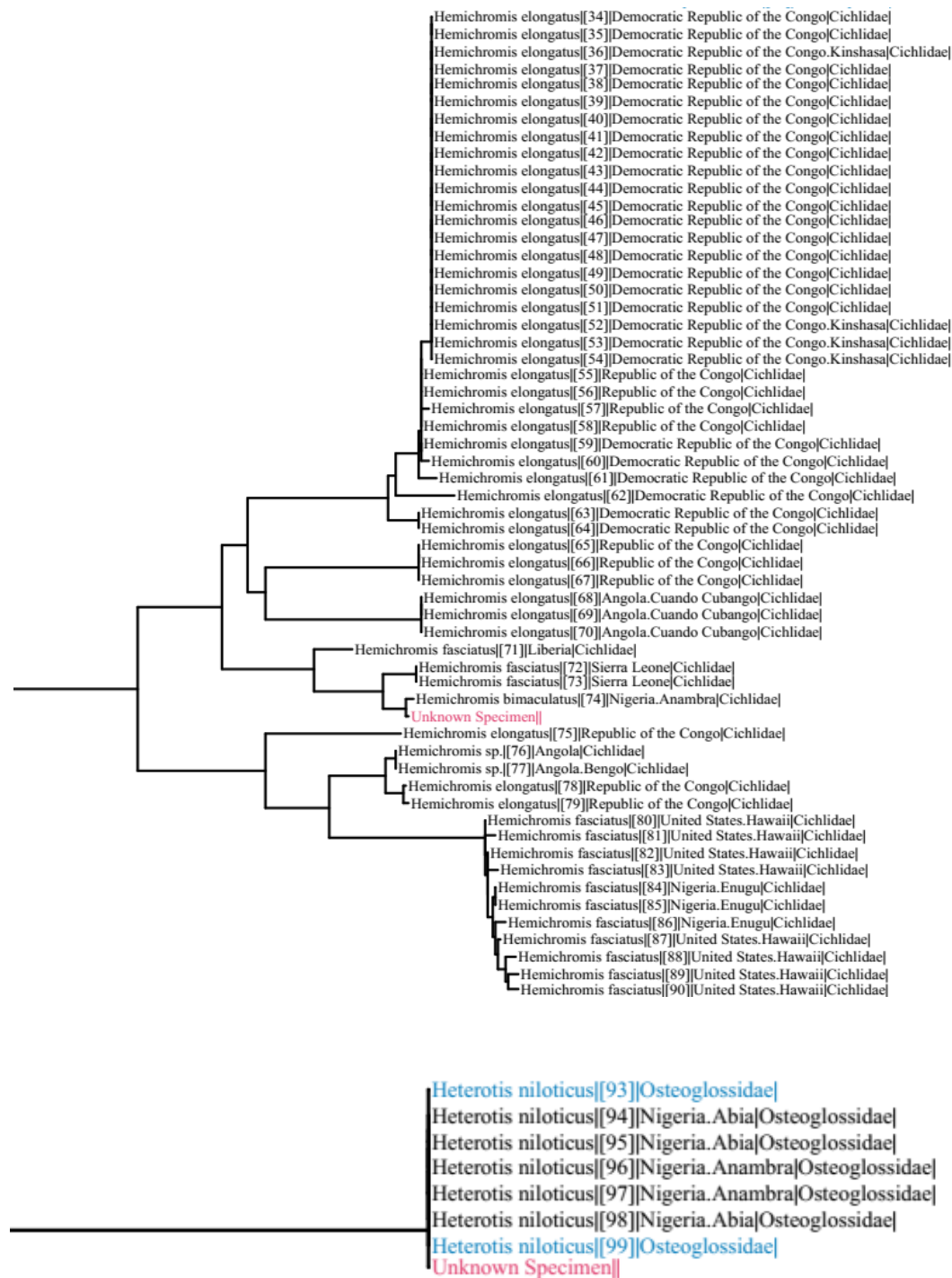


Figure 4.3i: Phylogenetic neighbour-joining tree based on COI barcode using K2P distance generated in BOLD database (www.barcodinglife.org). Unknown specimen shows the *Hemichromis bimaculatus* and *Heterotis niloticus* sequence blast in this present study in BOLD

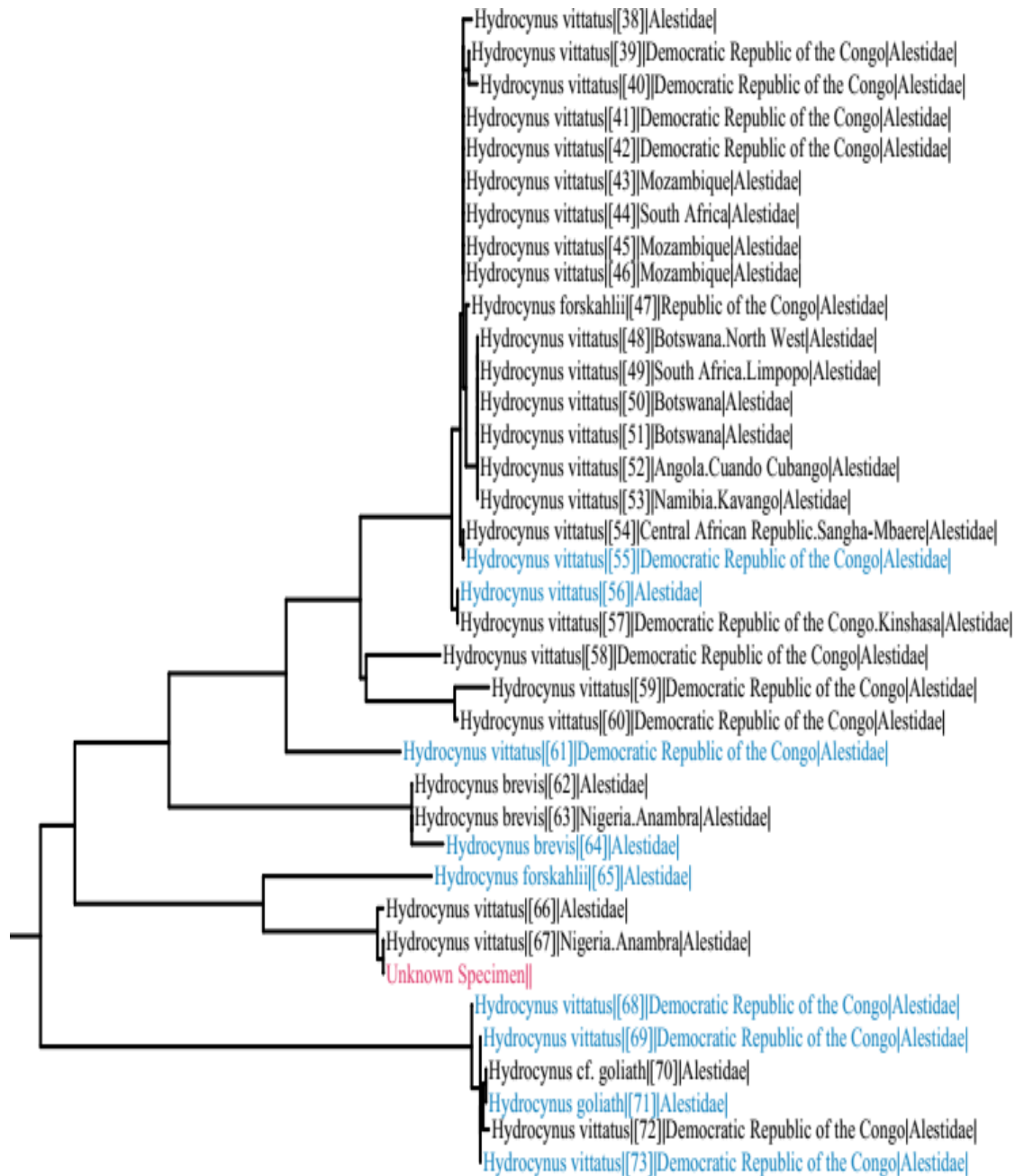


Figure 4.3j: Phylogenetic neighbour-joining tree based on COI barcode using K2P distance generated in BOLD database (www.barcodinglife.org). Unknown specimen shows the *Hydrocynus vittatus* sequence blast in this present study in BOLD

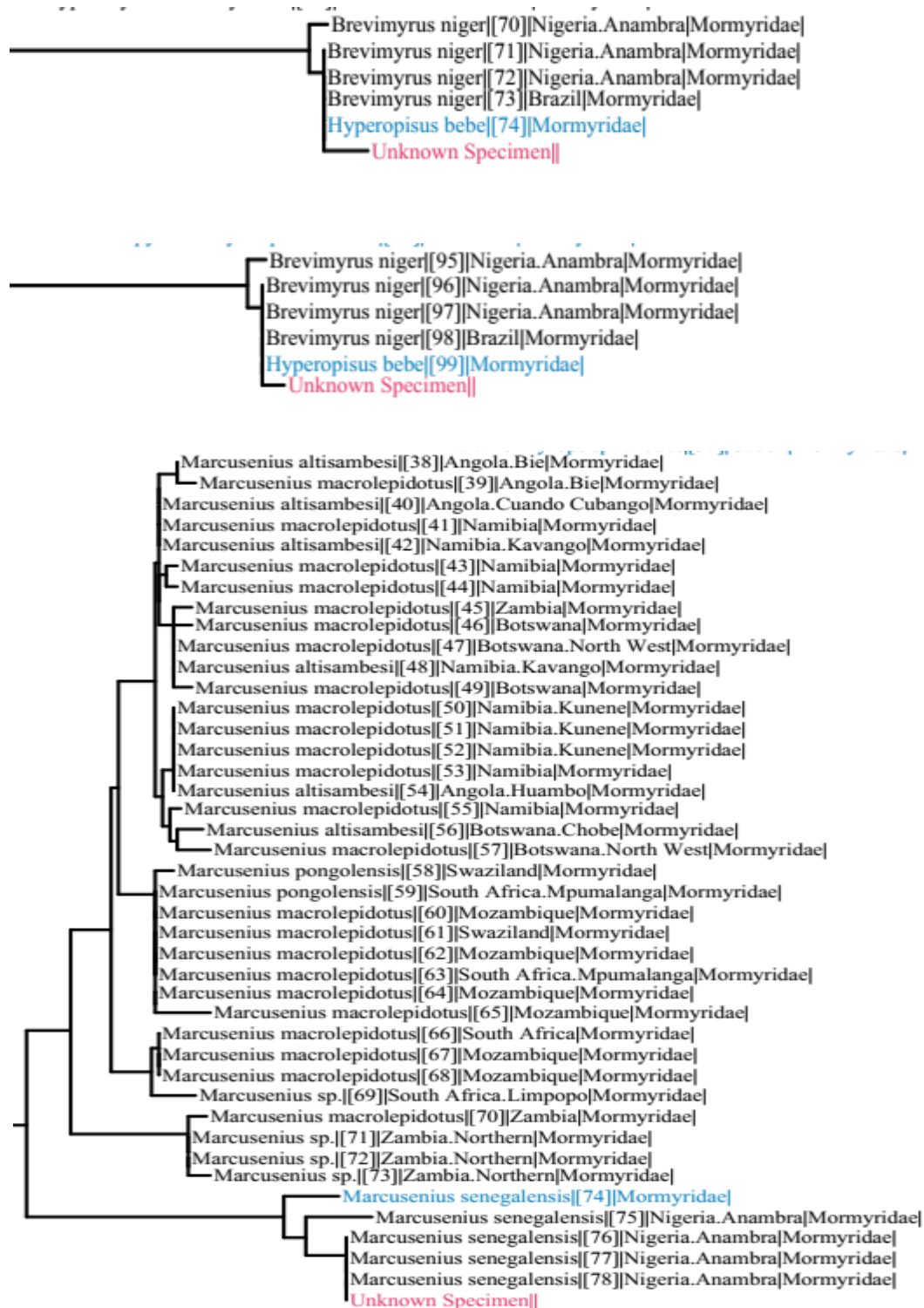


Figure 4.3k: Phylogenetic neighbour-joining tree based on COI barcode using K2P distance generated in BOLD database (www.barcodinglife.org). Unknown specimen shows the *Brevimyrus niger*, *Hyperopisus bebe* and *Marcusenius senegalensis* sequence blast in this present study in BOLD

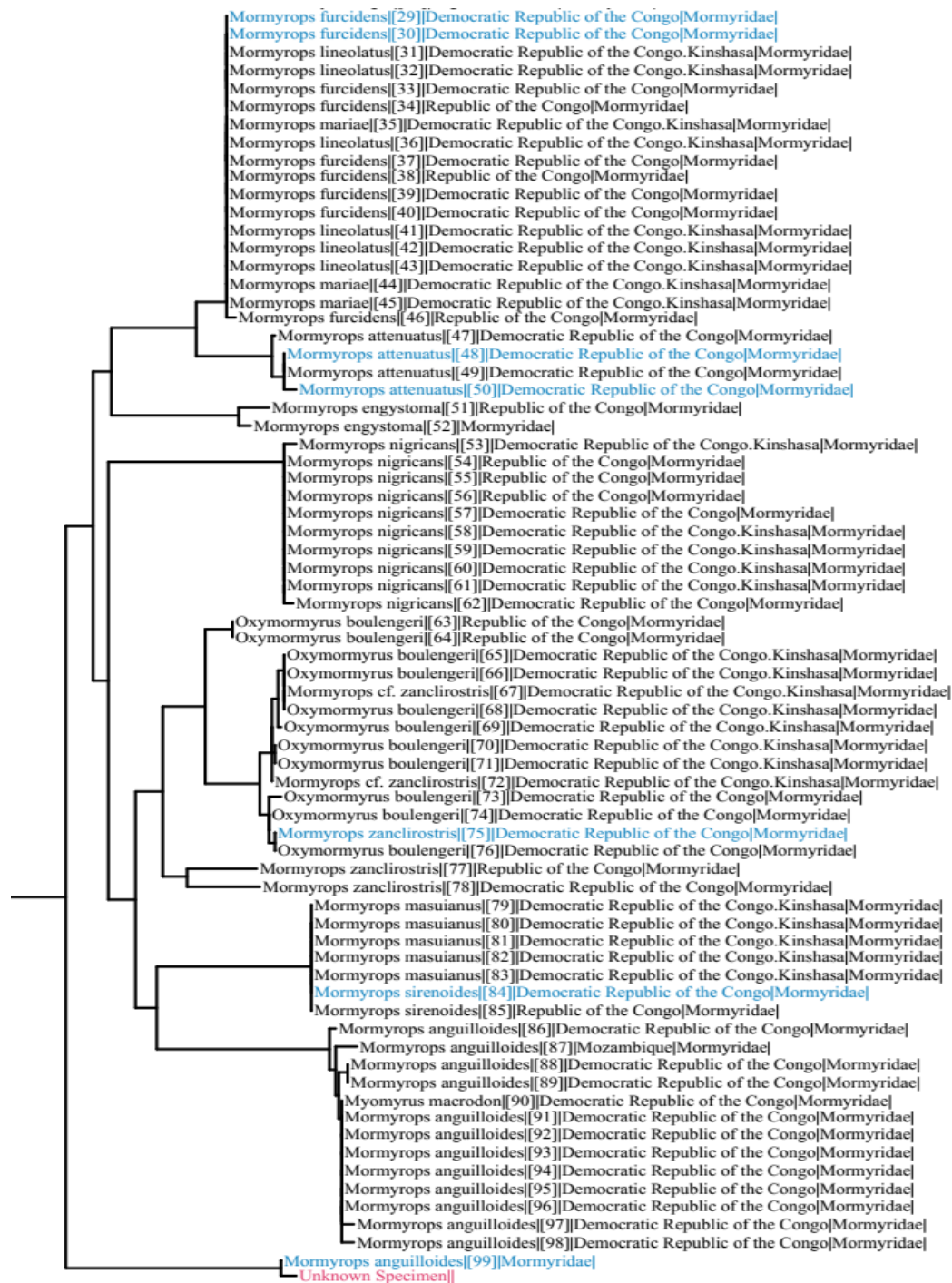


Figure 4.31: Phylogenetic neighbour-joining tree based on COI barcode using K2P distance generated in BOLD database (www.barcodinglife.org). Unknown specimen shows the *Mormyrops anguilloides* sequence blast in this present study in BOLD

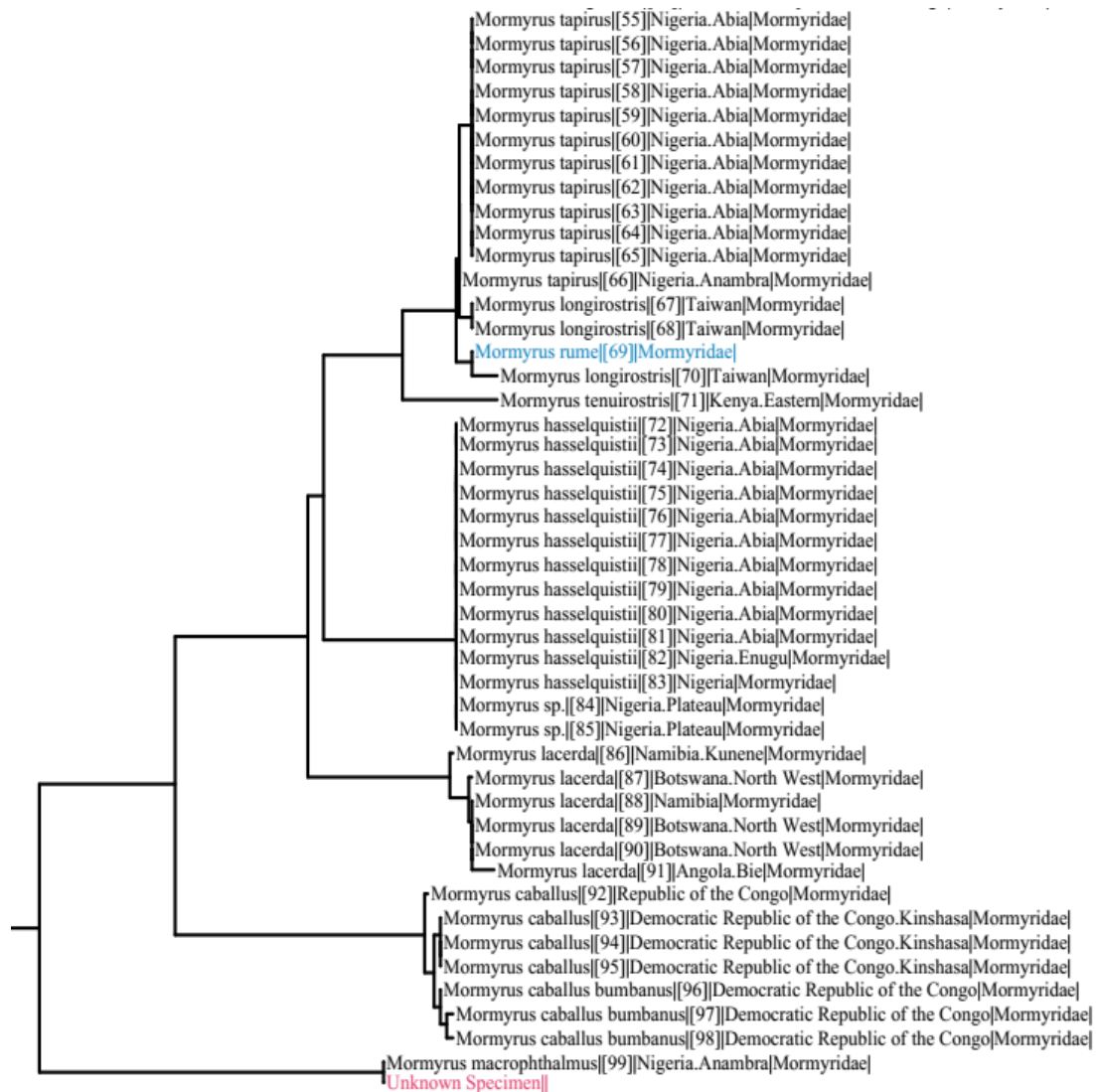


Figure 4.3m: Phylogenetic neighbour-joining tree based on COI barcode using K2P distance generated in BOLD database (www.barcodinglife.org). Unknown specimen shows the *Mormyrus macrophthalmus* sequence blast in this present study in BOLD

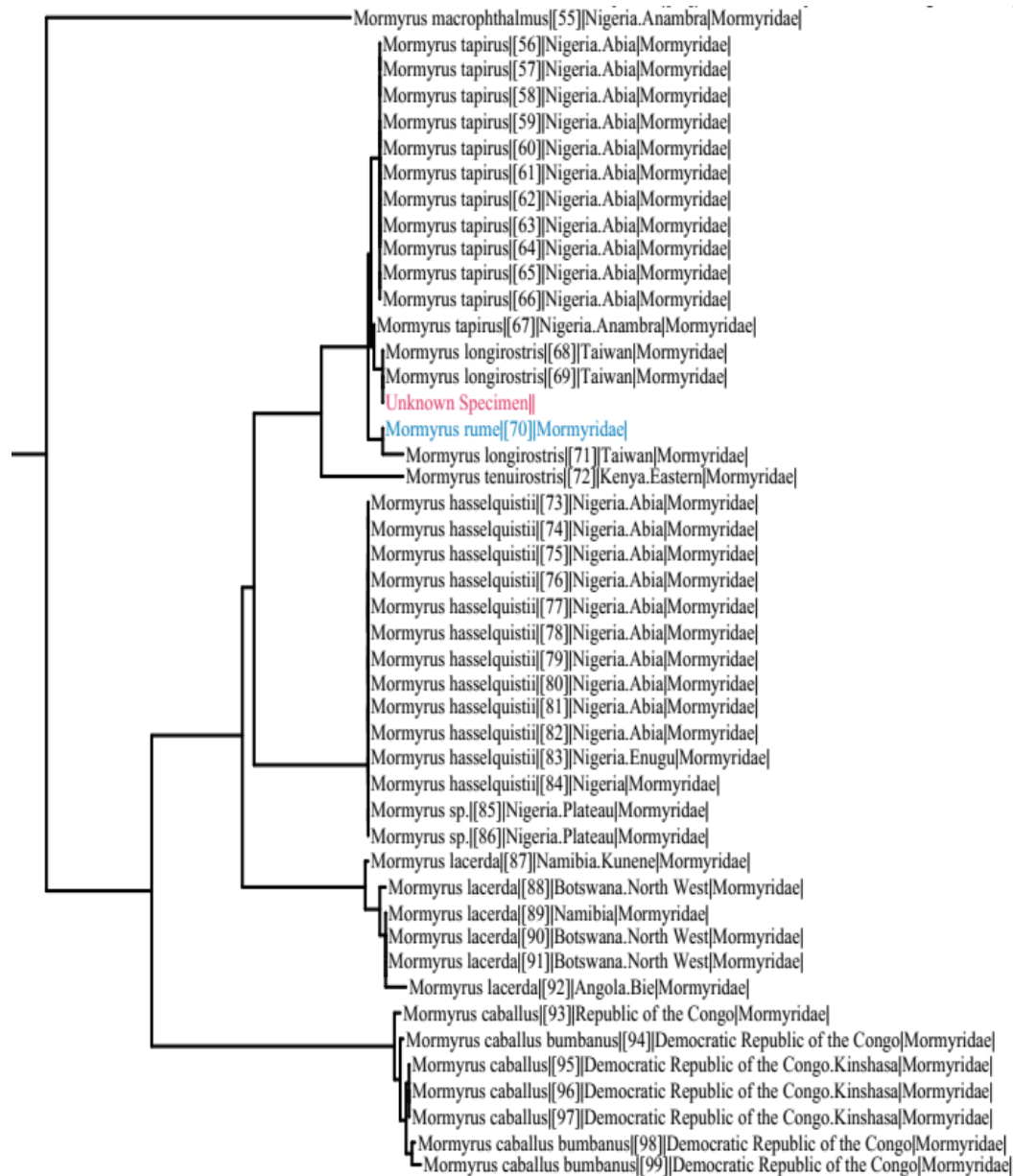


Figure 4.3n: Phylogenetic neighbour-joining tree based on COI barcode using K2P distance generated in BOLD database (www.barcodinglife.org). Unknown specimen shows the *Mormyrus longirostris* sequence blast in this present study in BOLD



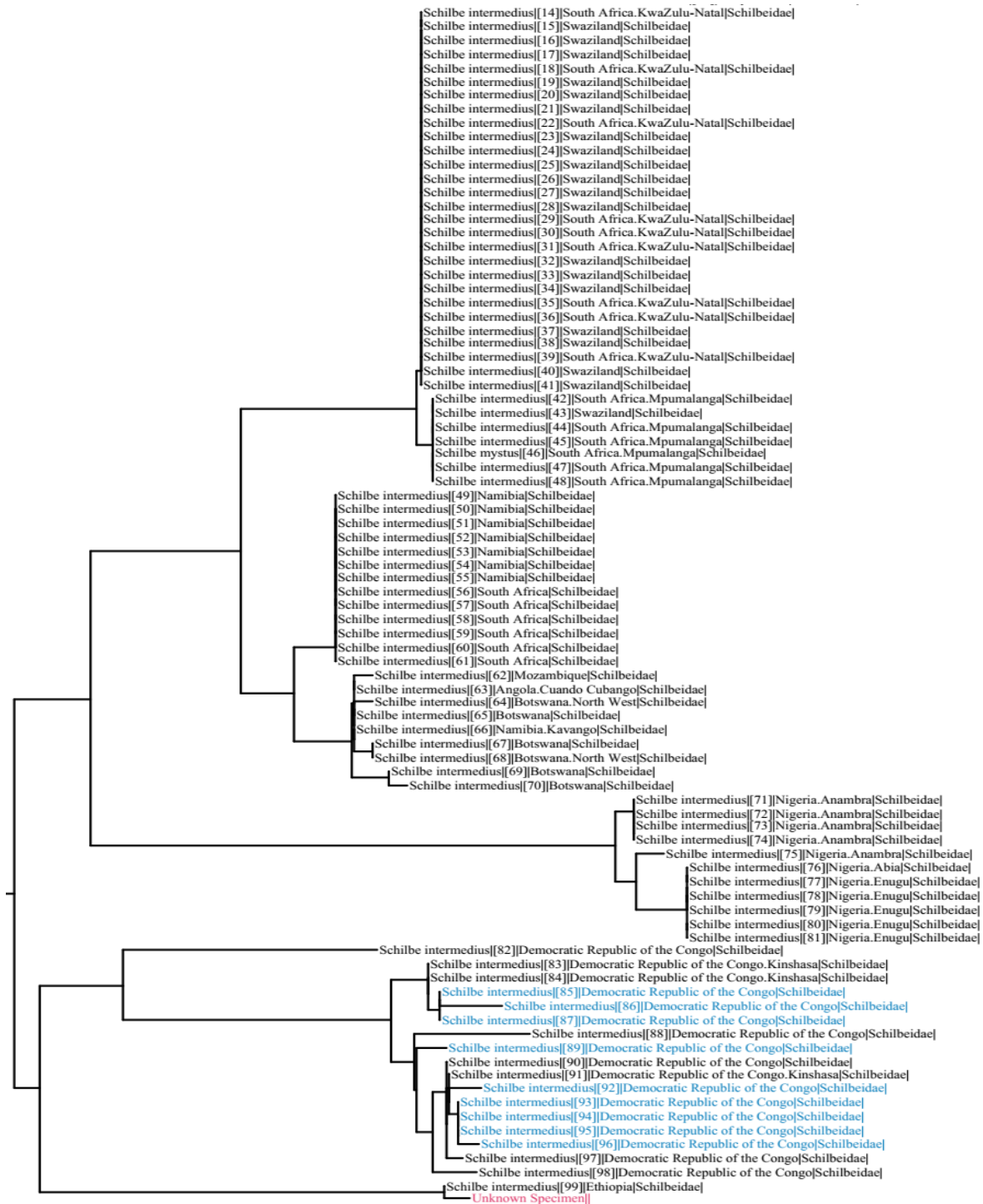


Figure 4.3p: Phylogenetic neighbour-joining tree based on COI barcode using K2P distance generated in BOLD database (www.barcodinglife.org). Unknown specimen shows the *Schilbe intermedius* sequence blast in this present study in BOLD

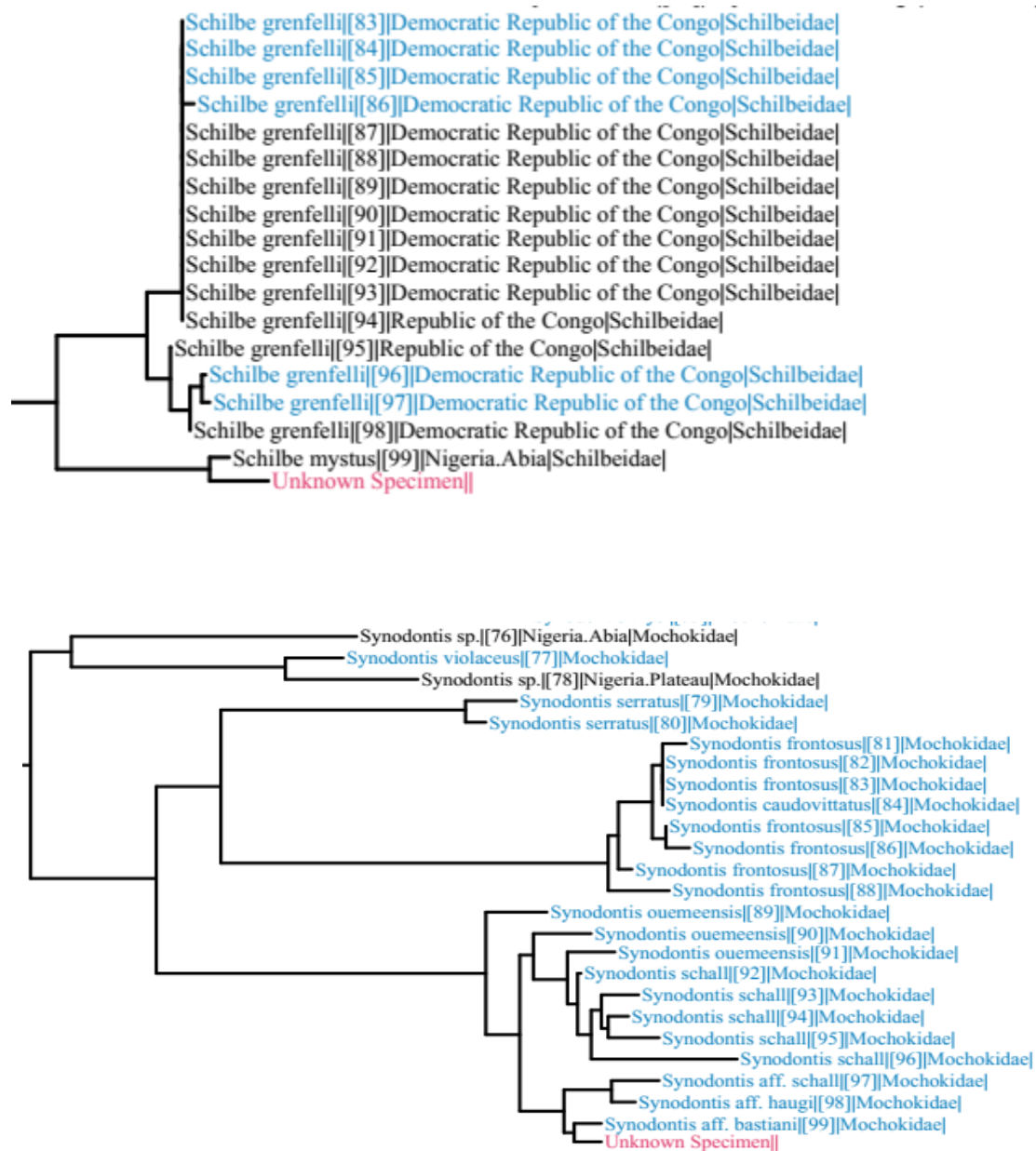


Figure 4.3q: Phylogenetic neighbour-joining tree based on COI barcode using K2P distance generated in BOLD database (www.barcodinglife.org). Unknown specimen shows the *Schilbe mystus* and *Synodontis aff. bastiani* sequence blast in this present study in BOLD

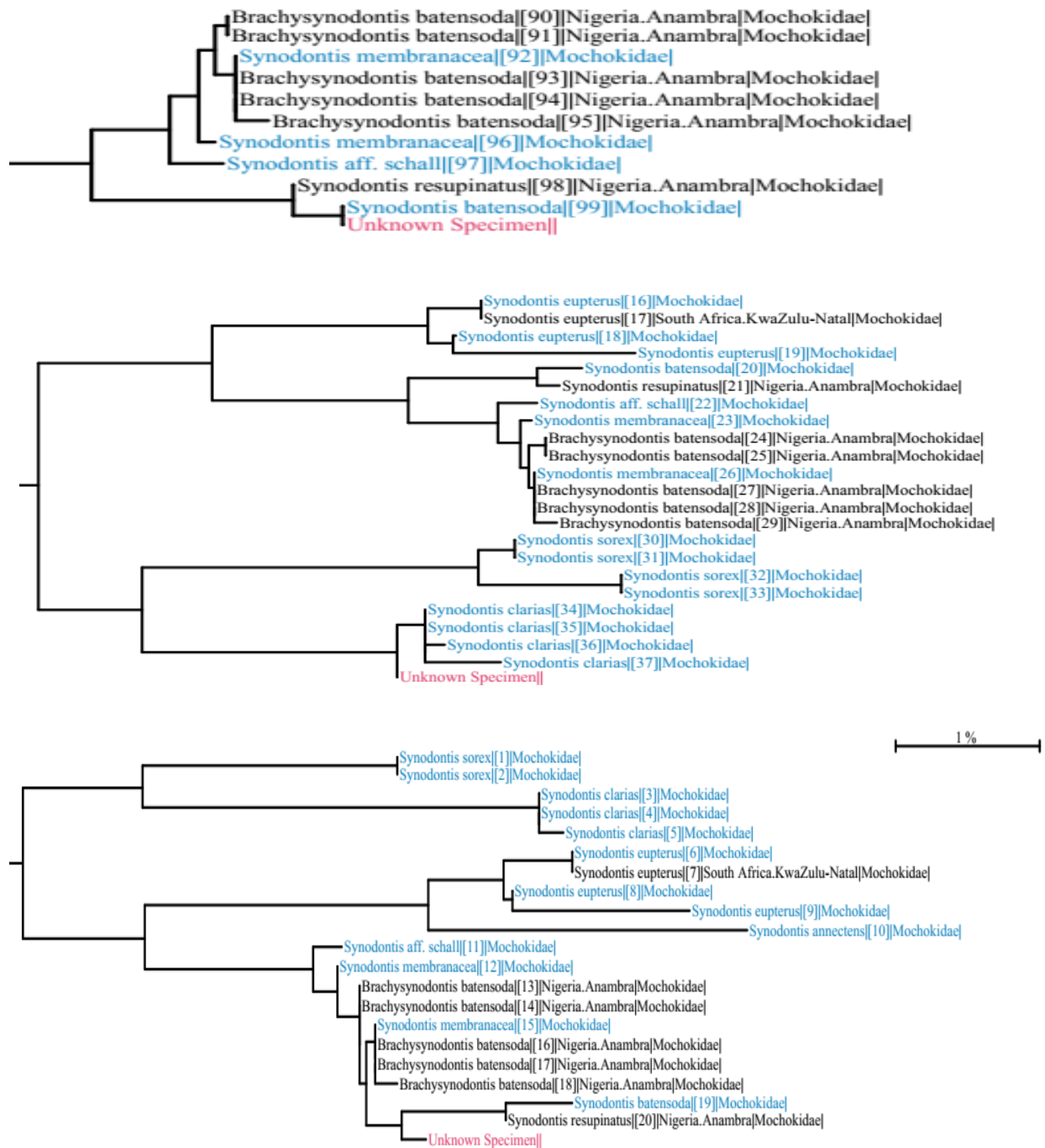


Figure 4.3r: Phylogenetic neighbour-joining tree based on COI barcode using K2P distance generated in BOLD database (www.barcodinglife.org). Unknown specimen shows the *Synodontis batensoda*, *Synodontis clarias* and *Synodontis resupinatus* sequence blast in this present study in BOLD

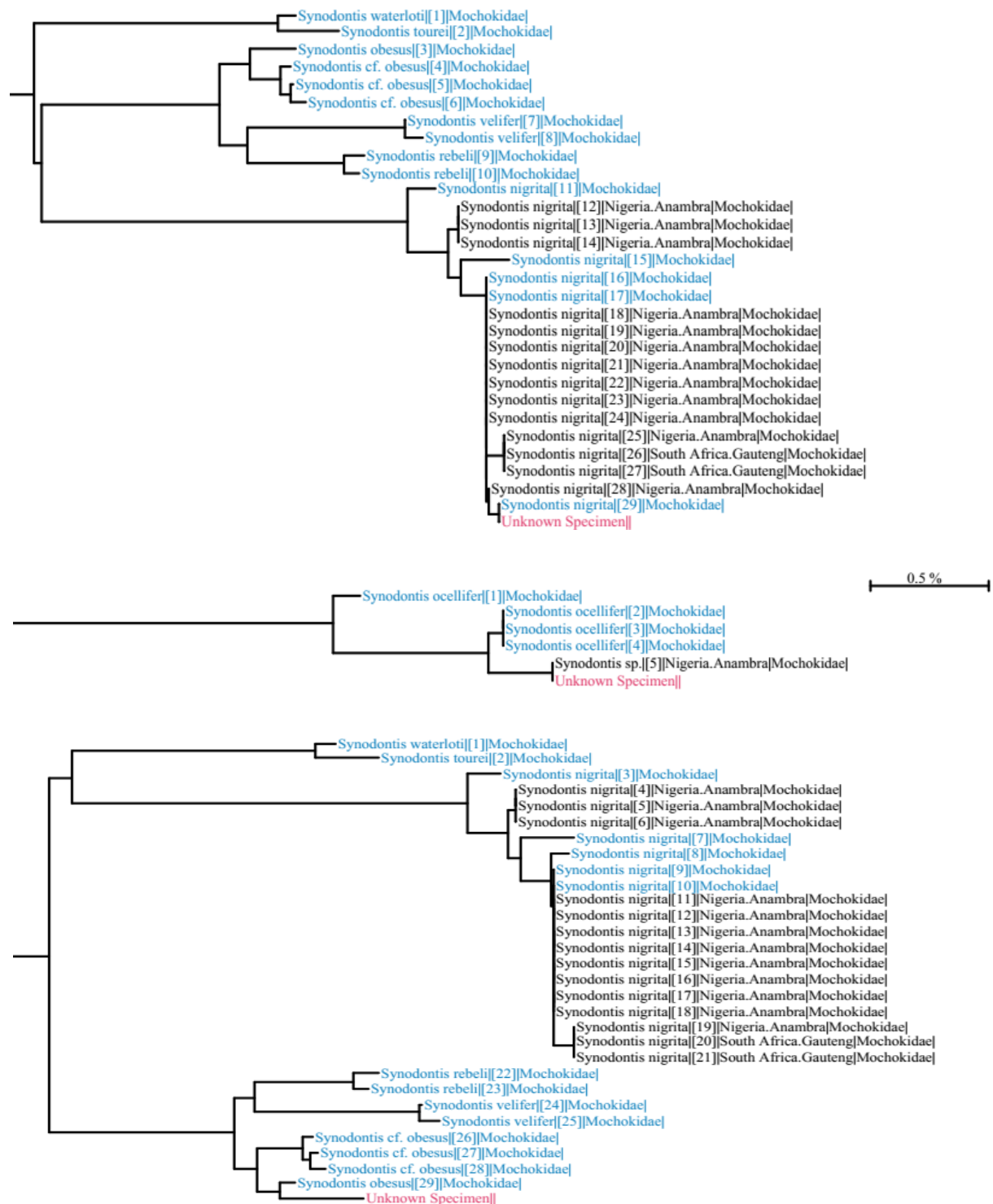


Figure 4.3s: Phylogenetic neighbour-joining tree based on COI barcode using K2P distance generated in BOLD database (www.barcodinglife.org). Unknown specimen shows the *Synodontis nigrita*, *Synodontis occillifer* and *Synodontis obesus* sequence blast in this present study in BOLD

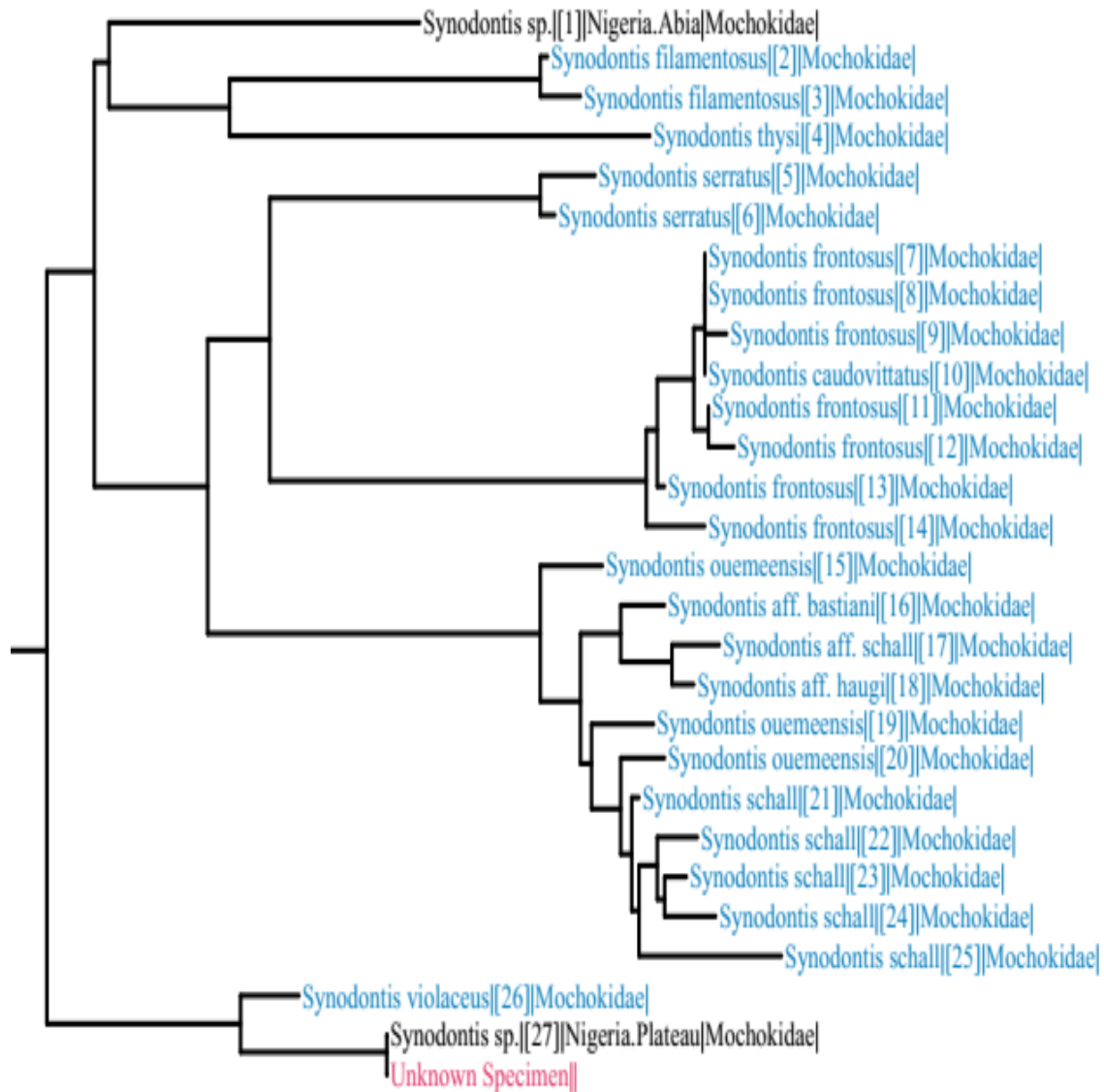


Figure 4.3t: Phylogenetic neighbour-joining tree based on COI barcode using K2P distance generated in BOLD database (www.barcodinglife.org). Unknown specimen shows the *Synodontis* spsequence blast in this present study in BOLD

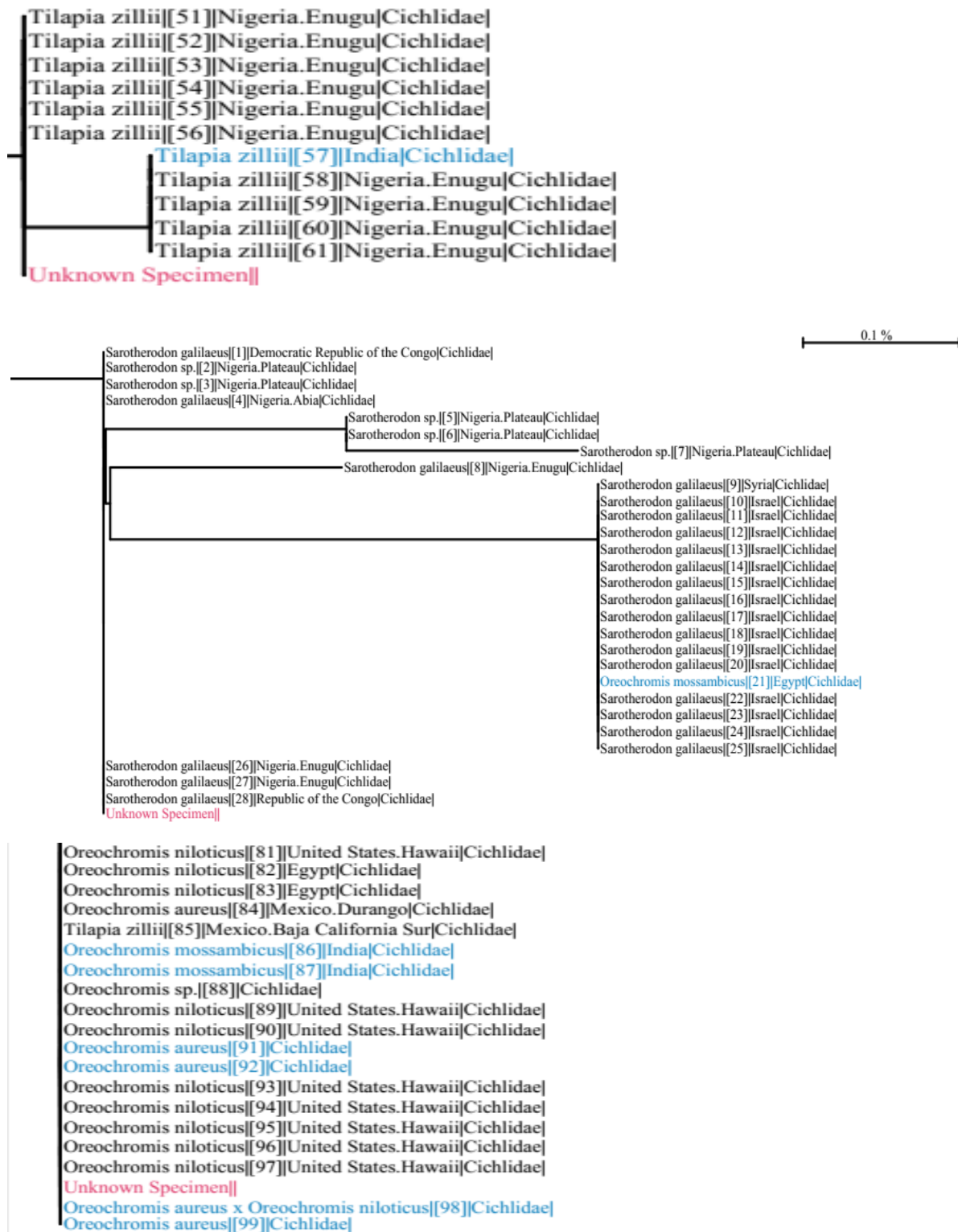


Figure 4.3u: Phylogenetic neighbour-joining tree based on COI barcode using K2P distance generated in BOLD database (www.barcodinglife.org). Unknown specimen shows the *Tilapia zillii*, *Sarotherodon galilaeus* and *Oreochromis aureus* sequence blast in this present study in BOLD

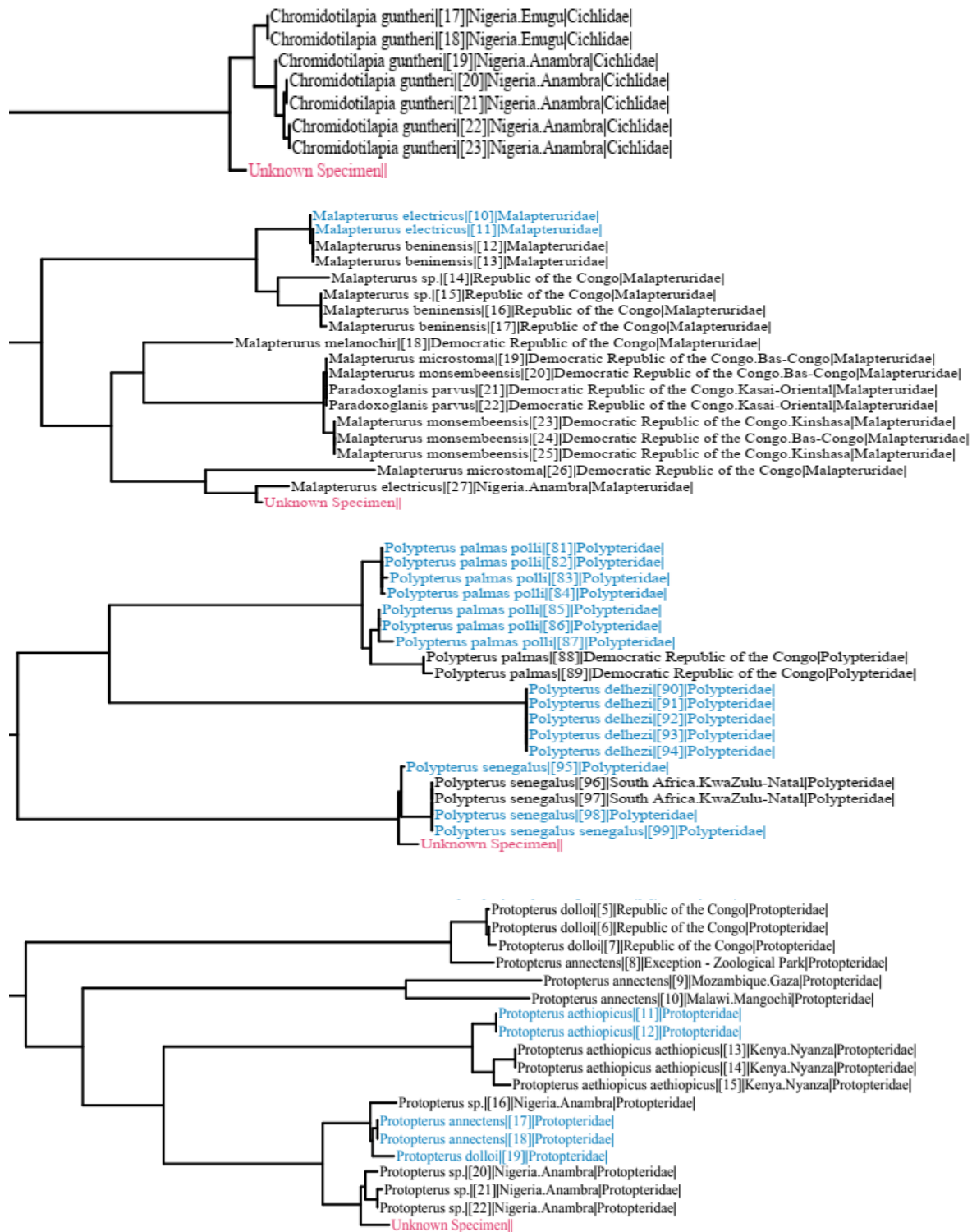


Figure 4.3v: Phylogenetic neighbour-joining tree based on COI barcode using K2P distance generated in BOLD database (www.barcodinglife.org). Unknown specimen shows the *Chromidotilapia guntheri*, *Malapterurus electricus* and *Polypterus senegalus* sequence blast in this present study in BOLD

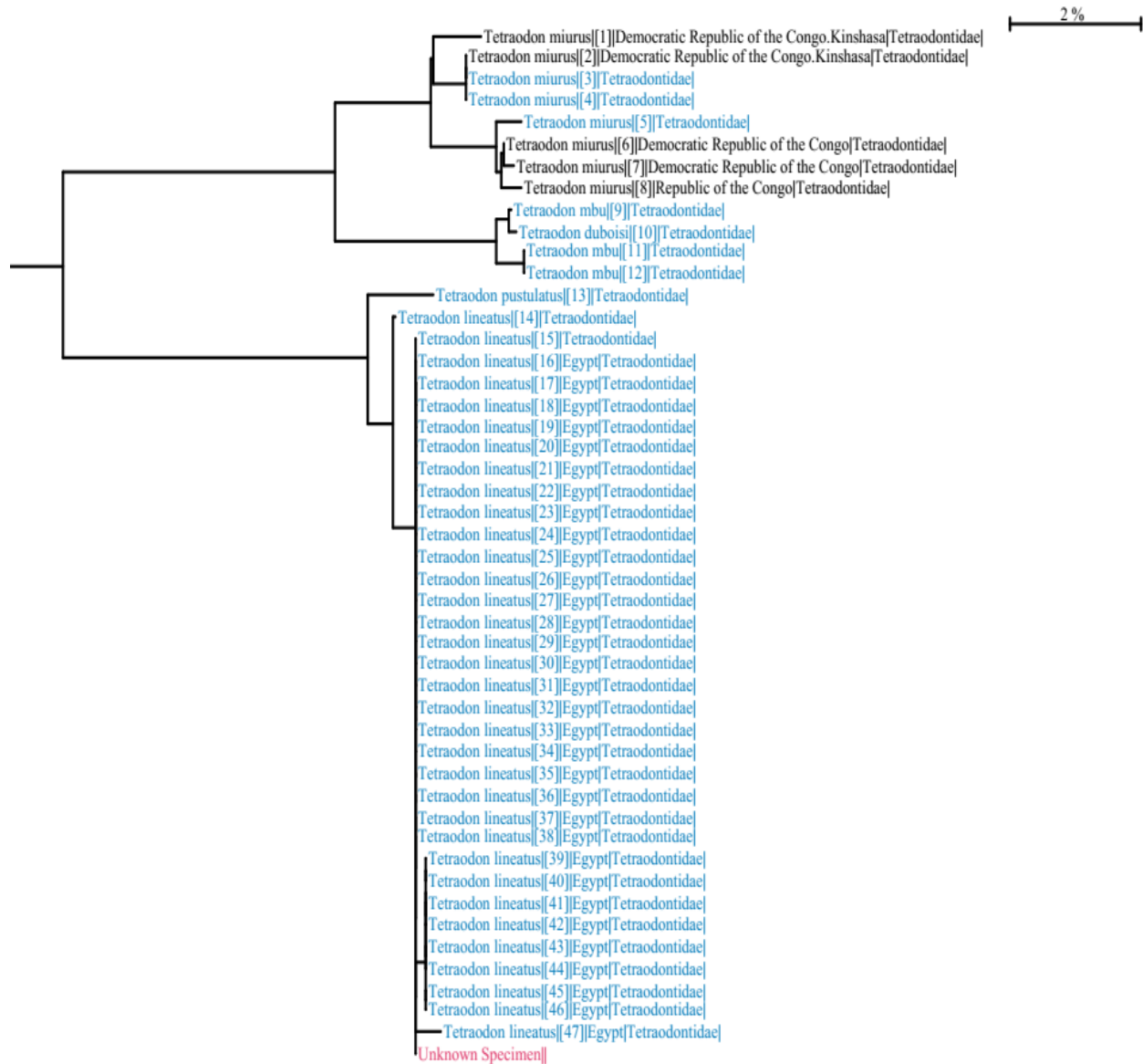


Figure 4.3w: Phylogenetic neighbour-joining tree based on COI barcode using K2P distance generated in BOLD database (www.barcodinglife.org). Unknown specimen shows the *Tetraodon lineatus* sequence blast in this present study in BOLD

4.4 Fish Composition, Abundance and Assemblage Structure

A total number of 9605 freshwater fish specimens identified belonging to 83 species, 43 genera, 24 families and 11 orders, recorded from up- and down-stream of JHPR (Table 4.1.4a). The upstream has higher number of catches with 5075 than the downstream of 4530 individual species, with rainy season and dry season giving 4821 and 4784 individuals respectively. Out of 83 species captured, 61 species were common to both dry and rainy seasons with 62 species caught during dry season and 82 species during rainy season. 80 species of fish was captured at the downstream which was higher than 68 species captured upstream.

Thirteen (13) families namely Gymnarcidae, Citharinidae, Malapteruridae, Centropomidae, Channidae, Tetraodontidae, Protopteruridae, Osteoglossidae, Dasyatidae, Anabantidae, Notopteridae, Polypteridae and Clupeidae were represented by a single species while the Mochokidae had the highest number of species (17) recorded within the family. Other families of fish recorded were Cyprinidae (9 species); Cichlidae (8 species); Mormyridae (8 species); Characidae (7 species); Claroteidae (7 species); Schilbeidae (4 species); Bagridae (3 species); Clariidae (2 species); Dischodontidae (2 species); and Ariidae (2 species).

The family Mochokidae and Cichlidae dominated the total catch with 2439 and 1759 respectively in term of abundance which accounts for 25.39% and 18.31% of the total catch. The family Dasyatidae and Protopteruridae had the least abundance in term of population catch with only 1 individual fish species each giving 0.01% of the total catch. The catch abundance in number and percentage occurrence of total catch of the other fish family present in up- and down-stream of Jebba reservoir include Characidae with 1050 fishes giving 10.93% of total catch, Claroteidae with 914 individual fishes of 9.57% total catch, Cyprinidae with 678 (7.06%), Citharinidae with 592 (6.16%), Mormyridae with 519 (5.40%) individual fishes and Bagridae

having 447 (4.65%) individual fishes. Dischodontidae had 356 individual species representing 3.71% of total fish species, while Schilbeidae, Cetropomidae, and Aridae have 327 (3.40%), 302 (3.14%), 98 (1.02%). Others include Clariidae 49 (0.51%), Gymnarcidae 36 (0.38%), Tetraodontidae 23 (0.24%), Malapteruridae 8 (0.08%), Polypteruridae 6 (0.06%), Osteoglossidae 4 (0.04%) and Clupeidae 3 (0.03%) of the total catch.

The fish species with high number and percentage of total catch include *Citharinus citharus* 592 (6.16%), *Oreochromis niloticus* 573 (5.97%), *Hydrocynus forskalii* 454 (4.73%), *Tillapia zilli* 389 (4.05%), *Brysonodontis batenensoda* 345 (3.59%), *Distichondus rostratus* 343 (3.71%), *Synodontis budgetti* 339 (3.53%), *Synodontis schall* 316 (3.29%), *Lates niloticus* 302 (3.14%), *Achenoglanis bisculatus* 291 (3.03%), *Hemisynodontis membranaceus* 281 (2.93%), *Sarotherodon galileus* 278 (2.89%), *Synodontis gambiansis* 242 (2.52%), *Achenoglanis occidentalis* 233 (2.43%), *Clarotes laticeps* 183 (1.91%), *Hydrocynus vittatus* 210 (2.19%), *Bagrus docmac* 204 (2.12%), *Tillapia guinensis* 188 (1.96%), *Brycinus nurse* 177(1.84%) and *Labeo coubie* 159 (1.66%).

Eleven families' of Gymnarcidae, Malapteruridae, Tetraodontidae, Protopteruridae, Osteoglossidae, Dasyatidae, Anabantidae, Notopteridae, Polypteridae and Clupeidae out of the thirteen families that were being represented by single species were rare in the reservoir. The other two families of Citharinidae and Centropomidae were frequently encountered especially at the upstream of the reservoir.

Table 4.4a: Ichthyodiversity, Abundance and Percentage Composition in Up- and Down-stream of JHPR.

Order	Family	Genera	Species	Dry season Upper Stream	Lower Stream	Wet Season Upper Stream	Lower Stream	Total (%)
Mormyriformes	Mormyridae	<i>Heperopisus</i>	<i>Heperopisus bebe</i>	32	31	36	47	146(1.520%)
			<i>Mormyrus</i>					
			<i>Mormyrus hasselquisti</i>	6	4	4	32	46(0.479%)
			<i>M. rume</i>	7	8	32	40	87(0.906%)
			<i>M. macrothalamus</i>	1	0	0	20	21(0.219%)
			<i>M. anguilloides</i>	8	19	18	36	81(0.843%)
		<i>Mormyrops</i>	<i>Mormyrops deliciosus</i>	29	29	25	8	91(0.947%)
			<i>Petrocephalus</i>					
		<i>Petrocephalus</i>	<i>Gnathonemus cyprynoides</i>	1	0	21	16	38(0.396%)
			<i>Marcusenius senegalensis</i>	0	0	3	6	9(0.094%)
		Total (%)		84(3.125%)	91(4.342%)	139(5.823%)	205(8.422%)	519(5.403%)
	Gymnarchidae	<i>Gymnarchus</i>	<i>Gymnarchus niloticus</i>	14	15	7	0	36(0.375%)
			Total (%)	14(0.521%)	15 (0.716%)	7 (0.293%)	0 (0%)	36(0.375%)
Characiformes	Characidae	<i>Hydrocynus</i>	<i>Hydrocynus forskalli</i>	179	148	72	58	454(4.727%)
			<i>Hydrocynus vittatus</i>	72	88	20	30	210(2.186%)
		<i>Alestes</i>	<i>Alestes baremose</i>	3	21	33	48	106(1.104%)
			<i>A. dentex</i>	0	18	27	14	59(0.614%)
		<i>Brycinus</i>	<i>Brycinus nurse</i>	19	26	69	63	177(1.843%)
			<i>B. intermedius</i>	0	0	0	10	10(0.104%)
		<i>Miralestes</i>	<i>Miralestes occidentalis</i>	0	0	0	34	34(0.354%)
			Total (%)	273 (10.156%)	302(14.408%)	218 (9.133%)	257(10.559%)	1050(10.932%)
	Distichodontidae	<i>Distichodus</i>	<i>Distichodus rostratus</i>	173	80	41	49	343(3.571%)
			<i>Distichodus encyphalus</i>	2	5	0	6	13(0.135%)
			Total (%)	175 (6.510%)	85 (4.055%)	41 (1.718%)	55(2.260%)	356(3.706%)
	Citharinidae	<i>Citharinus</i>	<i>Citharinus citharus</i>	201	109	204	78	592(6.163%)
			Total (%)	201 (7.478%)	109(5.200%)	204(8.546%)	78 (3.205%)	592(6.163%)
Cypriniformes	Cyprinidae	<i>Labeo</i>	<i>Labeo senegalensis</i>	0	49	42	44	135(1.406%)
			<i>Labeo branchypoma</i>	0	0	2	0	2(0.021%)

Siluriformes	Bagridae	Barbus	L. coubie	52	33	23	52	159(1.655%)	
			Barbus callipterus	0	0	12	15	27(0.281%)	
		B. occidentalis	56	92	91	81	320(3.332%)		
		B. lagoensis	21	0	0	0	21(0.219%)		
		Leptocypris	Leptocypris	0	0	1	7	8(0.083%)	
		Garra	Garra waterloti	0	0	0	1	1(0.010%)	
		Raimas	Raimas Senegalensis	0	0	0	5	5(0.052%)	
		Total (%)		129(4.799%)	173 (8.254%)	171 (7.164%)	195 (8.012%)	678(7.059%)	
		Bagrus	Bagrus filamentosus	46	6	60	38	150(1.562%)	
			B. docmac	17	8	116	63	204(2.124%)	
			B. bayad	13	19	44	17	93(0.968%)	
			Total (%)		76 (2.827%)	33 (1.574%)	220 (9.217%)	118 (4.848%)	447(4.654%)
	Clariidae	Clarias	Clarias geriepinus	13	0	3	15	28(0.323%)	
			C. anugularis	4	0	0	14	18(0.187%)	
		Total (%)		17 (0.632%)	0 (%)	3 (0.125%)	29 (1.192%)	49(0.510%)	
		Malapteruridae	Malapterurus	Malapterurus electricus	0	1	4	3	8(0.083%)
	Total (%)			0 (0%)	1 (0.048%)	4(0.1688%)	3 (0.123%)	8(0.083%)	
	Schilbeidae	Schilbe	Schilbe mystus	9	0	10	35	54(0.562%)	
			S. intermedius	85	0	53	66	200(2.082%)	
			S. uranoscopus	0	0	40	30	70(0.729%)	
			Parailia	Parailia pelucida	0	0	0	3	3(0.031%)
		Total (%)		94 (3.497%)	0 (0%)	103(4.315%)	130 (5.341%)	327(3.404%)	
		Claroteidae	Achenoglanis	Achenoglanis bisculatatus	165	54	44	38	291(3.030%)
				A. occidentalis	91	64	36	42	233(2.426%)
			Clarotes	Clarotes laticeps	32	0	92	57	183(1.905%)
			Chrysichthys	Chrysichthys auratus	66	3	24	0	93(0.968%)
				C. nigrodigitatus	0	2	53	24	79(0.822%)
				C. filamentous	0	0	19	10	29 (0.302%)
				Chrisichthys walker	0	0	1	5	6(0.062%)
	Total (%)		356 (13.244%)	113 (5.391%)	269 (11.269%)	276 (11.339%)	914(9.568%)		

Perciformes	Ariidae	Arius	Arius heudeloti	0	19	18	27	64(0.666%)
			A. gigas	17	8	7	2	34 (0.354%)
			Total (%)	17 (0.632%)	27 (1.288%)	25 (1.047%)	29 (1.192%)	98 (1.020%)
	Mockokidae	Brysynodontis	Brysynodontis bensoda	59	125	19	142	345(3.592%)
		Hemisynodontis	Hemisynodontis membranaceus	29	119	0	133	281(2.926%)
		Synodontis	Synodontis budgetti	57	197	25	60	339(3.529%)
			S. gambiansis	118	51	21	52	242(2.520%)
			S. eupterus	0	97	4	37	138(1.437%)
			S. violaceus	66	45	3	56	170(1.770%)
			S. schall	47	157	43	69	316(3.290%)
			S. clarias	35	56	5	15	111(1.156%)
			S. occelifer	0	21	11	13	45(0.469%)
			S. vemiculatus	0	44	0	40	84(0.875%)
			S. clarias	0	0	23	56	79(0.822%)
			S. omias	0	75	10	39	124(1.291%)
			S. resupinatus	0	0	30	65	95(0.989%)
			S. sorex	0	0	0	15	15(0.156%)
			S. thomasi	0	0	0	14	14(0.146%)
			S. filamentosus	0	0	11	6	17(0.177%)
		Chiloglanis	Chiloglanis batesii	0	9	0	15	24(0.250%)
			Total (%)	411(15.290%)	996 (47.519%)	205 (8.588%)	827 (33.977%)	2439(25.393%)
	Centropomidae	Lates	Lates niloticus	113	27	106	56	302(3.144%)
			Total (%)	113 (4.204%)	27 (1.288%)	106 (4.441%)	56 (2.301%)	302(3.144%)
	Cichlidae	Oreochromis	Oreochromis niloticus	230	85	145	103	573(5.966%)
			Oreochromis aureus	28	0	41	23	92(0.958%)
		Tillapia	Tillapia zilli	161	22	148	58	389(4.050%)
			T. guinensis	0	2	178	8	188(1.957%)
			T. dagetti	88	6	8	10	107(1.166%)
		Sarotherodon	Sarotherodon galileaus	153	10	88	27	278(2.894%)
			S. macrocephalus	61	9	30	6	106(1.104%)

		<i>Hemichromis</i>	<i>Hemichromis bimaculatus</i>	0	0	20	1	21(0.219%)
			Total (%)	721 (26.823%)	134 (6.393%)	658 (27.565%)	246 (9.902%)	1754(18.261%)
	Anabatidae	Ctenopoma	<i>Ctenopoma kingsleyae</i>	0	0	0	1	1(0.010%)
			Total (%)	0	0	0	1	1(0.010%)
	Channidae	Parachanna	<i>Parachanna obscura</i>	0	0	0	5	5(0.052%)
			Total (%)	0(0%)	0(0%)	0(0%)	5 (0.205%)	5(0.052%)
Tetraodontiformes	Tetraodontidae	<i>Tetraodon</i>	<i>Tetraodon lineatus</i>	7	0	14	2	23(0.239%)
			Total (%)	7 (0.260%)	0 (%)	14 (0.587%)	2 (0.082%)	23(0.239%)
Lepidosireniformes	Protopteruridae	<i>Protopterus</i>	<i>Protopterus annectans</i>	0	0	0	1	1 (0.010%)
			Total (%)	0 (0%)	0 (%)	0 (0%)	1 (0.041%)	1 (0.010%)
Osteoglossidae	Osteoglossidae	<i>Heterotis</i>	<i>Heterotis niloticus</i>	0	0	0	3	3(0.032%)
			Total (%)	0(0%)	0(0%)	0(0%)	3 (0.164%)	4(0.032%)
	Notopteridae	<i>Xynomystus</i>	<i>Xynomystus nigri</i>	0	0	0	1	1 (0.010%)
			Total (%)	0(0%)	0(0%)	0(0%)	1 (0.041%)	1 (0.010%)
Rajiformes	Dasyatidae	<i>Dasyatis</i>	<i>Dasyatis garouaensis</i>	0	0	0	1	1(0.010%)
			Total (%)	0(0%)	0(0%)	0(0%)	1 (0.041%)	1(0.010%)
Polypteriformes	Polypteridae	<i>Polypterus</i>	<i>Polypterus senegalus</i>	0	0	0	6	6(0.062%)
			Total (%)	0(0%)	0(0%)	0(0%)	6 (0.247%)	6(0.062%)
Clupeiformes	Clupeidae	<i>Laeviscutella</i>	<i>Laeviscutella dekimpel</i>	0	0	0	3	3(0.031%)
			Total (%)	0(0%)	0(0%)	0(0%)	3 (0.123%)	3(0.031%)
Grand Total (%)				2688 (27.985%)	2096(21.822%)	2387(24.852%)	2434(25.341%)	9605(100%)

Abundance of fish species indicates that 68 species were present at the upstream and 80 species at the downstream (Table 4.4b). Sixteen (16) species were found to be common and nine (9) occasional at both up- and down-stream. Three (3) species namely *Labeo branchypoma*, *Barbus lagoensis*, *Clarias lazera* were not encountered at the downstream while fourteen species, namely *Brycinus intermedius*, *Miralestes occidentalis*, *Garra waterloti*, *Raimas Senegalensis*, *Parailia pelucida*, *Synodontis vemiculatus*, *S. sorex*, *S. thomasi*, *Chiloglanis batesii*, *Protopterus annectans*, *Heterotis niloticus*, *Dasyatis garouaensis*, *Polypterus senegalus senegalus* and *Laeviscutella dekimpel* were not encountered at the upstream out of all the 83 species recorded. All the above named species were all rare at the locations at which they were present. At the upstream, 24 species were common, 18 species were occasional while 26 species were rare. The downstream shows 26 fish species to be common, 19 species occasional and 35 species rare. The family Mochokidae and Cichlidae constituted about 40% of the total catch abundance with Cichlidae dominance at the upstream and Mochokidae at the downstream. Other families with large number of total catch abundance include Claroteidae, Characidae Ariidae, Mormyridae and Citharinidae.

The relative monthly abundance of the fish family recorded in up- and down-stream of Jebba reservoir is shown in Figures 4.4a to 4.4r. Only thirty-eight (38) percent of the total fish families encountered during the survey were caught all year round. These families have multiple numbers of species represented in the group. The families that were not caught all year round but were in abundance include Distichodontidae, Citharinidae, Bagridae and Centropomidae making up of about twenty-four (24) percent of the encountered family (Figure 4.4a to 4.4d). Others that were caught once or few times in certain months of the year include Clariidae, Gymnarcidae,

Malapteruridae, Tetraodontidae, Protopteruridae, Osteoglossidae, Dasyatidae, Polypteridae and Clupeidae (Figure 4.4e to 4.4m). They are all being represented by single species in the family.

In the family Mormyridae, *Heperopisus bebe*, *Mormyrops anguilloides* and *Mormyrops deliciosus* were caught throughout the study period while others were only encountered in the months of July and August when catch abundance was high. Decline in catches of the family was observed in the early period of each season between October and December for dry season and March to May for rainy season (Figure 4.4n). The peak catch was observed in July, 2018 at the downstream. There is no statistical ($p > 0.05$) difference in locations and seasons having same range in the monthly catch in up- and down-stream during dry season, although downstream catch abundance was above the upstream catch abundance in the months of July and August, 2018.

The family Gymnarcidae was represented by *Gymnarchus niloticus* with statistical ($p < 0.05$) difference among locations. It was only encountered at the upstream having the peak of occurrence in the month of February, 2017 (Figure 4.4f). It was recorded in just five months out of twenty-four months of sampling survey. No record of the fish species at downstream.

The Characids were present throughout the sampling months having *Hydrocynus forskalii* and *Hydrocynus vittatus* to dominate the catch in the family. The monthly catch abundance ranged between four (4) samples species in May, 2018 to eighty (80) samples species in November, 2018. The monthly catch was higher at the downstream throughout the twenty-four month of the survey except in the months of January to March, 2017 (Figure 4.4o). Statistical ($p < 0.05$) difference was observed between seasons with the monthly catch abundance giving high catch index in dry seasons.

Table 4.4b: List of Fishes Collected from the Up and Down-Stream of JHPR Depicting the Qualitative Abundance

Order	Family	Genera	Name of species	Up Stream	Down Stream
Mormyriformes	Mormyridae	<i>Heperopisus</i>	<i>Heperopisus bebe</i>	XXX	XXX
		<i>Mormyrus</i>	<i>Mormyrus hasselquisti</i>	XX	XX
			<i>M. rume</i>	XX	XX
			<i>M. macrothalamus</i>	X	X
			<i>M. anguilloides</i>	XX	XX
		<i>Mormyrops</i>	<i>Mormyrops deliciosus</i>	XX	XX
		<i>Petrocephalus</i>	<i>Gnathonemus cyprynoides</i>	X	X
			<i>Marcusenius senegalensis</i>	X	X
	Gymnarchidae	<i>Gymnarchus</i>	<i>Gymnarchus niloticus</i>	X	X
Characiformes	Characidae	<i>Hydrocynus</i>	<i>Hydrocynus forskalli</i>	XXX	XXX
			<i>Hydrocynus vittatus</i>	XXX	XXX
		<i>Alestes</i>	<i>Alestes baremose</i>	XX	XXX
			<i>A. dentex</i>	XX	XX
		<i>Brycinus</i>	<i>Brycinus nurse</i>	XXX	XXX

Cypriniformes	Dischodontidae	<i>Miralestes</i>	<i>B. intermedius</i>		X
			<i>Miralestes occidentalis</i>		X
		<i>Distichodus</i>	<i>Distichodus rostratus</i>	XX	XX
			<i>Distichodus encyphalus</i>	X	X
	Citharinidae	<i>Citharinus</i>	<i>Citharinus citharus</i>	XXX	XXX
	Cyprinidae	<i>Labeo</i>	<i>Labeo senegalensis</i>	XX	XXX
			<i>Labeo branchypoma</i>	X	
			<i>L. cubie</i>	XX	XXX
		<i>Barbus</i>	<i>Barbus callipterus</i>	X	X
			<i>B. occidentalis</i>	XXX	XXX
			<i>B. lagoensis</i>	X	
		<i>Leptocypris</i>	<i>Leptocypris</i>	X	X
		<i>Garra</i>	<i>Garra waterloti</i>		X
		<i>Raimas</i>	<i>Raimas Senegalensis</i>		X
Siluriformes	Bagridae	<i>Bagrus</i>	<i>Bagrus filamentosus</i>	XXX	XX
			<i>B. docmac</i>	XXX	XXX

		<i>B. bayad</i>	XX	XX
Clariidae	<i>Clarias</i>	<i>Clarias geriepinus</i>	X	X
		<i>C. anugularis</i>	X	X
		<i>C. camerunensis</i>	X	X
		<i>C. lazera</i>	X	
Malapteruridae	<i>Malapterurus</i>	<i>Malapterurus electricus</i>	X	X
Schilbeidae	<i>Schilbe</i>	<i>Schilbe mystus</i>	X	XX
		<i>S. intermedius</i>	XXX	XXX
		<i>S. uranoscopus</i>	XX	XX
	<i>Parailia</i>	<i>Parailia pelucida</i>		X
Claroteidae	<i>Achenoglanis</i>	<i>Achenoglanis bisculatatus</i>	XXX	XXX
		<i>A. occidentalis</i>	XXX	XXX
	<i>Clarotes</i>	<i>Clarotes laticeps</i>	XXX	XXX
	<i>Chrysichthys</i>	<i>Chrysichthys auratus</i>	XX	X
		<i>C. nigrodigitatus</i>	XX	XX
		<i>C. filamentous</i>	X	X

		<i>Chrisichthys walker</i>	X	X
Ariidae	Arius	<i>Arius heudeloti</i>	X	XX
		<i>A. gigas</i>	X	X
Mockokidae	Brysynodontis	<i>Brysynodontis bensoda</i>	XX	XXX
	Hemisyndontis	<i>Hemisyndontis membranaceus</i>	XX	XXX
	Synodontis	<i>Synodontis budgetti</i>	XXX	XXX
		<i>S. gambiansis</i>	XXX	XXX
		<i>S. eupterus</i>	X	XXX
		<i>S. violaceus</i>	XXX	XXX
		<i>S. schall</i>	XXX	XXX
		<i>S. clarias</i>	XX	XXX
		<i>S. ocellifer</i>	X	X
		<i>S. vemiculatus</i>		XX
		<i>S. clarias</i>	X	XX
		<i>S. omias</i>	XX	XXX
		<i>S. resupinatus</i>	XX	XX

			<i>S. sorex</i>		X
			<i>S. thomasi</i>		X
			<i>S. filamentosus</i>	X	X
		<i>Chiloglanis</i>	<i>Chiloglanis batesii</i>		X
Perciformes	Centropomidae	<i>lates</i>	<i>Lates niloticus</i>	XXX	XXX
	Cichlidae	<i>Oreochromis</i>	<i>Oreochromis niloticus</i>	XXX	XXX
			<i>Oreochromis aureus</i>	XX	X
		<i>Tillapia</i>	<i>Tillapia zilli</i>	XXX	XX
			<i>T. guinensis</i>	XXX	X
			<i>T. dagetti</i>	XXX	XX
		<i>Sarotherodon</i>	<i>Sarotherodon galileaus</i>	XXX	XX
			<i>S. macrocephalus</i>	XXX	XX
		<i>Hemichromis</i>	<i>Hemichromis faciantus</i>	X	X
		<i>Chromidotillapia</i>	<i>Chromidotillapia guntheri</i>	X	
Tetraodontiformes	Tetraodontidae	<i>Tetraodon</i>	<i>Tetraodon lineatus</i>	X	X
Lepidosireniformes	Protopteruridae	<i>Protopterus</i>	<i>Protopterus annectans</i>		X

Osteoglossidae	Osteoglossidae	<i>Heterotis</i>	<i>Heterotis niloticus</i>	X
Rajiformes	Dasyatidae	Dasyatis	<i>Dasyatis garouaensis</i>	X
Polypteriformes	Polypteridae	<i>Polypterus</i>	<i>Polypterus senegalus senegalus</i>	X
Clupeiformes	Clupeidae	<i>Laeviscutella</i>	<i>Laeviscutella dekimpel</i>	X

Key: Abundant: XXX, Common; XX, Occasional; X, Rare.

The monthly catch abundance of the upstream was higher than the downstream in the family Distichodontidae and Citharinidae (Figure 4.4a and b). Similarly, the catch abundance was higher during the dry season in family Distichodontidae with the peak recorded in April, 2017. No catch was recorded in August, September and December 2017, likewise in May and June, 2018. The family Citharinidae was represented by a single species. The monthly catch abundance was higher at the upstream than the downstream except in January and December, 2018. The highest catch was recorded in March, 2017 with no catch in September, 2017, May and June, 2018. Distichodontidae show a seasonal statistical ($p < 0.05$) difference in the upstream while no statistical ($p > 0.05$) difference was observed in the downstream. In the case of Citharinidae, statistical ($p < 0.05$) seasonal variation was observed.

The family Cyprinidae was frequently caught all year round except in the month of January (Figure 4.4p). Similarly, there was also a drastic decline in number of catch in the month of October. Abundant catches were frequent and higher at the downstream than the upstream throughout the sampling period with the peak recorded in the month of April, 2018. Bagridae show a record of high catch abundance during the rainy season with the peak in the month of July. The month of January and February show no catch in both up- and down-stream. The family showed statistical ($p < 0.05$) different in seasons and locations

Clariidae shows low abundance in the total catch and were encountered in few months of the sampling period (Figure 4.4e). It was encountered once at the upstream in November, 2017. The highest catch was recorded in the month of April, 2017 at the downstream. Same occurrence was also recorded in the family Malapteruridae. It was recorded in only five months of the sampling period and represented by just a species with one sample in most occasions (Figure 4.4g).

The family Mochokidae had the highest catch abundance in term of number and species. There was increase incatch abundance during dry season between the months of February and May. Statistical ($p<0.05$) difference was observed in locations with the low frequency of occurrence and abundance at the upstream all year round except in month of March where they had relatively high abundance. The highest catch was recorded in month of March, 2018 and lowest in the month of October, 2017 (Figure 4.4q).

Centropomidae had high abundance at the upstream with statistical ($p<0.05$) difference in locations (Figure 4.4d). No catch was made in the months of September and December, 2017, January and June, 2018 in up- and down-stream. The peak occurrence was recorded in the month of June, 2017 with drastic decline in month of July, 2017. The Cichlids presented the highest frequency of occurrence in term of number and monthly catch at the upstream with occasional catch at the downstream showing statistical ($p<0.05$) difference in locations (Figure 4.4r). There is no difference in Cichlids cacth abundance in both up- and down-stream in October, 2017 with no catch in May, 2018 at both up- and down-stream.

The family Tetraodontidae, Protopteruridae, Osteoglossidae, Dasyatidae, Polypteridae and Clupeidae were only represented by only one species and were rare in catch abundance (Figure 4.4e-4.4m).

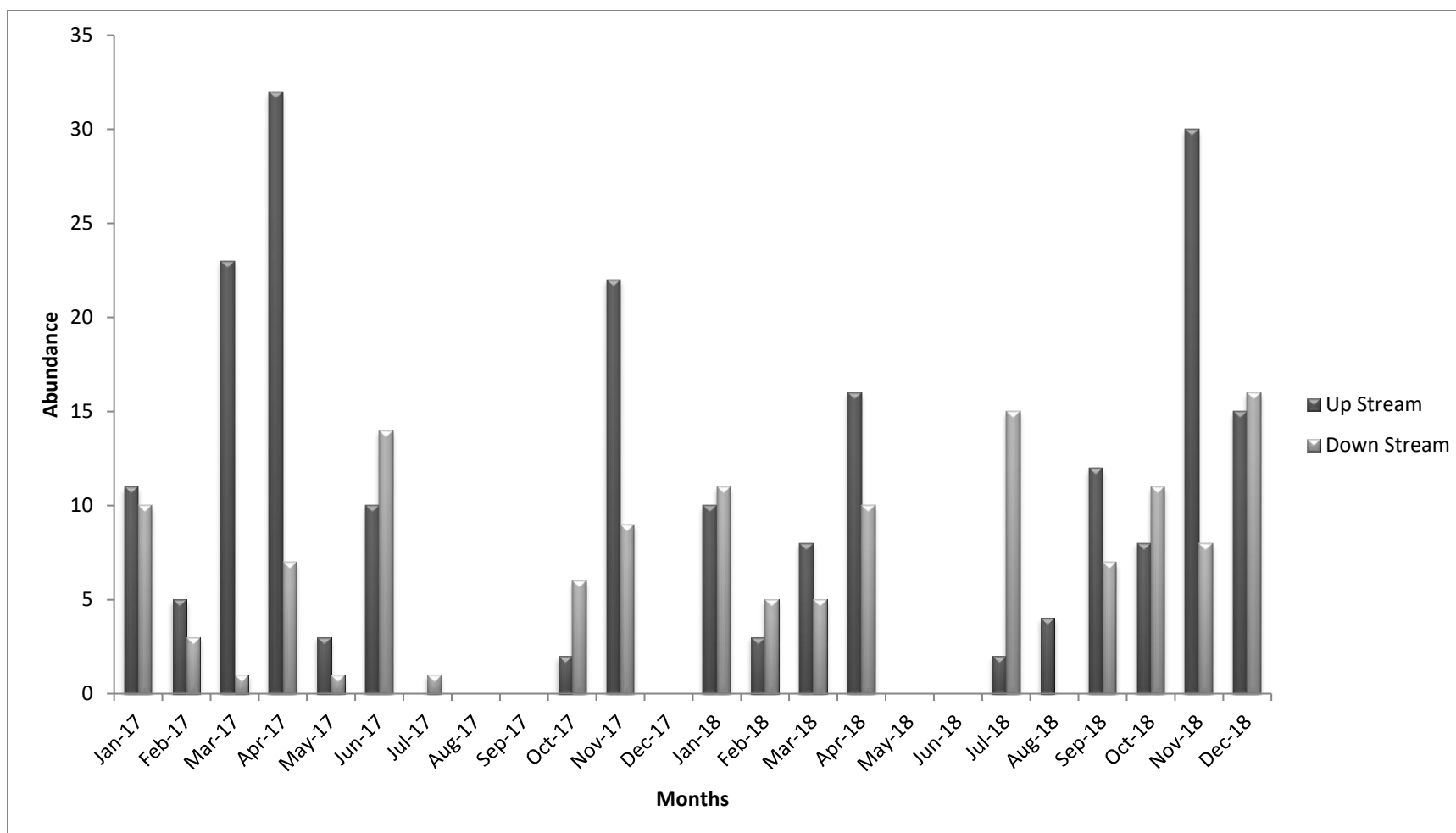


Figure 4.4a: Fish Catch Abundance Variations in family Distichodontidae in Up- and Down-stream of JHPR

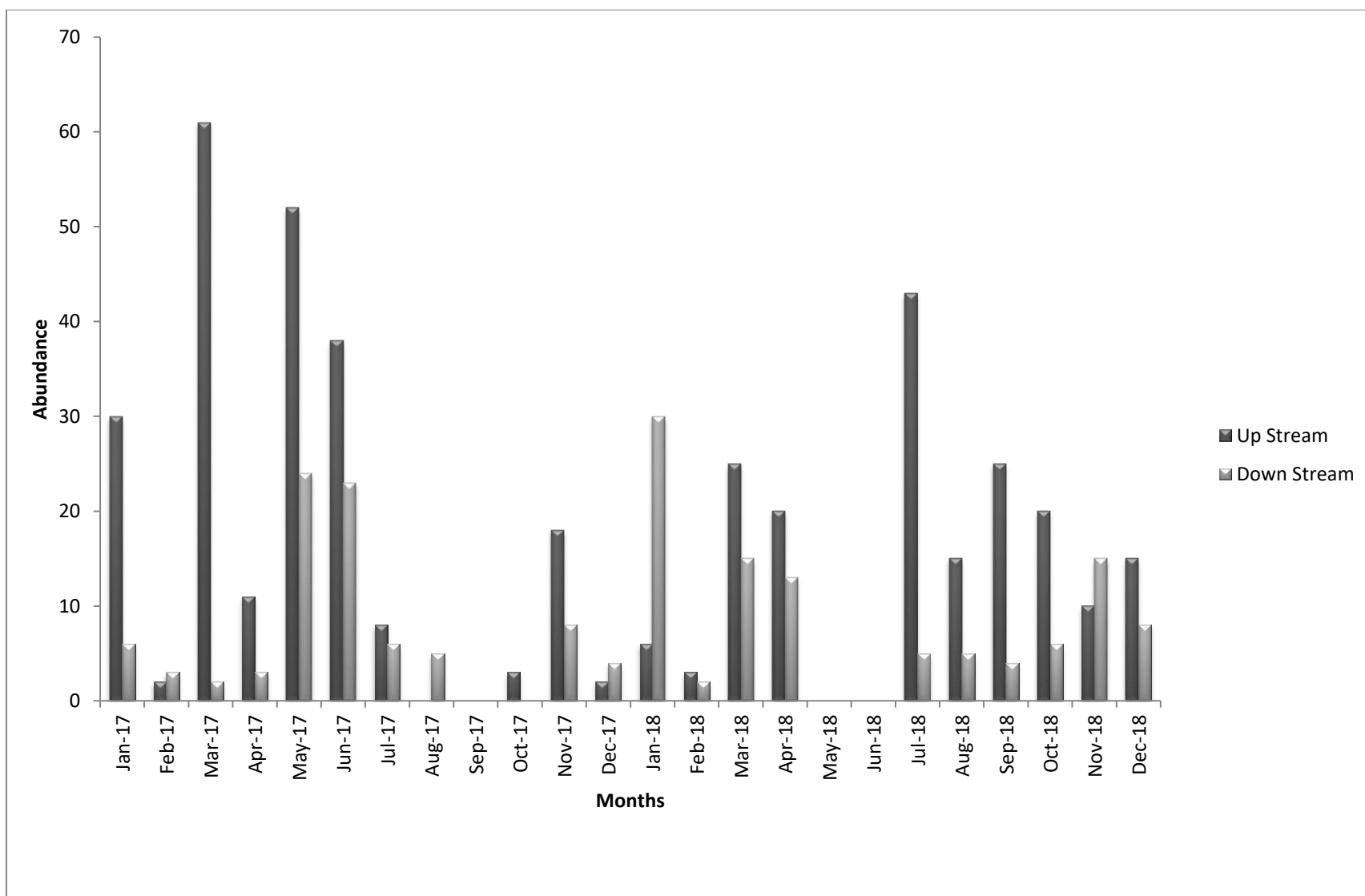


Figure 4.4b: Fish Catch Abundance Variations in family and Citharinidae in Up- and Down-stream of JHPR.

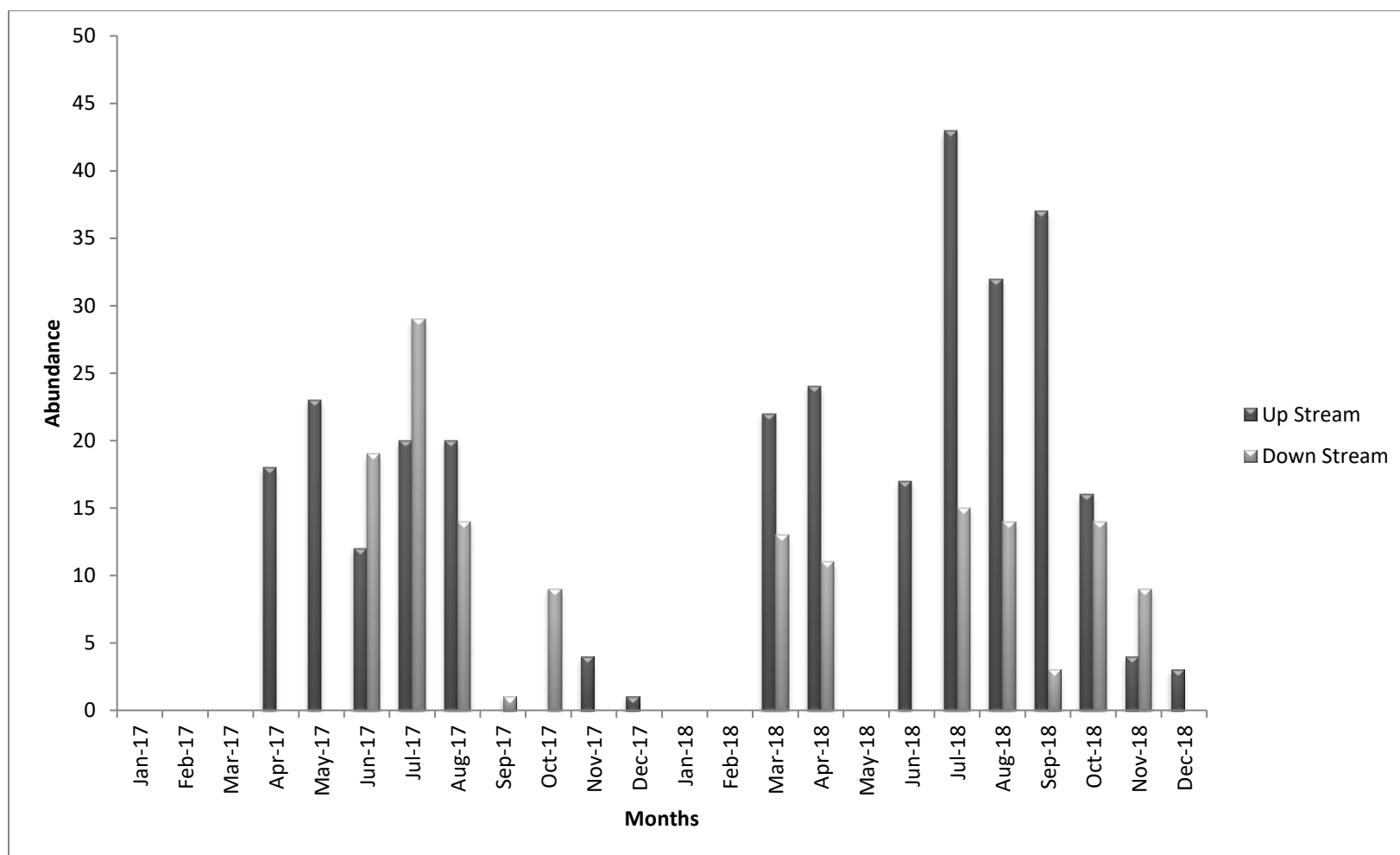


Figure 4.4c: Fish Catch Abundance Variations in Family Bagridae in Up- and Down-stream of JHPR.

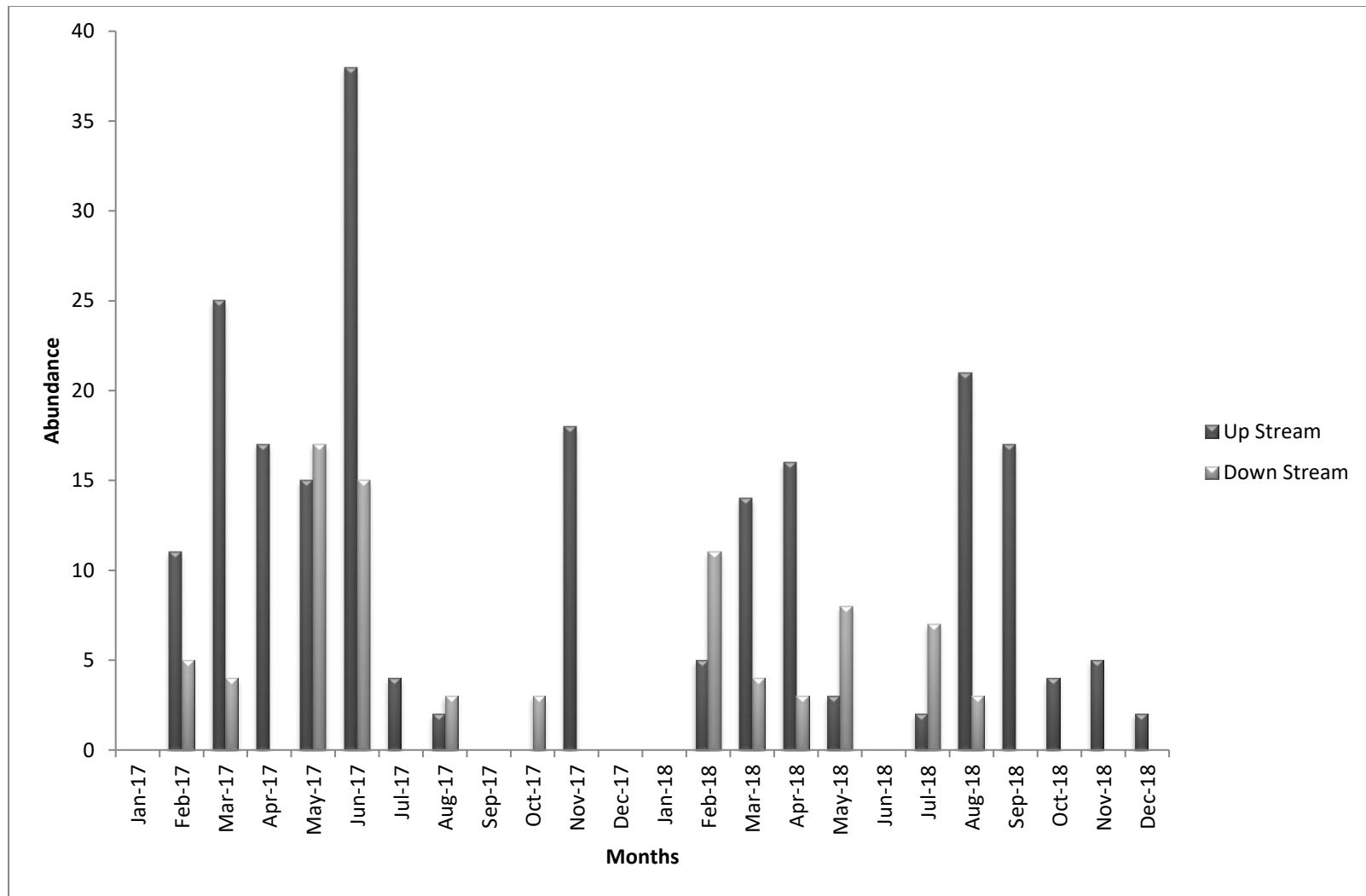


Figure 4.4d: Fish Catch Abundance Variations in Family Centropomidae in Up- and Down-stream of JHPR.

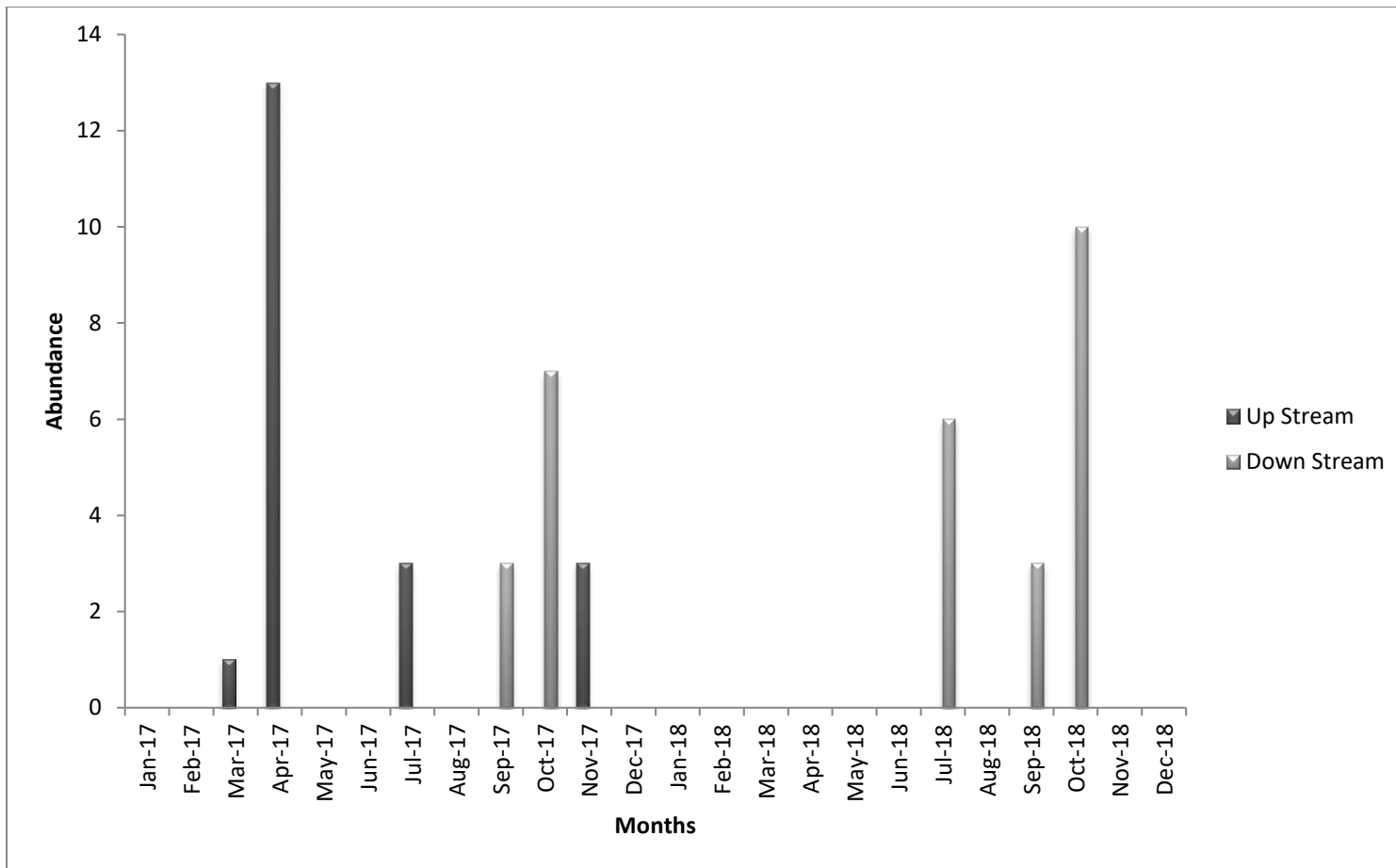


Figure 4.4e: Fish Catch Abundance Variations in Family Clariidae in Up- and Down-stream of JHPR.

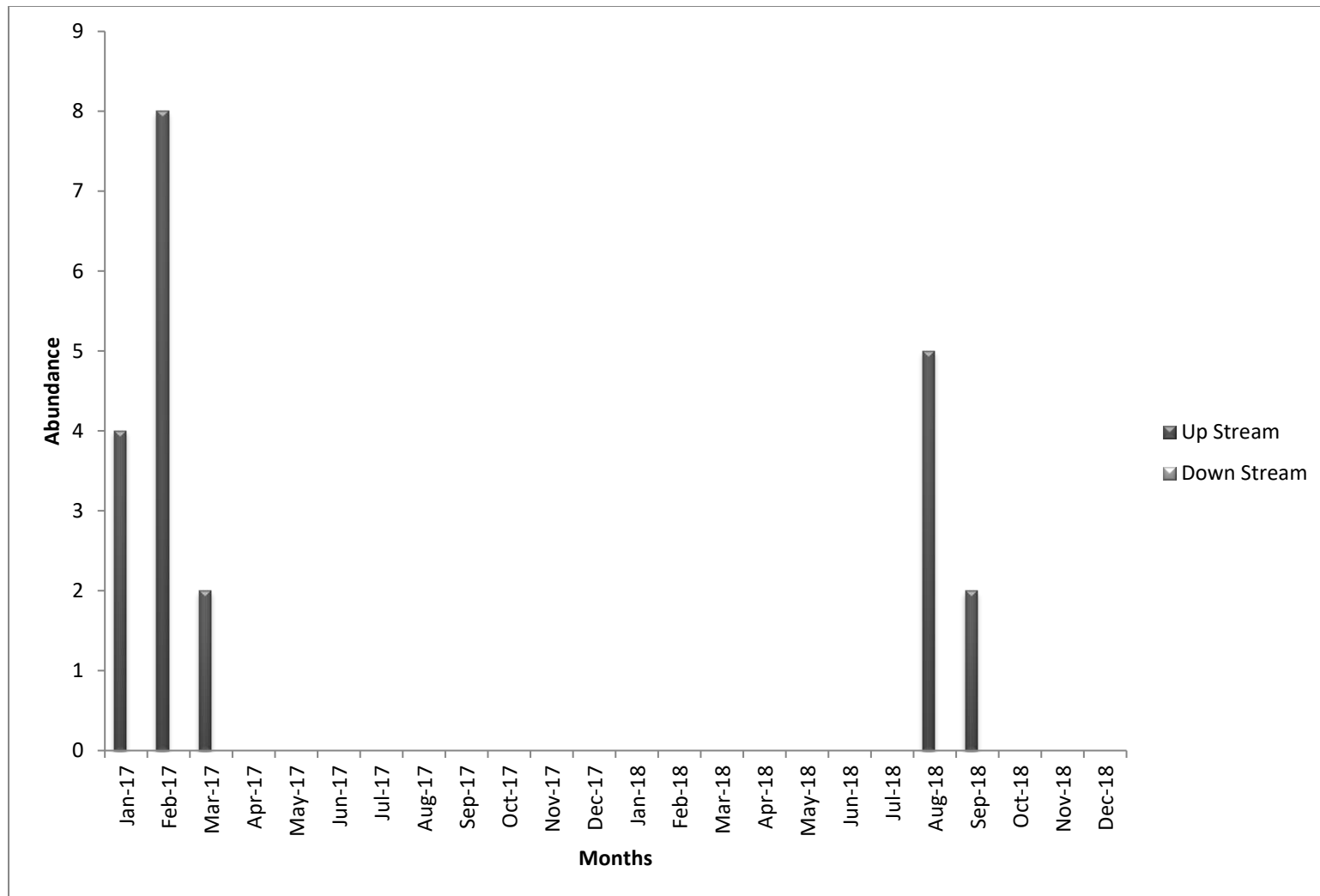


Figure 4.4f: Fish Catch Abundance Variations in Family Gymnarcidae in Up- and Down-stream of JHPR.

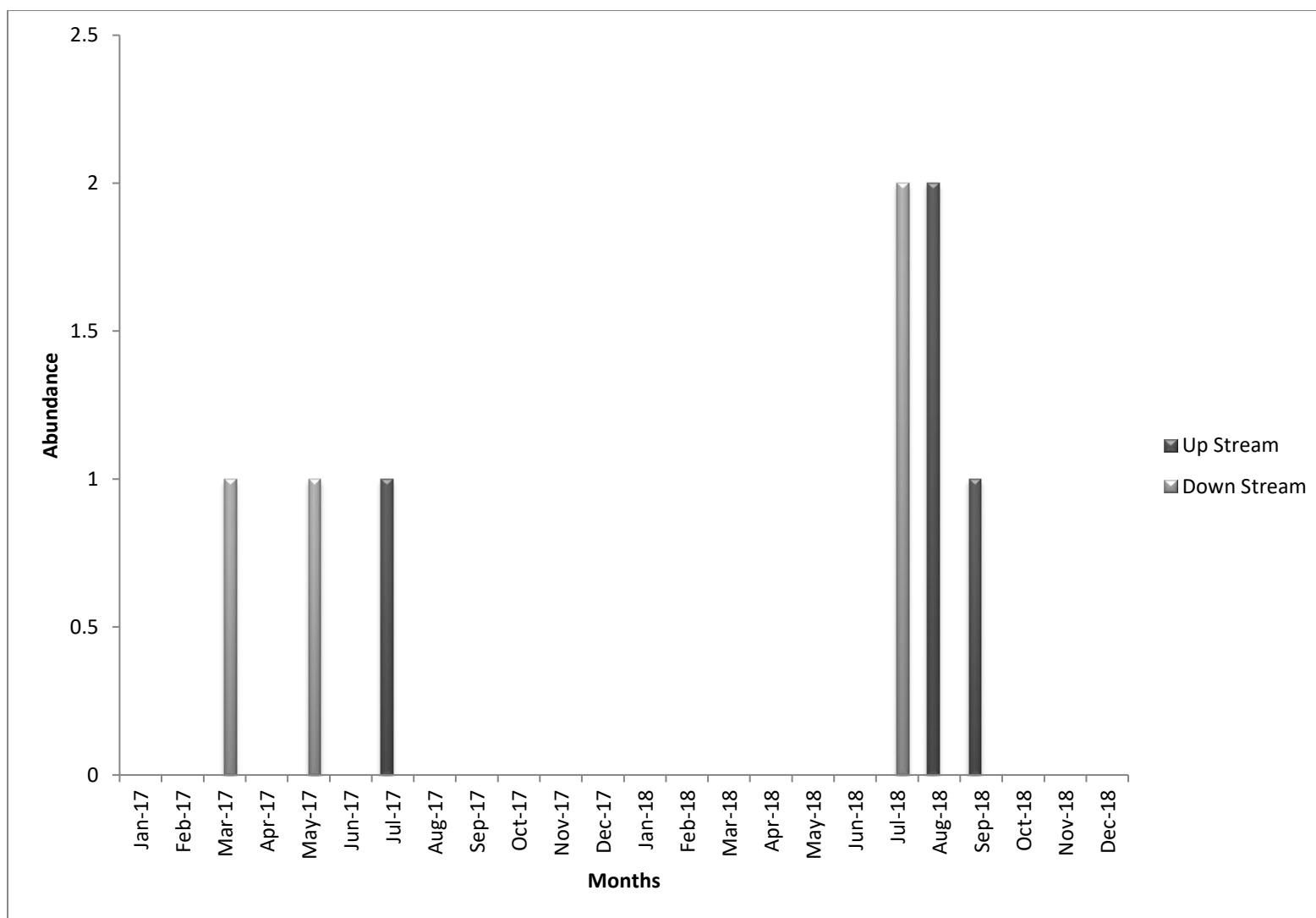


Figure 4.4g: Fish Catch Abundance Variations in Family Malapteruridae in Up- and Down-stream of JHPR.

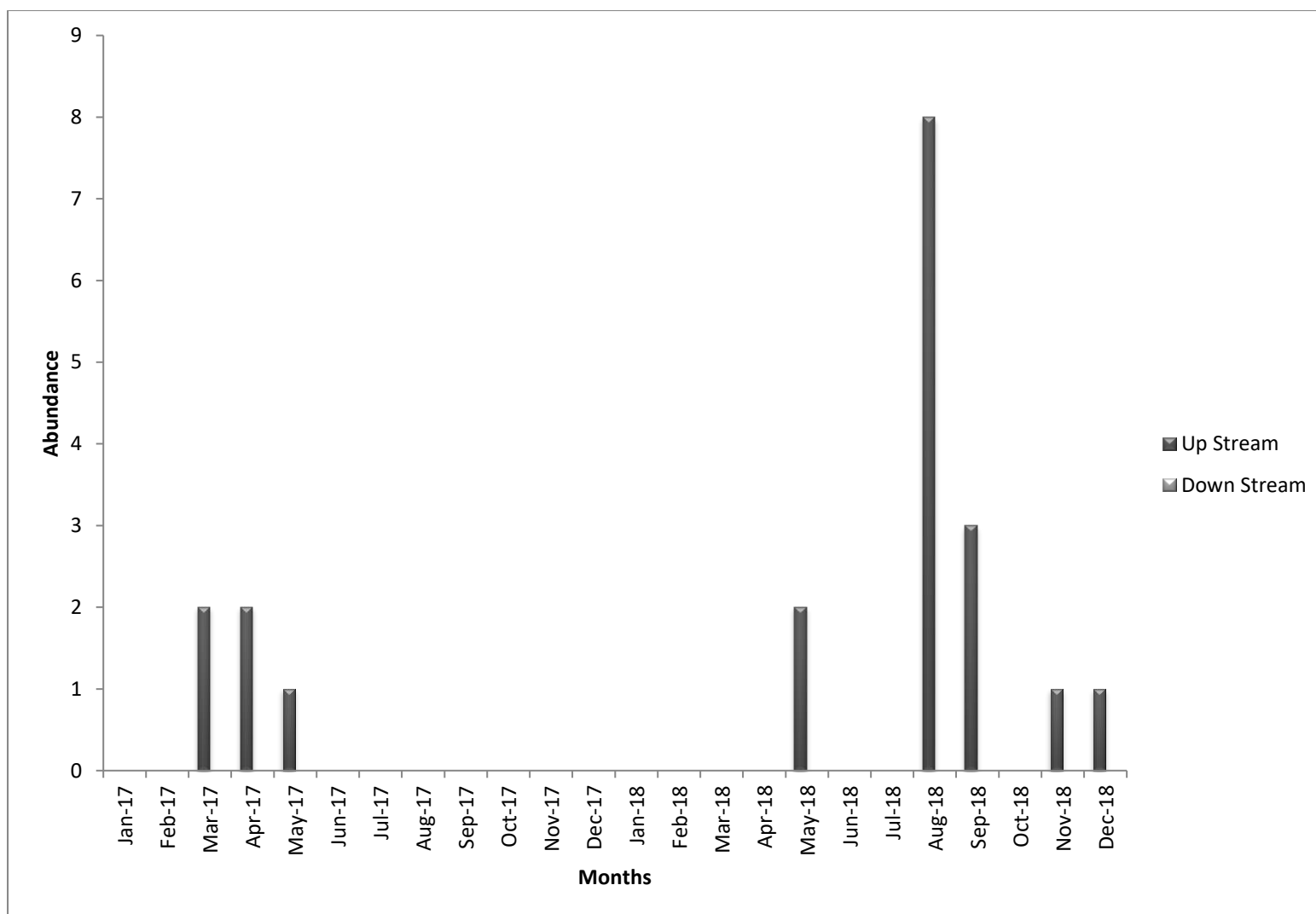


Figure 4.4h: Fish Catch Abundance Variations in Family Tetraodontidae in Up- and Down-stream of JHPR.

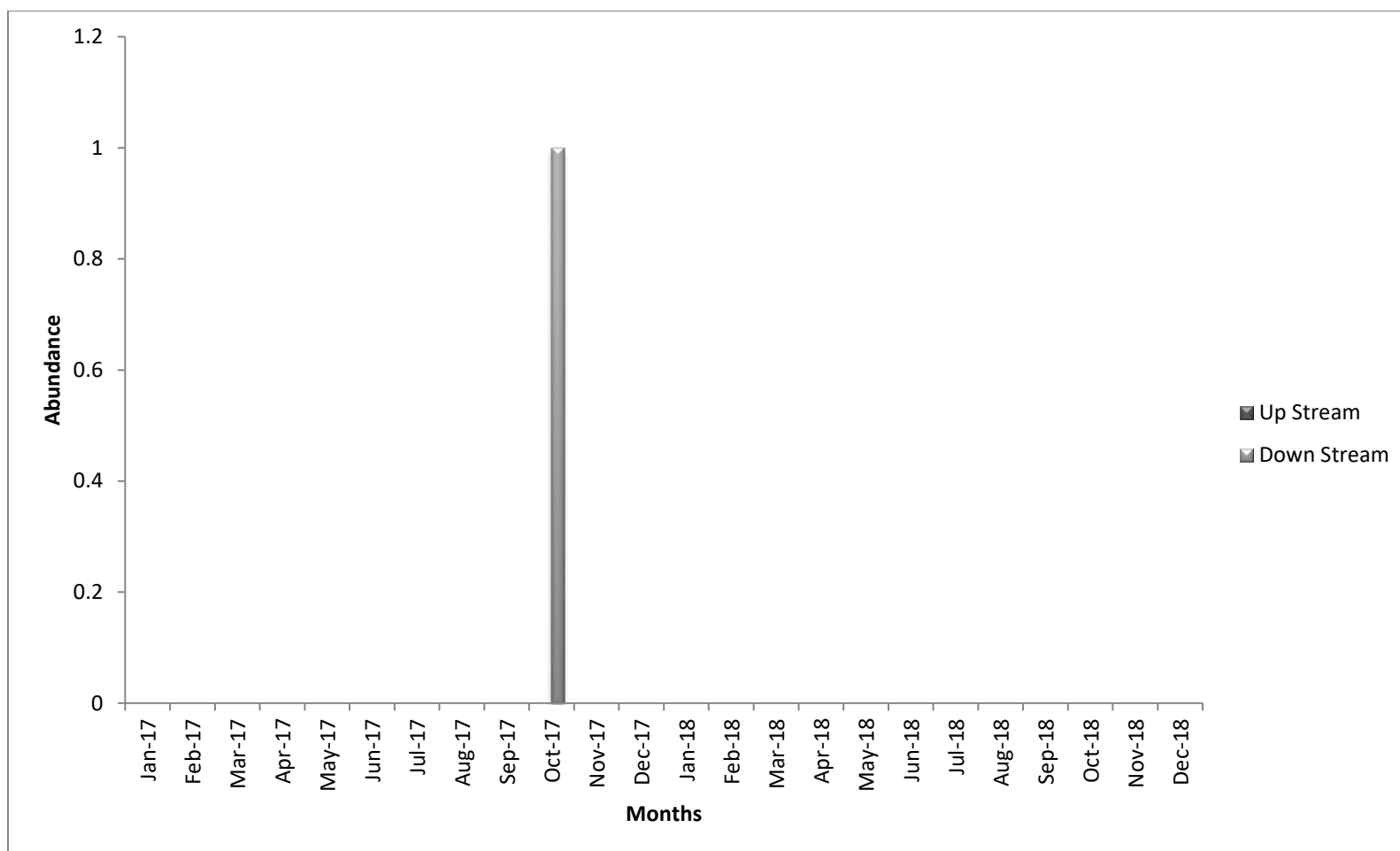


Figure 4.4i: Fish Catch Abundance Variations in Family Protopteridae in Up- and Down-stream of JHPR.

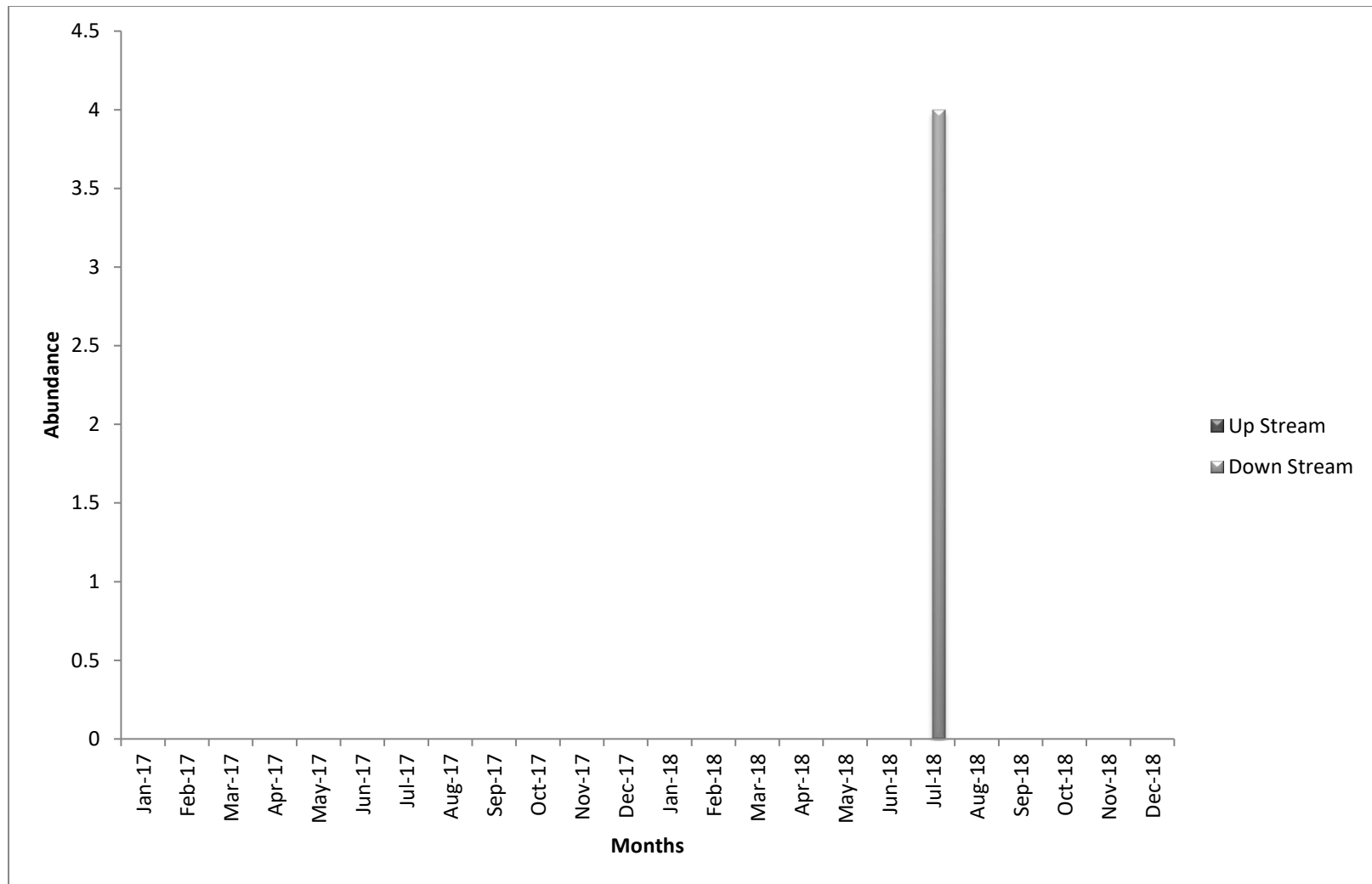


Figure 4.4j: Fish Catch Abundance Variations in Family Osteoglossidae in Up- and Down-stream of JHPR.

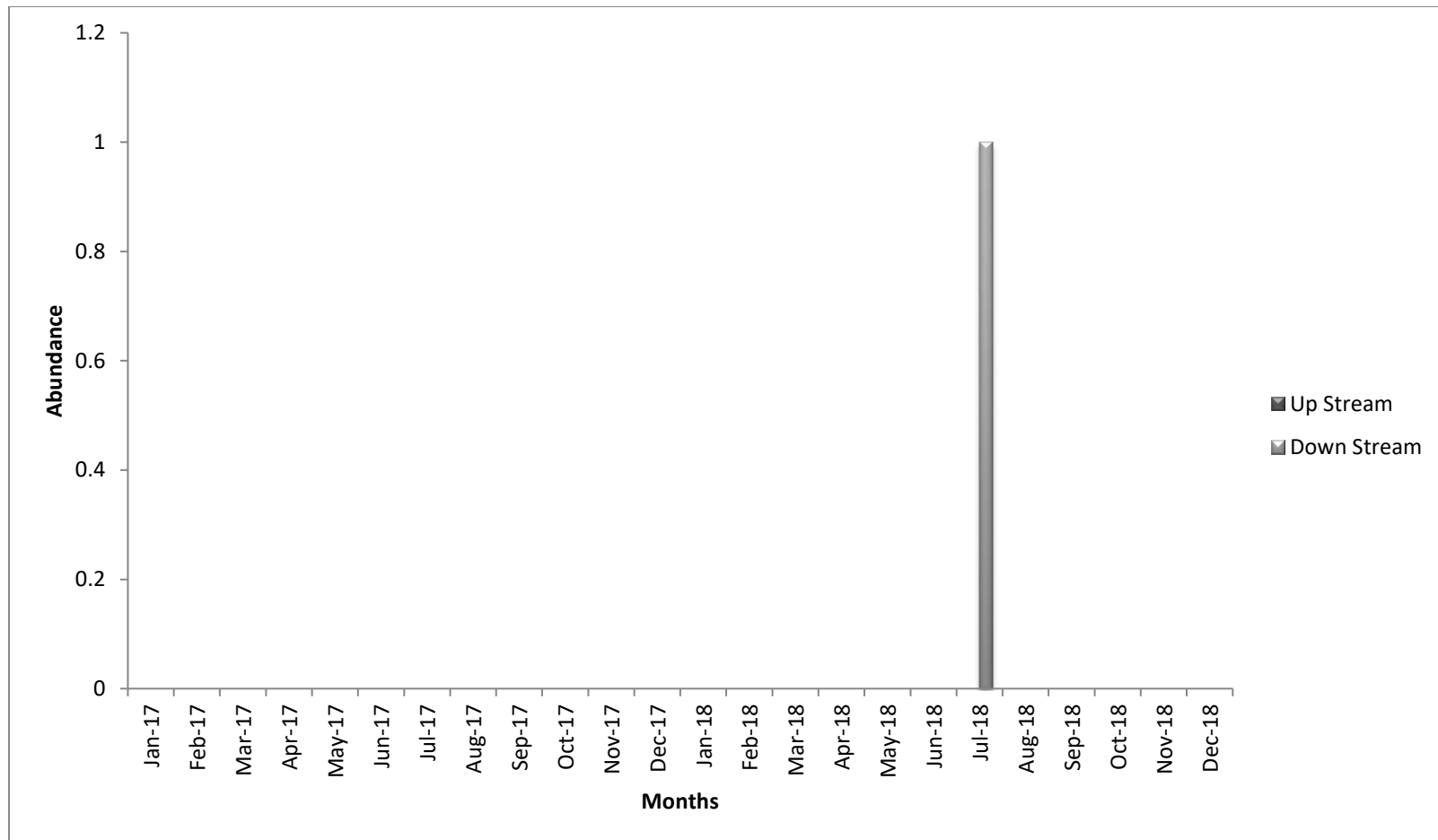


Figure 4.4k: Fish Catch Abundance Variations in Family Dasyatidae in Up- and Down-stream of JHPR.

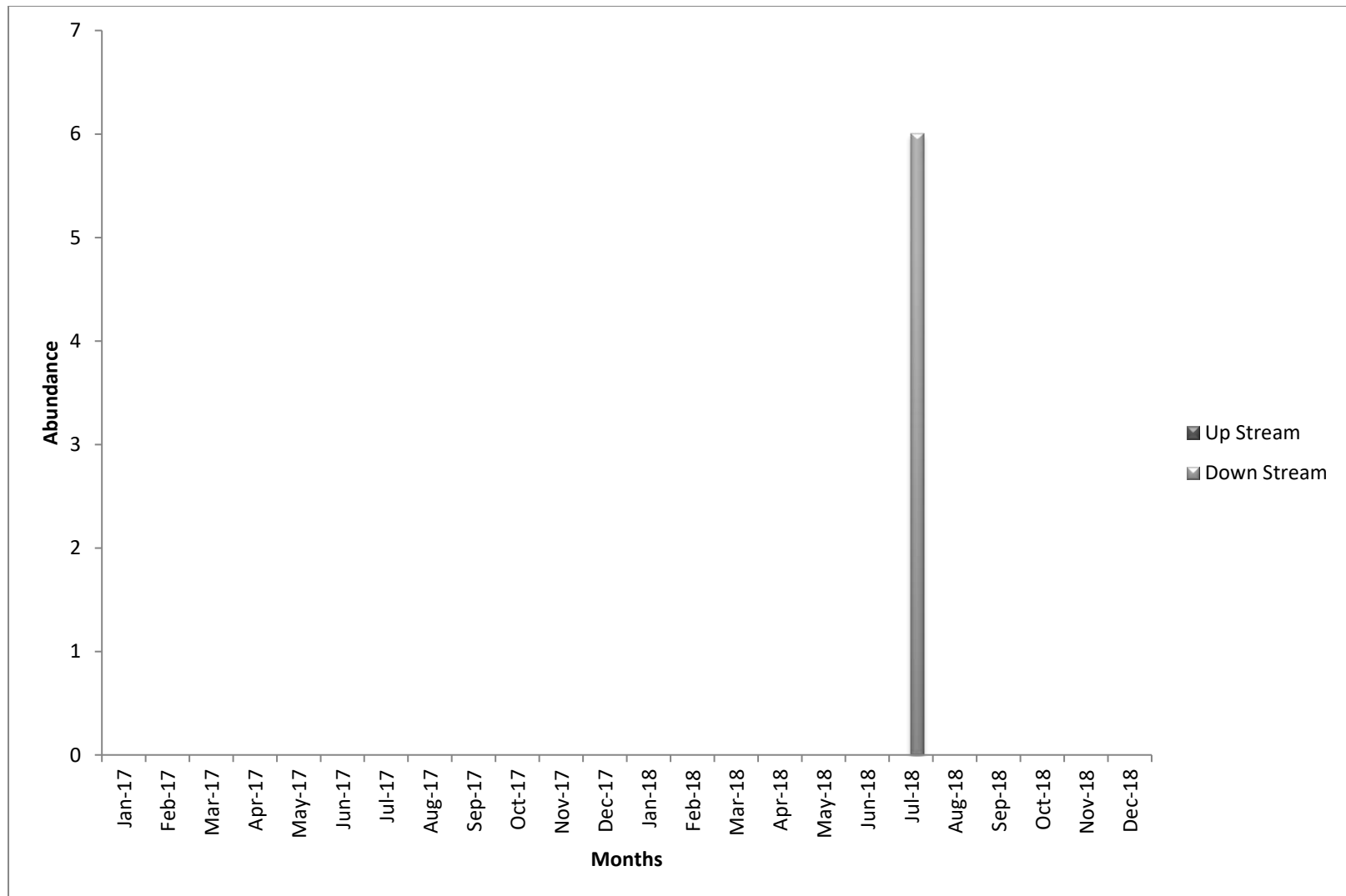


Figure 4.4I: Fish Catch Abundance Variations in Family Polypteridae in Up- and Down-stream of JHPR.

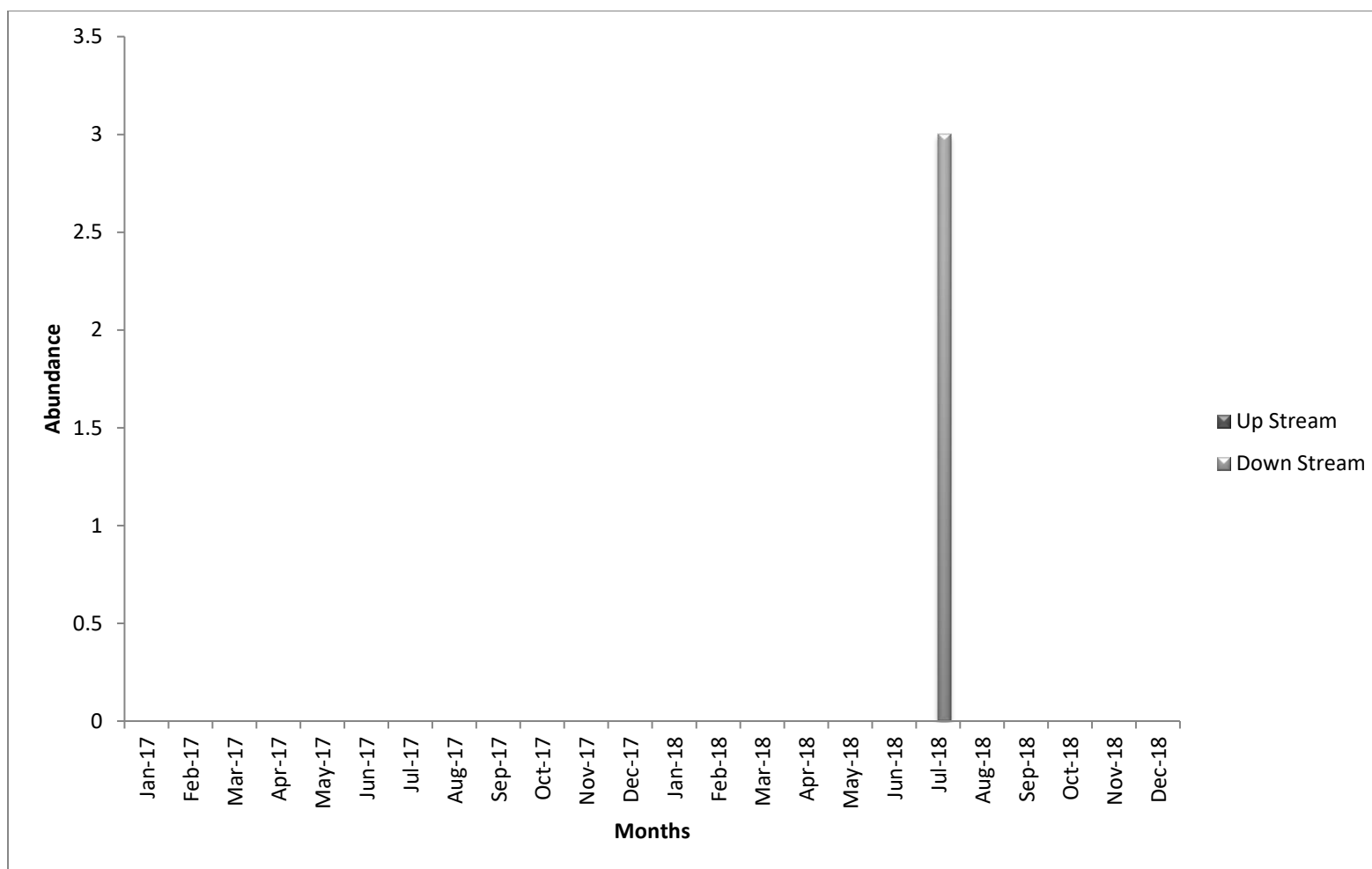


Figure 4.4m: Fish Catch Abundance Variations in Family Clupeidae in Up- and Down-stream of JHPR

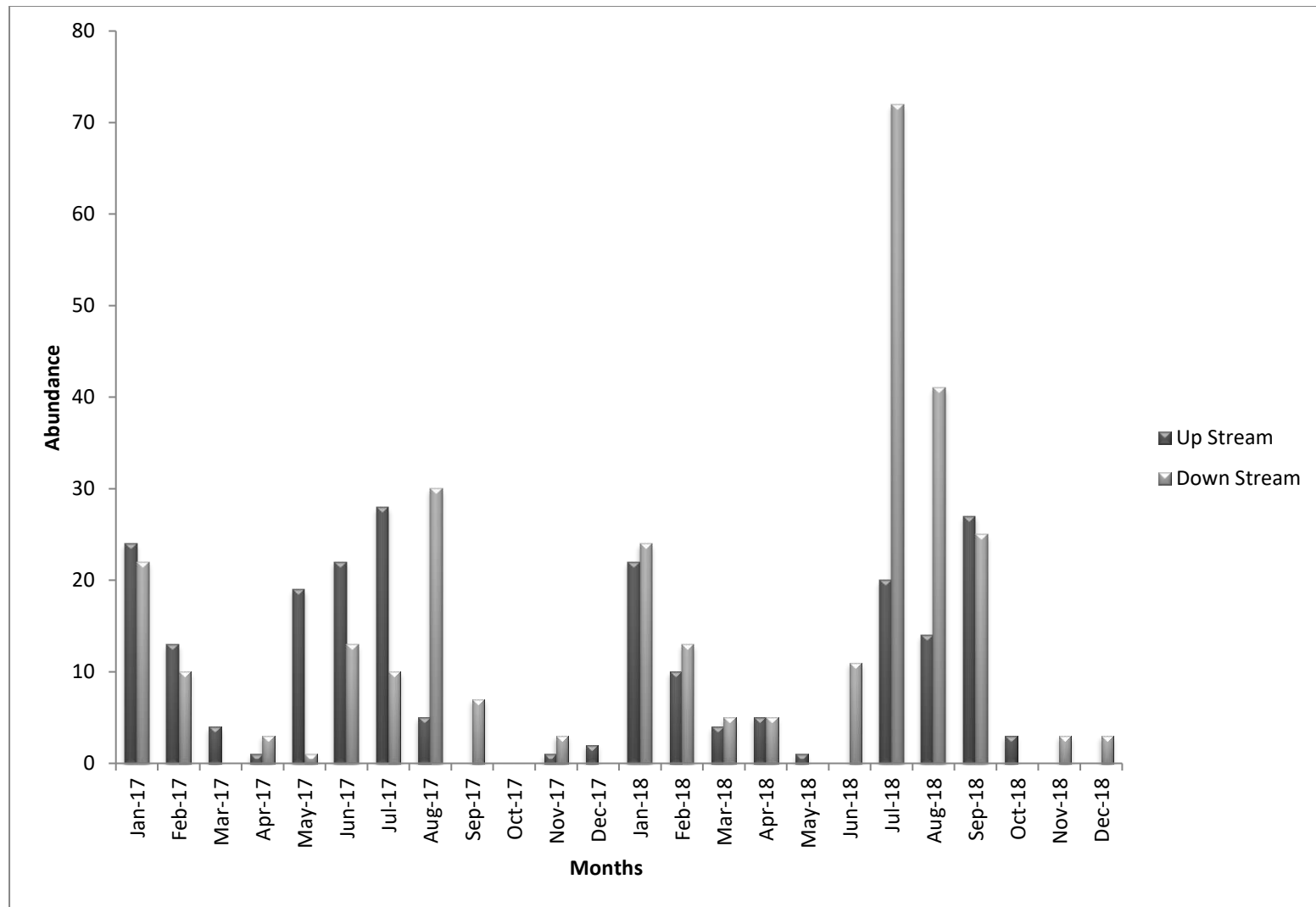


Figure 4.4n: Fish Catch Abundance Variations in Family Mormyridae in Up- and Down-stream of JHPR.

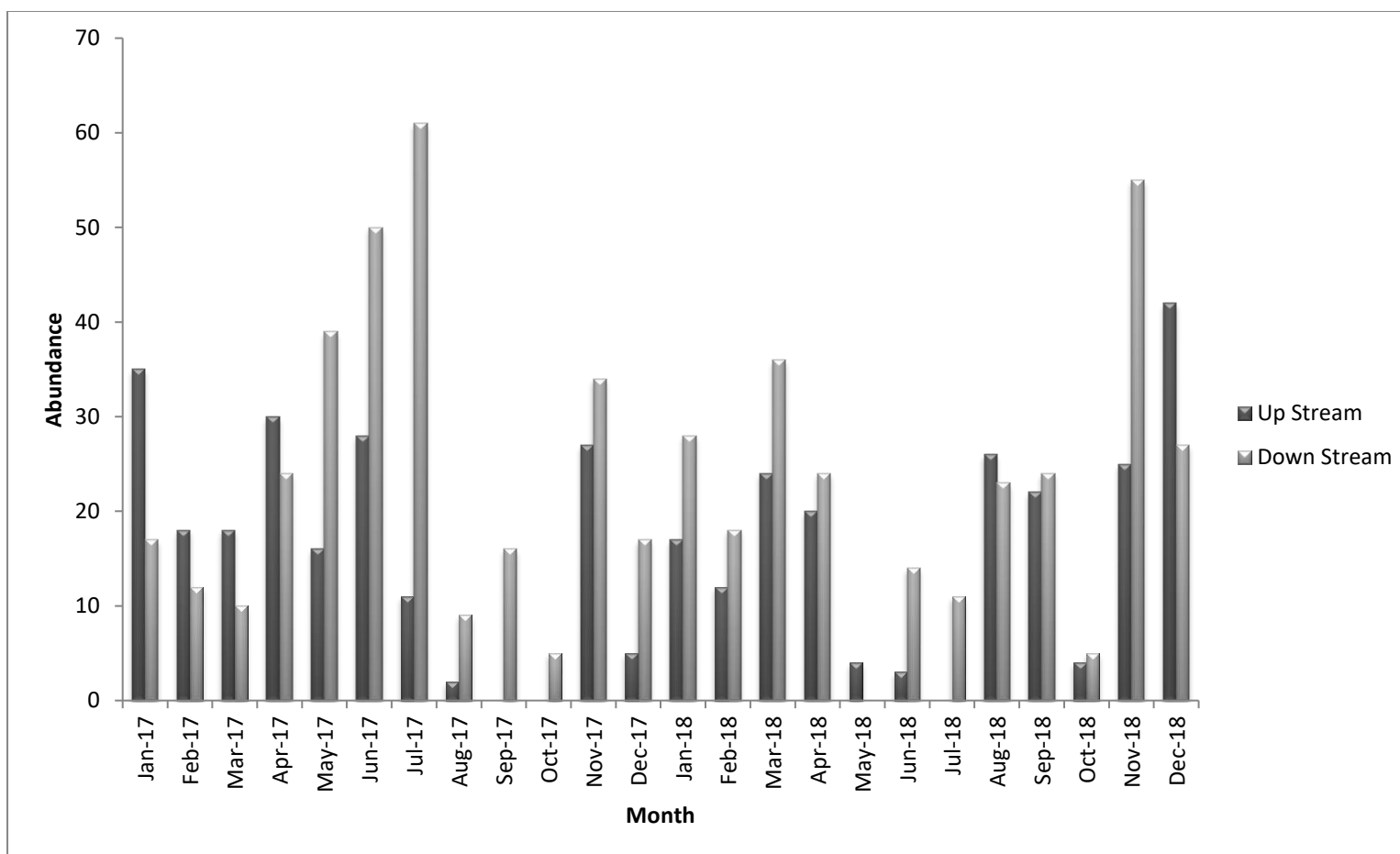


Figure 4.4o: Fish Catch Abundance Variations in Family Characidae in Up- and Down-stream of JHPR.

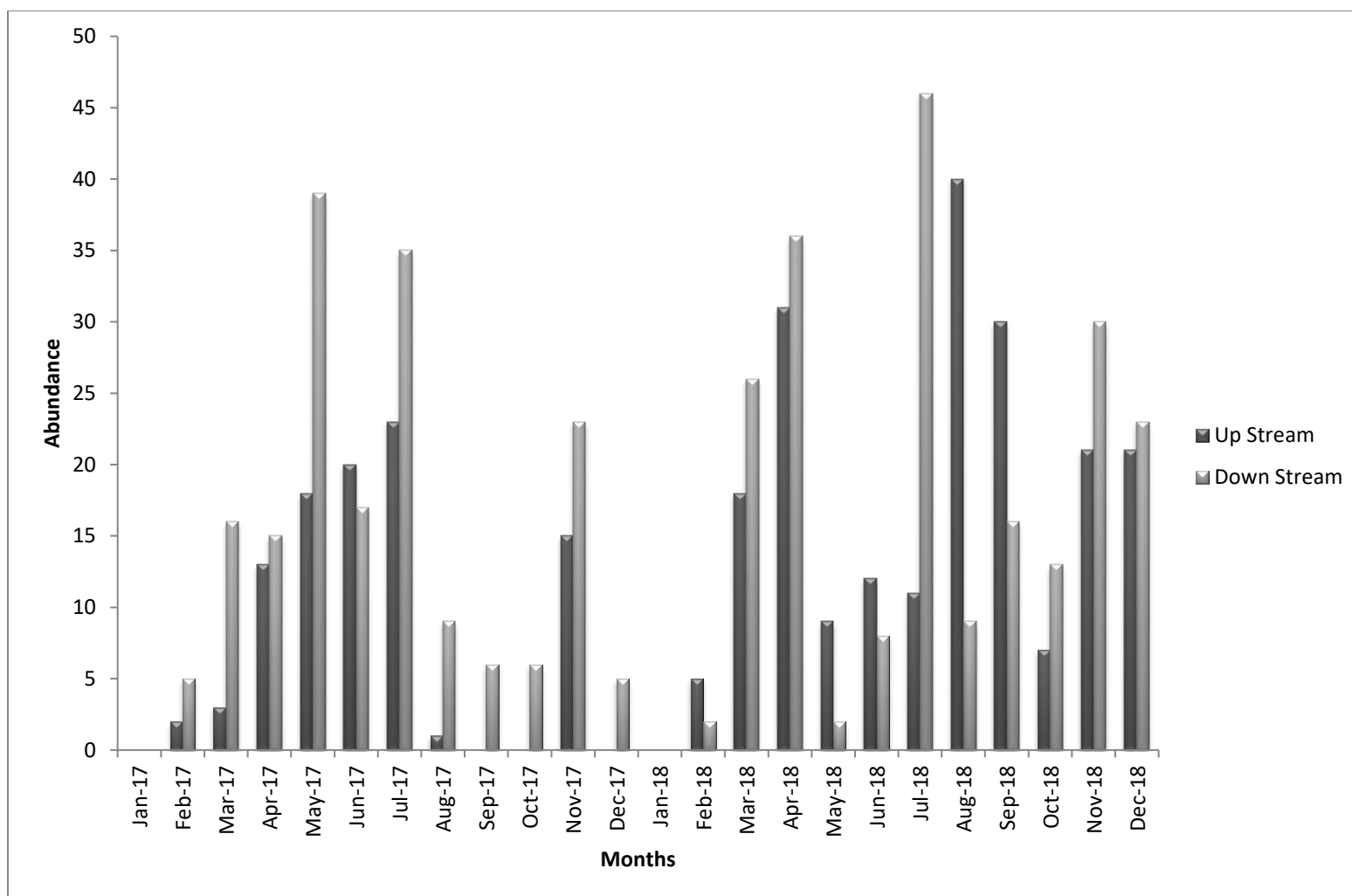


Figure 4.4p: Fish Catch Abundance Variations in Family Cyprinidae in Up- and Down-stream of JHPR.

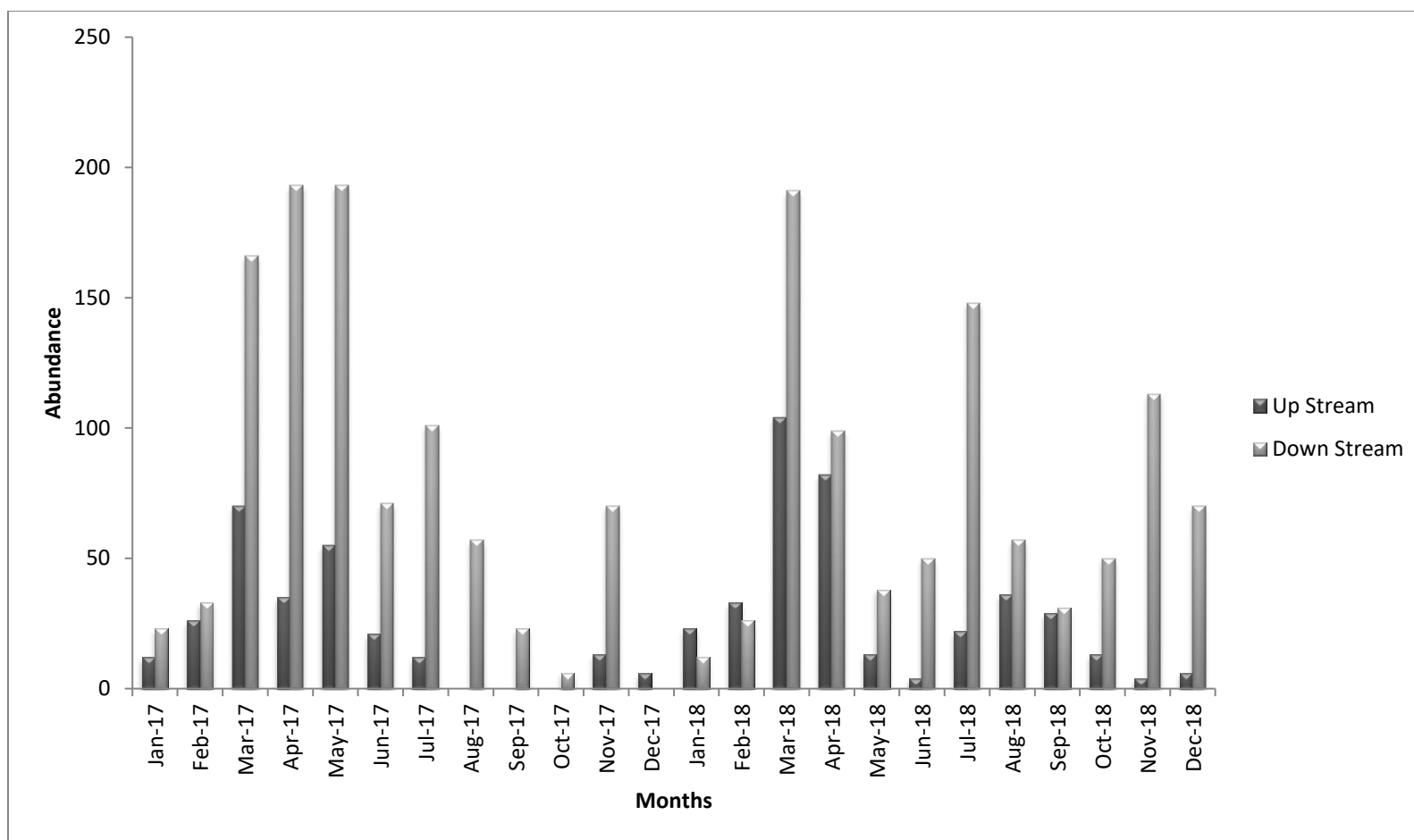


Figure 4.4q: Fish Catch Abundance Variations in Family Mochokidae in Up- and Down-stream of JHPR.

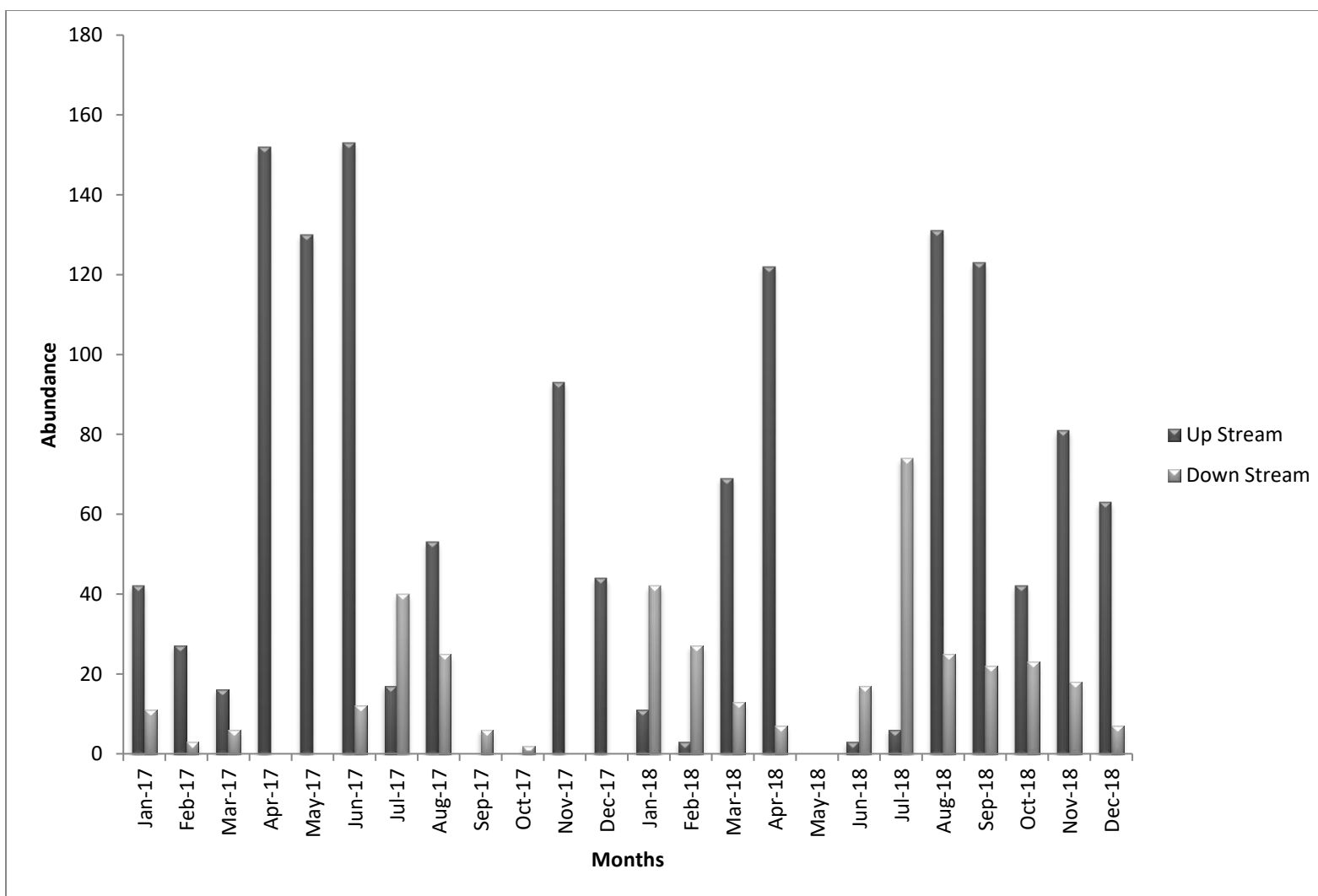


Figure 4.4r: Fish Catch Abundance Variations in Family Cichlidae in Up- and Down-stream of JHPR.

4.5 Seasonal Diversity Indexes of Fish Species

Overall, there was variability in locations and seasons on the fish diversity. The fish diversity and richness were different at the upstream in dry ($H=3.37$; Margalef = 5.81) and rainy season ($H=3.58$; Margalef= 7.47) (Table 4.5 and Figure 4.5). Similarly, at the downstream, the following diversity index were recorded in dry ($H= 3.37$; Margalef= 6.26) and rainy season ($H= 3.95$; Margalef = 9.73) respectively.

The locations and seasons shows that, up- and down-stream fish diversity during the dry season were not different having $H = 3.37$, however the species richness of Margalef = 5.81 and Margalef= 6.26 were obtained at the upstream and downstream respectively. Higher level of diversity was seen during the rainy season at the downstream compared to upstream section. The species diversity of $H=3.58$, at the upstream, $H= 3.95$ at the downstream and richness at upstream (Margalef= 7.47), downstream (Margalef= 9.73) were different (Figure 4.5). Trends in diversity and richness changes show in the resilience of each site to seasons and environmental variability.

Dominance index in site locations and seasons are 0.044 (dry season upstream), 0.044 (dry season downstream), 0.038 (rainy season upstream) and 0.024 (rainy season downstream) indicating low level of dominance.

Table 4.5: Seasonal Diversity Indexes of Fish Species in Up-and Down-Stream of JHPR.

Season	Dry		Rainy	
Indexes/Site	Up Stream	Down Stream	Up Stream	Down Stream
Taxa_S	47	49	59	78
Individuals	2728	2129	2347	2464
Dominance_D	0.04375	0.0439	0.038	0.02401
Simpson_1-D	0.9562	0.9561	0.962	0.976
Shannon_H	3.368	3.374	3.583	3.948
Evenness_e^H/S	0.6174	0.5957	0.6097	0.6731
Margalef	5.814	6.264	7.473	9.732

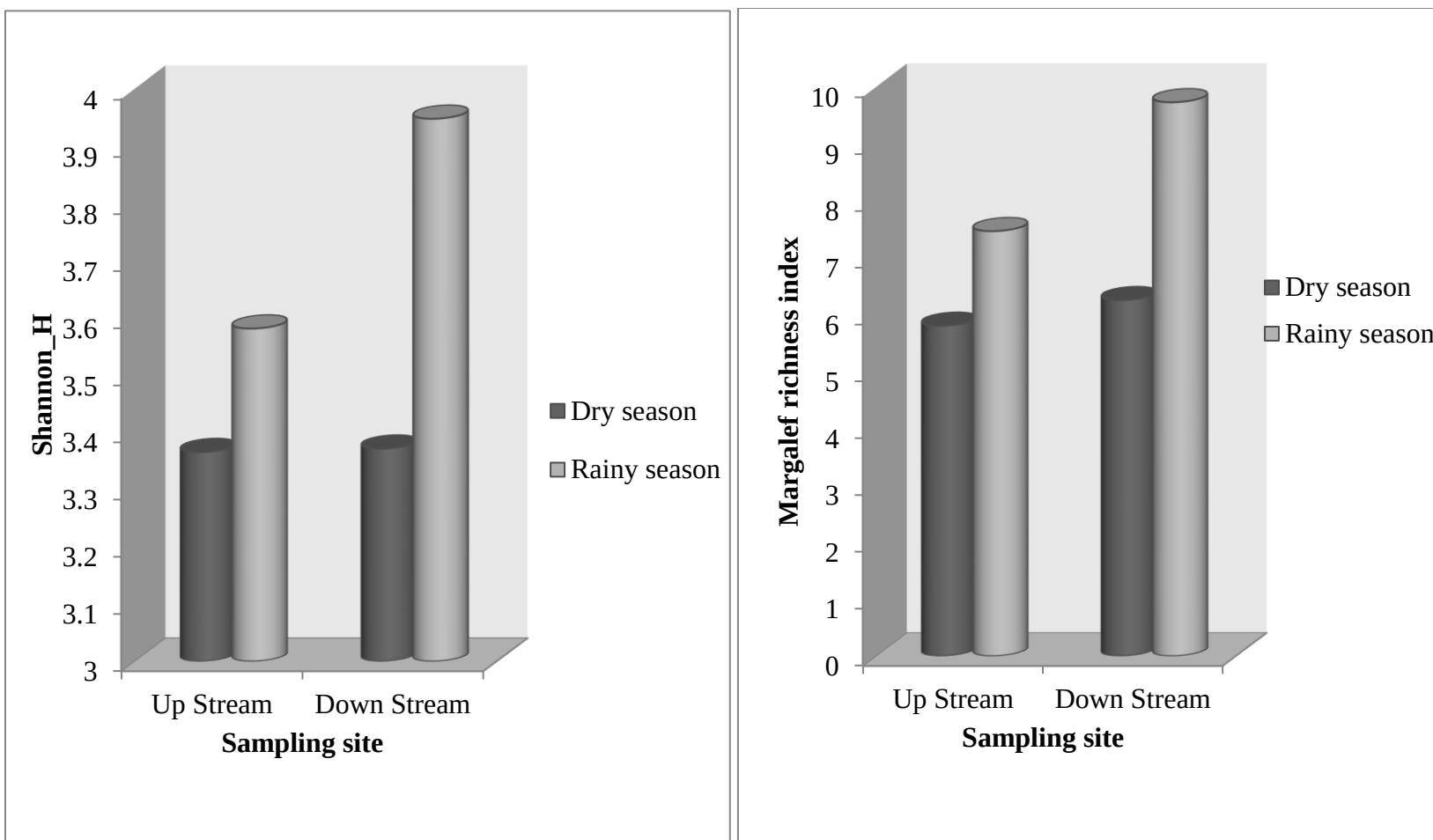


Figure 4.5: Seasonal Changes in Fish Species Richness and Diversity in Up and Down-Stream of JHPR

4.6 The physico-chemical parameters, abundance and distribution of fish species relationship in Up- and Down-stream of JHPR.

4.6.1 Factor Analysis and Correlation Matrix

The physico-chemical parameters and its relationship with fish family abundance in up- and down-stream of Jebba reservoir were presented in figure 4.6.1. The factors loading F1 and F2 accounted for 55.29% and 30.23% respectively explaining relationship of physico-chemical parameters variations influencing the catch abundance, occurrence, distribution and diversity of fish families in up- and down-stream of Jebba reservoir giving a total of 85.52% (Table 4.6.1a). Only F1 and F2 were plotted since both account for about 85.52% of the variability considering the physico-chemical parameters and fish family abundance. The relative length of the vector from the bi-plot shows positive relationship between the fish family Cichlidae, Centropomidae, Cithariniidae, Claroteidae and Tetraodontidae (Figure 4.6.1). Similarly, family Mochokidae and Characidae abundance were influenced by increase in calcium ion, COD, TS and Nitrate concentrations. The Malapteruridae catch was influenced by the increase in turbidity and TSS, Bagridae by Hydrogen carbonate and Mormyridae by DO.

In the factor analysis, physico-chemical parameters described as factor 1 while the fish family abundance as factor 2. The family Gymnarcidae (0.890), Characidae (0.889), Distichodontidae (0.639), Mormyridae (-0.830), Bagridae (-0.876), Malapteruridae (-0.884), Schilbedae (-0.8333) had a strong positive and negative loading with F1. This implies that increase or decrease in water quality parameters influence the catch abundance of the above listed fish families. The families Cithariniidae (-0.992), Centropomidae (-0.907), Cichlidae (-0.955), Tetraodontidae (-0.804), Cypriniidae (0.824), Arridae (0.838), Mochokidae (0.892),

Protopteruridae (0.685), Osteoglossidae (0.685), Dasyatidae (0.685), Polypteridae (0.685) and Clupeidae (0.685) shows positive and negative strong correlation with F2.

All the physico-chemical parameters, temperature (-0.993), pH (-0.892), TDS (0.725), DO (-0.839), Turbidity (-0.976), Nitrate concentration (0.808), Phosphate concentration (0.923), Calcium hardness (0.983, Magnesium hardness (0.998), TS (-0.855), Total hardness (0.997), BOD (0.849), Chloride (0.972), Hydrogen carbonate (-0.881), Potassium ion (-0.915), Sodium ion (0.993), Magnesium ion (0.992) correlated with F1 either positively or negatively except Calcium ion (0.771) and COD (0.759) that showed positive correlation with F2.

A correlation matrix of the factor analysis was used to bring out individual relationships between physico-chemical parameters and the fish family abundance (Table 4.6.1b). Mormyridae showed negative correlation with family Gymnarcidae, Distichodontidae and positive correlation with Cyprinidae, Protopteruridae, Malapteruridae, Osteoglossidae, Clupeidae, Dasyatidae and Polypteridae. The family Claroteidae, Centropomidae, Cichlidae and Tetraodontidae had positive correlation with family Citharinidae.

The DO had a positive relationship with all the fish families' abundance except Claroteidae, Mochokidae, centropomidae, Cichlidae and Tetraodontidae. In contrast, Turbidity had a positive correlation with family Mormyridae, Bagridae, Malapteruridae and Schilbedae, and negative correlation with Gymnarcidae, Characidae and Distichodontidae,

4.6.2 Correspondence Analysis

The correspondence analysis presents the relationship within and between the locations, seasons, physico-chemical parameters and fish family abundance. The first two eigenvalue variance present 93.5% suggesting the spatial separation of the fish family and the physico-chemical parameters factors in respect to locations and seasons (Figure 4.6.2). The turbidity,

chloride, conductivity, calcium hardness, magnesium hardness, total hardness and COD were the physico-chemical parameters contributing to the coordinate length of the fish family distribution with turbidity having positive correlation with the rainy season.

The relative length of the vector shows that turbidity and chloride were the most important physico-chemical parameters factors influencing the abundance and distribution of fish species encountered, bringing about changes in site and season occurrence to predict the fish catch abundance. The vector length of the fish family indicates that, catch abundance of Mochokidae tends toward the downstream, increase during the dry season. The upstream associate with the higher catch abundance of families Cichlidae, Distichodontidae, Claroteidae, Centropomidae, and Citharinidae in dry season while Tetraodontidae, Schilbeidae, Bagridae show more catch abundance during the rainy season. Protopteridae, Ariidae, Cyprinidae, Mormyridae, Clariidae, Polypteridae, Malapteruridae, and Osteoglossidae associate with the downstream in raining season. There was a strong relationship in family Mochokidae and Characidae abundance at the downstream during dry season. Turbidity vector length shows high loading towards raining season while chloride tends towards dry season with other hydrological variable having high loading and cluster at the center of the coordinates close to downstream (Figure 4.6.2).

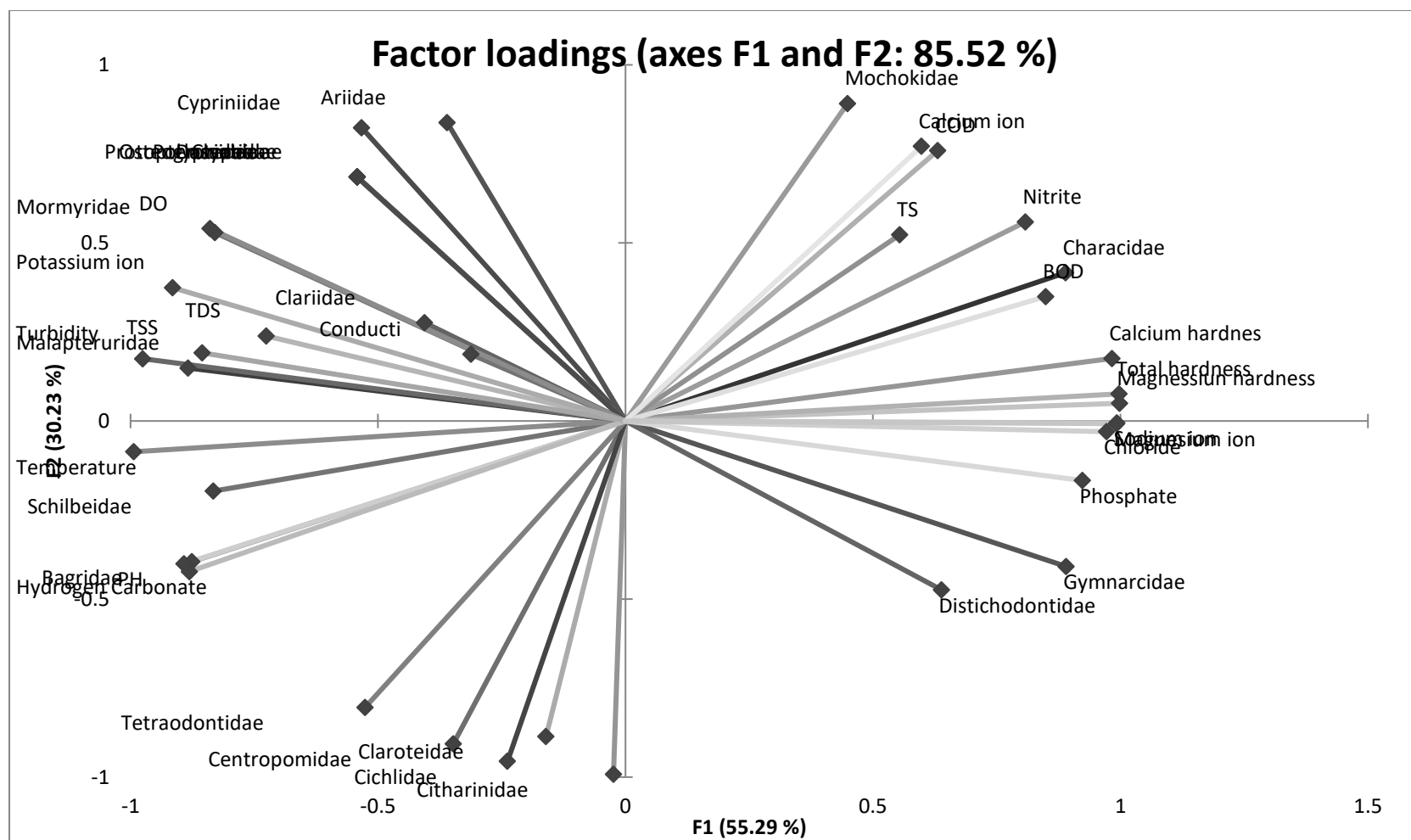


Figure 4.6.1: Factor analysis bi-plot of fish family abundance and physico-chemical parameters measured in up- and down-stream of JHPR.

Key: The first two factors described 55.29% and 30.23% which jointly explained 85.52%. DO: Dissolved oxygen; COD: Chemical Oxygen Demand; BOD: Biological Oxygen Demand; TS: Total Solids; TDS: Total Dissolved Solids

Table 4.6.1a: Eigene vectors of the Factor pattern in fish family abundance and water quality variables

Fish family	F1	F2	F3
Mormyridae	-0.83	0.529	0.178
Gymnarcidae	0.89	-0.409	-0.2
Characidae	0.889	0.416	0.189
Distichodontidae	0.639	-0.474	0.606
Citharinidae	-0.024	-0.992	-0.124
Cyprinidae	-0.533	0.824	-0.193
Bagridae	-0.876	-0.395	-0.276
Clariidae	-0.406	0.276	0.871
Malapteruridae	-0.884	0.149	-0.444
Schilbeidae	-0.833	-0.197	0.517
Claroteidae	-0.161	-0.886	0.436
Ariidae	-0.36	0.838	-0.409
Mochokidae	0.449	0.892	0.06
Centropomidae	-0.348	-0.907	0.239
Cichlidae	-0.238	-0.955	0.174
Tetraodontidae	-0.526	-0.804	-0.277
Protopteruridae	-0.542	0.685	0.487
Osteoglossidae	-0.542	0.685	0.487
Dasyatidae	-0.542	0.685	0.487
Polypteridae	-0.542	0.685	0.487
Clupeidae	-0.542	0.685	0.487
Temperature	-0.993	-0.086	-0.076
PH	-0.892	-0.401	0.208
Conducti	-0.312	0.187	-0.931
TDS	-0.725	0.239	-0.646
DO	-0.839	0.54	0.062
Turbidity	-0.976	0.175	-0.133
Nitrite	0.808	0.559	-0.187
Phosphate	0.923	-0.167	-0.346
Calcium hardnes	0.983	0.176	-0.049
Magnesium hardness	0.998	0.05	0.032
TSS	-0.855	0.191	-0.481
TS	0.554	0.523	-0.648
Total hardness	0.997	0.076	-0.009
BOD	0.849	0.35	0.396
COD	0.631	0.759	0.159
Chloride	0.972	-0.03	0.233
Hydrogen Carbonate	-0.881	-0.423	0.212
Potassium ion	-0.915	0.374	-0.152

Table 4.6.1b: Correlation matrix (Pearson (n)) of the fish family abundance and water quality variables

Variables	lomyrida	ymmarci	Characida	tichodoni	Citharini	Cyprinida	Bagridae	Clariidae	alapteru	Schilbeida	Clariidae	Ariidae	Mochokida	ntropomi	Cichlidae	traodonti	topteruric	teoglossi	Dasyatida	olypterida	Clupeidae
Mommyrid	1	-0.991	-0.484	-0.673	-0.527	0.844	0.469	0.638	0.733	0.679	-0.258	0.669	0.110	-0.148	-0.277	-0.039	0.899	0.899	0.899	0.899	0.899
Gymnarcia	-0.991	1	0.584	0.641	0.409	-0.773	-0.563	-0.649	-0.759	-0.765	0.132	-0.581	0.023	0.013	0.143	-0.084	-0.860	-0.860	-0.860	-0.860	-0.860
Characida	-0.484	0.584	1	0.485	-0.458	-0.168	-0.996	-0.081	-0.808	-0.725	-0.429	-0.049	0.782	-0.642	-0.577	-0.855	-0.105	-0.105	-0.105	-0.105	-0.105
Distichodidae	-0.673	0.641	0.485	1	0.380	-0.848	-0.539	0.137	-0.904	-0.125	0.582	-0.876	-0.100	0.353	0.407	-0.122	-0.377	-0.377	-0.377	-0.377	-0.377
Citharinidae	-0.527	0.409	-0.458	0.380	1	-0.780	0.447	-0.372	-0.071	0.151	0.828	-0.772	-0.903	0.878	0.932	0.845	-0.727	-0.727	-0.727	-0.727	-0.727
Cyprinidae	0.844	-0.773	-0.168	-0.848	-0.780	1	0.195	0.276	0.679	0.182	-0.728	0.962	0.484	-0.607	-0.694	-0.328	0.759	0.759	0.759	0.759	0.759
Bagridae	0.469	-0.563	-0.996	-0.539	0.447	0.195	1	0.006	0.838	0.665	0.370	0.098	-0.762	0.597	0.538	0.855	0.070	0.070	0.070	0.070	0.070
Clariidae	0.638	-0.649	-0.081	0.137	-0.372	0.276	0.006	1	0.014	0.734	0.200	0.021	0.116	0.099	-0.016	-0.250	0.833	0.833	0.833	0.833	0.833
Malapteru	0.733	-0.759	-0.808	-0.904	-0.071	0.679	0.838	0.014	1	0.477	-0.183	0.625	-0.291	0.067	-0.009	0.468	0.365	0.365	0.365	0.365	0.365
Schilbeida	0.679	-0.765	-0.725	-0.125	0.151	0.182	0.665	0.734	0.477	1	0.534	-0.077	-0.518	0.592	0.477	0.453	0.568	0.568	0.568	0.568	0.568
Clariidae	-0.258	0.132	-0.429	0.582	0.828	-0.728	0.370	0.200	-0.183	0.534	1	-0.863	-0.836	0.963	0.960	0.676	-0.308	-0.308	-0.308	-0.308	-0.308
Ariidae	0.669	-0.581	-0.049	-0.876	-0.772	0.962	0.098	0.021	0.625	-0.077	-0.863	1	0.561	-0.732	-0.786	-0.371	0.570	0.570	0.570	0.570	0.570
Mochokidae	0.110	0.023	0.782	-0.100	-0.903	0.484	-0.762	0.116	-0.291	-0.518	-0.836	0.561	1	-0.950	-0.948	-0.970	0.397	0.397	0.397	0.397	0.397
Centropom	-0.148	0.013	-0.642	0.353	0.878	-0.607	0.597	0.099	0.067	0.592	0.963	-0.732	-0.950	1	0.991	0.846	-0.316	-0.316	-0.316	-0.316	-0.316
Cichlidae	-0.277	0.143	-0.577	0.407	0.932	-0.694	0.538	-0.016	-0.009	0.477	0.960	-0.786	-0.948	0.991	1	0.845	-0.441	-0.441	-0.441	-0.441	-0.441
Tetraodon	-0.039	-0.084	-0.855	-0.122	0.845	-0.328	0.855	-0.250	0.468	0.453	0.676	-0.371	-0.970	0.846	0.845	1	-0.401	-0.401	-0.401	-0.401	-0.401
Protopterus	0.899	-0.860	-0.105	-0.377	-0.727	0.759	0.070	0.833	0.365	0.568	-0.308	0.570	0.397	-0.316	-0.441	-0.401	1	1.000	1.000	1.000	1.000
Osteogloss	0.899	-0.860	-0.105	-0.377	-0.727	0.759	0.070	0.833	0.365	0.568	-0.308	0.570	0.397	-0.316	-0.441	-0.401	1.000	1	1.000	1.000	1.000
Dasyatida	0.899	-0.860	-0.105	-0.377	-0.727	0.759	0.070	0.833	0.365	0.568	-0.308	0.570	0.397	-0.316	-0.441	-0.401	1.000	1.000	1	1.000	1.000
Polypterid	0.899	-0.860	-0.105	-0.377	-0.727	0.759	0.070	0.833	0.365	0.568	-0.308	0.570	0.397	-0.316	-0.441	-0.401	1.000	1.000	1.000	1	1.000
Clupeidae	0.899	-0.860	-0.105	-0.377	-0.727	0.759	0.070	0.833	0.365	0.568	-0.308	0.570	0.397	-0.316	-0.441	-0.401	1.000	1.000	1.000	1.000	1
Temperature	0.765	-0.834	-0.934	-0.640	0.119	0.473	0.925	0.313	0.899	0.805	0.203	0.317	-0.527	0.406	0.306	0.613	0.442	0.442	0.442	0.442	0.442
PH	0.565	-0.672	-0.921	-0.253	0.394	0.105	0.883	0.433	0.636	0.930	0.589	-0.100	-0.746	0.724	0.632	0.734	0.310	0.310	0.310	0.310	0.310
Conductivity	0.192	-0.168	-0.376	-0.852	-0.063	0.501	0.457	-0.633	0.717	-0.259	-0.522	0.651	-0.029	-0.284	-0.267	0.272	-0.156	-0.156	-0.156	-0.156	-0.156
TDS	0.613	-0.614	-0.668	-0.968	-0.139	0.708	0.720	-0.202	0.963	0.223	-0.376	0.726	-0.152	-0.118	-0.168	0.369	0.243	0.243	0.243	0.243	0.243
DO	0.993	-0.980	-0.510	-0.755	-0.523	0.880	0.505	0.544	0.795	0.624	-0.317	0.730	0.109	-0.183	-0.305	-0.010	0.855	0.855	0.855	0.855	0.855
Turbidity	0.878	-0.914	-0.820	-0.787	-0.133	0.690	0.822	0.329	0.947	0.709	-0.056	0.553	-0.290	0.149	0.042	0.409	0.584	0.584	0.584	0.584	0.584
Nitrite	-0.408	0.528	0.916	0.138	-0.551	0.066	-0.877	-0.336	-0.548	-0.879	-0.706	0.254	0.850	-0.832	-0.759	-0.823	-0.146	-0.146	-0.146	-0.146	-0.146
Phosphate	-0.916	0.960	0.686	0.459	0.186	-0.563	-0.647	-0.723	-0.687	-0.915	-0.151	-0.331	0.244	-0.252	-0.121	-0.255	-0.783	-0.783	-0.783	-0.783	-0.783
Calcium hardness	-0.732	0.814	0.938	0.515	-0.192	-0.370	-0.917	-0.393	-0.821	-0.879	-0.335	-0.187	0.595	-0.513	-0.411	-0.645	-0.436	-0.436	-0.436	-0.436	-0.436
Magnesium	-0.796	0.862	0.914	0.633	-0.077	-0.497	-0.903	-0.364	-0.889	-0.825	-0.190	-0.331	0.494	-0.385	-0.280	-0.574	-0.492	-0.492	-0.492	-0.492	-0.492
TSS	0.725	-0.744	-0.772	-0.929	-0.109	0.707	0.807	-0.019	0.998	0.426	-0.242	0.666	-0.242	0.009	-0.063	0.429	0.361	0.361	0.361	0.361	0.361
TS	-0.299	0.410	0.588	-0.287	-0.451	0.260	-0.513	-0.645	-0.124	-0.900	-0.834	0.504	0.676	-0.821	-0.744	-0.532	-0.258	-0.258	-0.258	-0.258	-0.258
Total hardness	-0.788	0.858	0.917	0.595	-0.099	-0.467	-0.901	-0.391	-0.866	-0.850	-0.231	-0.292	0.515	-0.418	-0.312	-0.583	-0.493	-0.493	-0.493	-0.493	-0.493
BOD	-0.449	0.534	0.976	0.616	-0.416	-0.241	-0.991	0.097	-0.874	-0.571	-0.273	-0.175	0.716	-0.518	-0.467	-0.837	-0.028	-0.028	-0.028	-0.028	-0.028
COD	-0.093	0.220	0.907	0.139	-0.788	0.258	-0.897	0.092	-0.515	-0.593	-0.704	0.344	0.970	-0.870	-0.848	-0.986	0.256	0.256	0.256	0.256	0.256
Chloride	-0.781	0.831	0.896	0.776	-0.023	-0.588	-0.904	-0.200	-0.967	-0.683	-0.028	-0.471	0.423	-0.255	-0.162	-0.552	-0.434	-0.434	-0.434	-0.434	-0.434
Hydrogen	0.545	-0.654	-0.920	-0.234	0.414	0.081	0.881	0.425	0.622	0.927	0.608	-0.123	-0.760	0.740	0.651	0.745	0.291	0.291	0.291	0.291	0.291
Potassium	0.930	-0.937	-0.686	-0.854	-0.330	0.825	0.696	0.343	0.932	0.610	-0.251	0.705	-0.086	-0.057	-0.166	0.222	0.678	0.678	0.678	0.678	0.678
Sodium ion	-0.805	0.862	0.903	0.709	-0.033	-0.557	-0.901	-0.300	-0.931	-0.764	-0.102	-0.411	0.448	-0.312	-0.210	-0.551	-0.484	-0.484	-0.484	-0.484	-0.484
Calcium ion	-0.127	0.261	0.812	-0.116	-0.752	0.359	-0.768	-0.220	-0.317	-0.763	-0.874	0.520	0.943	-0.959	-0.917	-0.874	0.098	0.098	0.098	0.098	0.098
Magnesium ion	-0.806	0.862	0.903	0.711	-0.032	-0.559	-0.900	-0.299	-0.932	-0.762	-0.100	-0.414	0.446	-0.309	-0.208	-0.550	-0.484	-0.484	-0.484	-0.484	-0.484

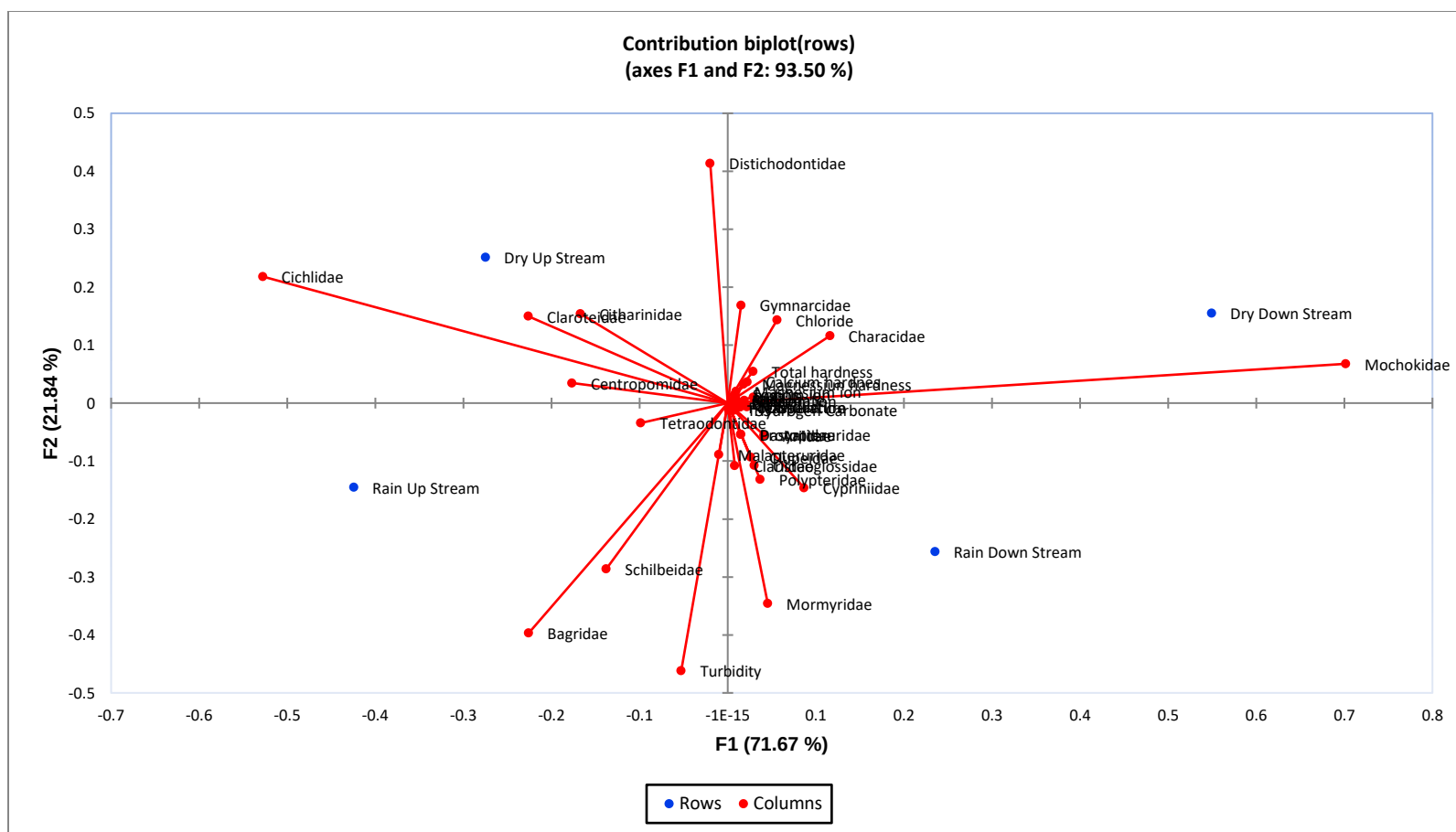


Figure 4.6.2: Correspondence analysis bi-plot on the fish family abundance (arrow), physico-chemical parameters (arrow) and location based on seasons (dots).

Key: The first two correspondence axes explain 71.67% and 21.84% of variance. DO: Dissolved oxygen; COD: Chemical Oxygen Demand; BOD: Biological Oxygen Demand; TS: Total Solids; TDS: TotalDissolved Solids.

4.7 Pair-Wise Intra and Inter-Specific Divergence in General and Species

Only 31 species out of the 55 studied species were estimated for mean intra-specific distance. A total number of 17 (30.91%) species show no distance within species while 25 (45.45%) species cannot be computed due to single sample species representation. The highest intraspecies K2P distance of 0.89% was observed in *protopterus* (Table 4.7a).

Genetic divergence of the genera for all the selected species was compared for which the mitochondrial COI sequence is available. In the intra-generic divergence, 8 out of the 33 genera namely *Ctenomopa*, *Dasyatis*, *Gymnarchus*, *Hyperopisus*, *Marcusenius*, *Sarotherodon*, *Xynomystus* and *Chromidotillapia* cannot be computed due to single sample species representation of the genera. 6(18.18%) show no distance within the group whereas *Brycinus* show the highest distance of 18.8% within the genera. Other groups where high percentage recorded include *Synodontis* (5.32%), *Schilbe* (11.37%), *Malapterurus* (8.49%), *Labeo* (2.27%), *Distichondus* (3.25%) and *Bagrus* (3.23%). In the listed genera, higher genetic distances were recorded due to representation of the group with more than one species except in *Malapterurus*.

The *Brienomyrus*, *Hemichromis*, *Heterotis*, *Hydrocynus*, *Parachana*, and *Tetraodon* show no distance within the genera, while *Citharinus*, *Clarotes*, *Lates*, *Polypterus*, *Coptodon*, *Oreochromis*, *Mormyrops*, *Mormyrus*, *Clarias* and *Achenoglanis* have low distance value of 0.07%, 0.06%, 0.04%, 0.07%, 0.11%, 0.32%, 0.12%, 0.06%, 0.10% and 0.12% respectively within the genera (Table 4.8b).

The highest distance group between genera were recorded in *Citharinus* and *Dasyatis*, *Protopterus* and *Oreochromis*, *Labeo* and *Dasyatis*, *Clarotes* and *Dasyatis*, *Protopterus* and *Bagrus*, *Protopterus* and *Chrysichthys*, *Protopterus* and *Labeo*; *Tetraodon* and *Protopterus*;

Mormyrops and *Lates*, *Mormyrus* and *Lates*, *Mormyrops* and *Bagrus*, *Heterotis* and *Chrysichthys*, *Gymnarchus* and *Chrysichthys* having 0.48, 0.45, 0.44, 0.44, 0.41, 0.41, 0.41, 0.42, 0.40, 0.40, 0.40, 0.41, 0.41 and 0.41 respectively. Similarly higher maximum distances between genera were also recorded in some groups namely; *Mormyrus* and *Bagrus* (0.39), *Distichondius* and *Mormyrops* (0.38); *Clarotes* and *Mormyrops* (0.39), *Protopterus* and *Achenoglanis* (0.38), *Coptodon* and *Gymnarchus* (0.38); *Tetraodon* and *Gymnarchus* (0.37); *Achenoglanis* and *Distichondus* (0.37), *Achenoglanis* and *Polypterus* (0.37), *Achenoglanis* and *Xynomystus* (0.37), *Chrysichthys* and *Xynomystus* (0.37), *Marcusenius* and *Xynomystus* (0.37), *Synodontis* and *Parachana* (0.37); *Sarotherodon* and *Malapterurus* (0.37); *Mormyrops* and *Hydrocynus* (0.37); *Lates* and *Gymnarchus* (0.37) (Table 4.8.1c).

Hyperopisus and *Brienomyrus* show no divergence between groups. Other family having lower divergence between groups are *Clarotes* and *Chrysichthys* (0.19); *Mormyrops* and *Mormyrus* (0.19); *Bagrus* and *Achenoglanis* (0.21); *Schilbe* and *Achenoglanis* (0.20), *Synodontis* and *Achenoglanis* (0.24); *Hydrocynus* and *Brycinus* (0.21); *Oreochromis* and *Hemichromis* (0.21); *Chromidotillapia* and *Hemichromis* (0.21); *Bagrus* and *Schilbe* (0.22); *Chrysichthys* and *Schilbe* (0.22); *Chrysichthys* and *Bagrus* (0.22); *Chrysichthys* and *Achenoglanis* (0.22)

Table 4.7a: Intraspecific Divergence among Sample Species Collected from Up- and Down-stream of JHPR

Species	Distance value
<i>Achenoglanis bisculatus</i>	n/c
<i>Achenoglanis occidentalis</i>	0.001224
<i>Bagrus bajad</i>	n/c
<i>Bagrus docmac</i>	n/c
<i>Brienomyrus niger</i>	0
<i>Brycinus nurse</i>	n/c
<i>Brycinus sp</i>	n/c
<i>Chrysichthys cf auratus</i>	0
<i>Chrysichthys nigrodigitatus</i>	0
<i>Chrysichthys sp</i>	0
<i>Citharinus citharus</i>	0.000735
<i>Clarias gariepinus</i>	0.001019
<i>Clarotes laticeps</i>	0.000611
<i>Ctenopoma</i>	n/c
<i>Distichondus engycephalus</i>	n/c
<i>Distichondus rostratus</i>	0
<i>Dasyatis sp</i>	n/c
<i>Gymnarchus niloticus</i>	n/c
<i>Hemichromis bimaculatus</i>	0
<i>Heterotis niloticus</i>	0
<i>Hydrocynus vittatus</i>	0
<i>Hyperopisus bebe</i>	n/c
<i>Labeo coubie</i>	0.001836
<i>Labeo horie</i>	n/c
<i>Labeo senegalensis</i>	0.000263
<i>Lates niloticus</i>	0.000407
<i>Malapterurus electricus</i>	n/c

<i>Malapterurus sp</i>	n/c
<i>Marcusenius senegalensis</i>	n/c
<i>Mormyrops anguilloides</i>	0.001222
<i>Mormyrus macrophthalmus</i>	0
<i>Mormyrus tapirus</i>	0.001833
<i>Oreochromis aureus</i>	0
<i>Oreochromis sp</i>	0
<i>Oreochromis niloticus</i>	0.001833
<i>Parachana insignis</i>	0
<i>Parachana obscura</i>	n/c
<i>Protopterus sp</i>	0.008938
<i>Polypterus senegalus</i>	0.000733
<i>Sarotherodon galilaeus</i>	n/c
<i>Schilbe intermedius</i>	n/c
<i>Schilbe mystus</i>	n/c
<i>Synodontis aff. Bastiani</i>	0.000942
<i>Synodontis batensoda</i>	n/c
<i>Synodontis clarias</i>	0
<i>Synodontis membranacea</i>	0
<i>Synodontis nigrita</i>	n/c
<i>Synodontis obesus</i>	0
<i>Synodontis ocellifer</i>	n/c
<i>Synodontis sp</i>	n/c
<i>Synodontis violacea</i>	0
<i>Tetraodon lineatus</i>	0
<i>Cotodon zilli</i>	0.001129
<i>Xynomystus nigri</i>	n/c
<i>Chromidotillapia</i>	n/c

Table 4.7b: Intra-generic Divergence in Sample Sequences Collected from Up- and Down-stream of JHPR

Genera	Distance value (%)
Auchenoglanis	3.69%
Bagrus	3.23%
Brienomyrus	0%
Brycinus	18.79%
Chromidotillapia	n/c
Chrysichthys	7.08%
Citharinus	0.07%
Clarias	0.10%
Clarotes	0.06%
Coptodon	0.11%
Ctenopoma	n/c
Distichodius	3.25%
Dasyatis	n/c
Gymnarchus	n/c
Hemichromis	0
Heterotis	0
Hydrocynus	0
Hyperopisus	n/c
Labeo	2.27%
Lates	0.04%
Malapterurus	8.49%
Marcusenius	n/c
Mormyrops	0.12%
Mormyrus	0.66%
Oreochromis	0.32%
Parachana	0
Protopterus	0.89%
Polypterus	0.07%
Sarotherodon	n/c
Schilbe	11.37%
Synodontis	5.32%
Tetraodon	0
Xynomystus	n/c

Table 4.7c: Inter-generic Divergence in Genera Sample Sequences Collected from Up- and Down-stream of JHPR

General	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32
1 Auchenoglanis																																
2 Bagrus	0.21																															
3 Brienomyrus	0.36	0.38																														
4 Brycinus	0.29	0.30	0.30																													
5 Chrysichthys	0.23	0.22	0.37	0.29																												
6 Citharinus	0.28	0.34	0.35	0.26	0.28																											
7 Clarias	0.28	0.23	0.30	0.30	0.27	0.34																										
8 Clarotes	0.24	0.23	0.37	0.29	0.19	0.28	0.25																									
9 Ctenopoma	0.30	0.33	0.31	0.31	0.31	0.29	0.36	0.30																								
10 Distichodus	0.36	0.32	0.35	0.30	0.34	0.24	0.29	0.33	0.35																							
11 Gymnarchus	0.34	0.33	0.33	0.37	0.36	0.41	0.28	0.34	0.37	0.36																						
12 Hemichromis	0.32	0.34	0.35	0.31	0.30	0.31	0.35	0.30	0.27	0.35	0.39																					
13 Heterotis	0.35	0.35	0.32	0.36	0.40	0.35	0.39	0.34	0.32	0.34	0.32	0.30																				
14 Hydrocynus	0.31	0.33	0.32	0.21	0.31	0.29	0.26	0.33	0.30	0.31	0.36	0.31	0.36																			
15 Hyperopisus	0.35	0.38	0.00	0.30	0.37	0.35	0.30	0.36	0.31	0.35	0.33	0.34	0.31	0.32																		
16 Labeo	0.36	0.32	0.30	0.34	0.32	0.33	0.29	0.30	0.27	0.30	0.30	0.33	0.30	0.37	0.31																	
17 Lates	0.36	0.36	0.33	0.33	0.36	0.34	0.37	0.37	0.30	0.30	0.36	0.38	0.31	0.34	0.32	0.36																
18 Malapterurus	0.25	0.27	0.31	0.31	0.27	0.29	0.28	0.25	0.29	0.29	0.34	0.38	0.31	0.35	0.32	0.34	0.34															
19 Marcusenius	0.34	0.35	0.14	0.31	0.36	0.37	0.28	0.35	0.34	0.33	0.32	0.35	0.35	0.31	0.14	0.33	0.32	0.32														
20 Mormyrops	0.35	0.40	0.16	0.35	0.35	0.37	0.36	0.39	0.33	0.38	0.33	0.36	0.34	0.37	0.16	0.35	0.40	0.33	0.21													
21 Mormyrus	0.33	0.38	0.21	0.35	0.36	0.34	0.35	0.37	0.35	0.37	0.33	0.35	0.36	0.35	0.21	0.32	0.40	0.33	0.21	0.19												
22 Oreochromis	0.31	0.31	0.36	0.32	0.26	0.27	0.33	0.29	0.29	0.32	0.38	0.21	0.30	0.29	0.35	0.30	0.33	0.36	0.35	0.32	0.32											
23 Parachana	0.32	0.36	0.38	0.32	0.36	0.31	0.40	0.35	0.30	0.34	0.37	0.32	0.37	0.33	0.38	0.34	0.35	0.37	0.39	0.36	0.37	0.31										
24 Protopterus	0.37	0.40	0.35	0.35	0.40	0.39	0.37	0.36	0.38	0.37	0.39	0.36	0.38	0.34	0.35	0.41	0.33	0.38	0.36	0.35	0.37	0.34	0.45									
25 Polypterus	0.36	0.32	0.38	0.30	0.33	0.38	0.31	0.33	0.29	0.33	0.30	0.35	0.31	0.31	0.38	0.31	0.35	0.32	0.34	0.39	0.38	0.35	0.38	0.37								
26 Sarotherodon	0.31	0.31	0.36	0.32	0.27	0.28	0.34	0.29	0.30	0.32	0.39	0.21	0.30	0.29	0.36	0.30	0.33	0.37	0.36	0.32	0.32	0.00	0.31	0.35	0.36							
27 Schilbe	0.20	0.22	0.33	0.27	0.22	0.30	0.27	0.24	0.29	0.32	0.33	0.31	0.31	0.28	0.32	0.31	0.28	0.24	0.31	0.30	0.33	0.27	0.34	0.36	0.30	0.28						
28 Synodontis	0.24	0.27	0.35	0.30	0.23	0.29	0.29	0.26	0.30	0.33	0.34	0.31	0.31	0.28	0.35	0.32	0.32	0.25	0.34	0.33	0.31	0.30	0.37	0.40	0.34	0.30	0.20					
29 Tetraodon	0.31	0.33	0.34	0.31	0.33	0.32	0.38	0.35	0.30	0.34	0.36	0.30	0.34	0.27	0.33	0.31	0.34	0.32	0.35	0.31	0.33	0.29	0.33	0.42	0.32	0.30	0.33	0.32				
30 Coptodon	0.32	0.33	0.33	0.31	0.27	0.26	0.35	0.29	0.27	0.36	0.38	0.21	0.31	0.27	0.32	0.31	0.34	0.33	0.30	0.34	0.32	0.13	0.31	0.37	0.35	0.13	0.30	0.30	0.28			
31 Xynomystus	0.36	0.35	0.27	0.31	0.37	0.30	0.36	0.36	0.28	0.37	0.31	0.33	0.31	0.30	0.27	0.34	0.30	0.32	0.28	0.26	0.30	0.32	0.35	0.38	0.34	0.33	0.28	0.32	0.29	0.28		
32 Chromidotillapia	0.27	0.25	0.32	0.28	0.26	0.30	0.30	0.27	0.28	0.30	0.38	0.21	0.31	0.29	0.32	0.30	0.32	0.29	0.31	0.34	0.31	0.18	0.31	0.31	0.29	0.18	0.27	0.28	0.30	0.20	0.33	
33 Dasys	0.39	0.40	0.39	0.38	0.37	0.48	0.42	0.44	0.40	0.43	0.36	0.39	0.39	0.40	0.39	0.44	0.39	0.42	0.39	0.42	0.42	0.40	0.41	0.44	0.40	0.40	0.40	0.38	0.39	0.39	0.38	0.39

CHAPTER FIVE

5.0 Discussion

5.1 Physico-chemical Variations in Up- and Down-Stream of JHPR

The physico-chemical properties in up- and down-stream of Jebba reservoir described the ecological dynamics of fish composition, abundance and distribution of the species found in this region. Several freshwater ecosystems studied from different regions in Nigeria suggested that physical and chemical properties of such ecosystem determine the nature, abundance, health and diversity of the species present (Imevbore, 1975; Egborge, 1987; Adeniji, 1991; Akinbuwa, 1999; Omotosho, 1998; Araoye, 1999; Castillo-Rivera *et al.*, 2002; Simier *et al.*, 2006 Mustapha, 2010; Oladipo *et al.*, 2018). The driving forces of the aquatic ecosystem are the water hydrology and nutrients that influences the population dynamics at different time and location (Mallin, 1994; Chalar and Tundisi, 1999; Mustapha, 2009).

Water temperature is one of the factors that affect the fish distribution in freshwater ecosystem. High water temperature has been known to enhance the growth of microorganisms and control water gas solubility to fish that affects the metabolic rate (IEPA 2001; SAWQG, 1996). The temperature recorded in this present work is in line with optimal water temperature for fish condition, maximum growth rate and proper food conversion (Ajibare, 2014). The surface water temperatures observed in up and down-stream of Jebba reservoir in this study were also in consonant with the temperature range recorded by Nsor and Obodai (2016). The higher temperature recorded during the dry season except in December and January was as result of harmattan resulting from north east trade winds (Mustapha, 2009). The rainy season water temperature might be as a result of low radiation and the cloud together with mixing of water from the rain. The temperature fluctuations in relation to season have been reported by many

Nigerian authors in freshwater ecosystem such as Ase river, Kainji lake, Jebba lake, Oyun reservoir and Apodu reservoir (Imevbore, 1975; Idodo-Umeh, 1987; Adeniji, 1991; Mustapha, 2009; Oladipo *et al.*, 2018). This justify the report by Talling (1969) which state that African lakes have their minimum temperature limited to rainy season with fish growth faster at warm water temperature range (Boyd and Lichtkoppler, 1979).

The level of availability of oxygen determines the inorganic nutrients solubility and dictates if environment is aerobic or anaerobic (Beadle, 1981). The main source of dissolved oxygen in water is through direct absorption which influenced by temperature (Plimmer, 1978; Kutty, 1987). The dissolved oxygen levels recorded in up- and down-stream of Jebba reservoir were generally low due to high temperature and continuos vertical mixing of the water but above the critical level of 2 mg/l for fish growth given by Nigeria Federal Ministry of Environment. The concentration ranged have lower dissolved oxygen concentration in year 2017 with no significant difference is both season and location than 2018. Higher dissolved oxygen concentration was observed during rainy season as a result of lower temperature and with proper mixing of the water. Studies through scientific investigation suggest 4 - 9 mg/L of DO as the optimal range for large and diverse fish population and growth of sensitive species of fishes may begin to find alternative route at about 3 mg/L (Howell. and Simpson, 1994; U.S. EPA, 2000; Abdus-Salamet *al.*, 2010). Following the recommendation by Bolarin and Hatton (1981), the DO concentration observed in this study often times lower than the desired range for warm water fish of 5mg/l-12mg/l. However, the range of the dissolved oxygen concentration observed in this work is similar to the range value observed by Ayoola and Kuto, (2009) in Lagos lagoon; Oyewo, (1998); Olaniyan (1969). Similarly, the seasonal higher value observed during the rainy season have also be reported by Adeniji (1991) in Jebba Lake, Imvebore, (1975) in Kainji Lake,

Mustapha, (2006; 2009) in Moro and Oyun reservoirs, and Yakubu, (2004) in Shiroro. This shows a typical value of DO obtainable in Nigerian freshwater ecosystem.

The pH range recorded in this study shows that the water is slightly alkaline and occasional acidic. The pH range of 7-8.5 is known to be ideal for biological activities and productivity while less than 4 are detrimental to aquatic life (Boyd, 1979). Wide fluctuation in pH for persistent period of time may cause death to aquatic organism (Ajibare, 2014). The photosynthetic activities determine the rate of carbon dioxide and bicarbonates assimilation that responsible for pH level (Simpi *et al.*, 2011). The pH serves as an indicator of water quality to determine the extent of pollution in aquatic system since low pH allow elements and compound to brings a condition that can endanger the aquatic life (APHA, 1995). The pH range of this work is in contrast to observation made in River Jamieson in Delta state and other work recorded in Nigeria due to level of pollution recorded in most of the rivers (Awachie, 1981; Ogbeibu and Victor, 1995; Imoobe and Oboh, 2003; Akubugwo and Duru, 2011) and agrees with report in Nkoro River, Niger Delta, Nigeria that little fluctuations in water pH are generally more conducive to aquatic life (Abowei, 2010).

The minimum turbidity was obtained in the dry season when there was little or no rain that brought in silt and debris from the catchment area. The suspended solid determines the turbidity level which tends to be low during the period of low debris and highest in the month of August during heavy downfall of rain (Mohammad and Saminu, 2012). The result agrees with the result obtained in Lake Kaptai, Bangladesh, Idian and Oyun reservoir, Nigeria indicating high level of transparency during the dry season and low transparency in rainy season (Khan and Choudhary, 1994; Mustapha, 2009).

The conductivity recorded was low and its monthly value could be related to other rivers in Nigeria. The reason for this could be availability of planktons and macrophytes as producers utilizing the dissolved salts and nutrient reducing suspended and dissolved materials (Amaringhe and Vijverberg, 2002). It is an important parameter in determining the water quality because evapotranspiration and pollution from the use of manure and fertilizers for irrigation activities (Waziri and Ogugbuaja, 2012). An ionic compound of the water determines the conductivity and low conductivity value have been reported in Nigerian freshwaters (Imevbore, 1975; Mustapha, 2009; Waziri and Ogugbuaja, 2012). The higher value of conductivity was noted in the month of August which similar to reports indicating of higher conductivity of water in the rains (Imevbore, 1975; Adeniyi, 1978; Adeniji, 1991 and Kemdiri, 2005)

The maximum total dissolved solute was recorded in the month of August. This shows the effect of the nutrient that have been brought as a result of flood caused by rainfall that brings dissolved solids from lands surrounding the river (Ajao, 1990; Akubugwo and Duru, 2011). The TDS value obtained throughout the period of study is below the Federal Ministry of Environment limit for fish production and this is also in line with other observations made by Mustapha, (2009), Manjare *et al.* (2010) and Singh *et al.* (2010).

The nutrient levels of the up- and down-stream of the study area were low during the dry season with increase during the rainy season showing seasonal variation. The nitrate concentration variance in seasons might be as a result of suspended sediment transportation due to water influx from the runoff and tributaries that happens during the rainy seasons. Similar report by Ayoola and Kuto, (2009) and Mustapha, (2009) indicating high nitrate concentration in rainy season compare to dry season and lower nitrate concentration in dry season in some eastern

Nigeria rivers (Akpan *et al.*, 1993). Nitrate is an essential nutrient that ensures primary productivity in water ecosystem, though high concentration causes alga bloom and toxic to the aquatic environment. Nitrate content of the surface water occur in trace amount of about 0.5mg/l under normal condition but the concentration is enhanced by the inputs from human activities and environmental factors which may limit the productivity (Bilger and Atkinson, 1997; Ajao, 1990).

Excess nutrient in the aquatic ecosystem may pose problem bringing unpleasant odour and taste as a result of decomposition of algae, destruction of food web and diversity loss (Hauson and Buttlar, 1994; Scheffer, 1998). Excessive nutrient that leads to eutrophication also reduce fish species composition and population hence reduced socio-economic function of the river for fisheries (Gliwicz and Warsaw, 1992). The phosphate which is also as an essential nutrient in aquatic system shows higher concentration than the mean value obtained at lower Niger river by Zakariya *et al.* (2011), Ganga River by Joshi *et al.* (2009) and Oyun reservoir by Mustapha, (2009).

The biological oxygen demand observed show similar to report of Akubugwo and Duru (2011) in Otamiri River, Imo State and report of Okayi *et al.* (2013) at Guma River, Benue State. The BOD level indicates that there is more nutrient in the water attributing to seasonal changes in BOD increasing effect of surface run-off and soil erosion into the receiving water body (Oyewo *et al.*, 1999). The high level of chemical oxygen demand shows high level of oxygen requirement in the water as a result of organic and inorganic decomposition. The combine effect BOD and COD result in the level of dissolved oxygen which is low when oxygen was used for decomposition process that generate gasses like methane and hydrogen sulphide (Wooton, 1992).

Generally, the water parameters of the up- and down-stream of Jebba reservoir shows to be within the range of permissible limit by WHO and Nigeria ministry of environment. It shows that it is safe for aquatic life together with the power generation which is the purpose by which it was created.

5.2 DNA Barcoding in Taxonomic Confirmation

DNA barcode goal is assigning species name to unknown samples and likewise to improve discovery of new and closely related species. This helps in species discrimination and identification in all life stages either microscopic or complex morphological structure (Hebert *et al.*, 2003). The study present DNA barcodes for some selected fish sample and developed a reference barcode library for fish species community in up- and down-stream of Jebba reservoir which helps to confirm some identified species encounter during the research survey. Fish species that are successfully identified were done combining both morphology and molecular analysis. These generate a small but relevant data towards having a comprehensive reference library of CO1 gene barcode for fish species in Nigerian freshwater ecosystem.

The use of DNA barcoding was very efficient in species identification for this present study. All the COI sequences of the studied species clustered together in the phylogenetic tree for specific and generic species which is line with many reports from fish studies. These reports includes the DNA barcode of fish species from southeastern Nigeria (Nwani *et al.*, 2011), use of DNA barcoding for improved biodiversity assessment and monitoring in Peru (Ulises *et al.*, 2018), DNA barcodes of Canadian freshwater fishes (Hubert *et al.*, 2008), fishes from Upper Parana River Basin (Pereira *et al.*, 2013), freshwater fishes from southwestern, Nigeria (Falade *et al.*, 2016), freshwater fishes from southeastern Nigeria (Nwakanma *et al.*, 2015), DNA barcoding

of commonly exploited fishes in Ghats, India (Qayoom *et al.*, 2018), DNA barcoding of Australia's fish species (Ward *et al.*, 2005), DNA barcoding of freshwater fish species from north-central Nigeria (Iyiola *et al.*, 2018), DNA barcoding of fish species in the Taiwan Strait (Bingpeng *et al.*, 2018) and DNA barcoding and genetic diversity analyses of fishes of Indo-Myanmar biodiversity hotspot in Kaladan River (Anindya *et al.*, 2017). All these studies have created a reference database that helps in Nigerian fish species identification using molecular tool and aid high identification rate of the present studied species.

This DNA barcoding was used to verify the taxonomy authentication of the identified species that was used to determine fish catch abundance and diversity. Most of the barcode species shows that morphometric and meristic method was effective for species identification except for few that have close resemblance in morphology. This justifies why morphological identification needs a taxonomist expert together with the tedious work involved in confirmation of the said species. Although, non-corresponding species names in morphology and blast results search may be as a result of either hybridization, incorrect identification of the original or present specimen (Verspoor and Hammar, 1991; Ward *et al.*, 2005). The NJ tree analysis indicated that sample morphologically identified as *Mormyrus rume* clustered with *M. longirostris* from the GenBank, hence, the specimen (*Mormyrus rume*) was refers as *M. longirostris*. In addition, the use of combined morphological and molecular approaches in this present study helped to unravel species identity sequences in Nigerian as well as discover possible potential new species (*Ctenopoma* sp, *Malapterurus* sp, *Dasyatis* sp and *Protopterus* sp) from the area. However, studies that would use of multiple molecular markers, morphological and ecological data are needed to ascertain if these species represent new species or records for the area. The Smooth

Freshwater Stingray, *Dasyatis garouaensis* sequence generated in this present work may be taken as the tentative species identification pending further revision.

The cases of mismatch identification experience in this study are few and include *Oreochromis*, *Malapterurus*, *Schilbe*, *Synodontis* and *Mormyrus*. The cases of mix-matched identification and close relationship in cluster NJ tree experience in this work had been reported by Sogbesan *et al.* (2017). He stated that the close similarities between *Sarotherodon galilaeus* and *Oreochromis niloticus* indicated in the phylogenetic tree is due to closeness in morphology as they are both mouth brooders in accordance with the hypothesis of Trewavas *et al.* (1980). This requires more sample and deeper analyses to justify the mismatch in the molecular identification as seen in NCBI and BOLD system for proper identification. The result also revealed possibility of a new species of *Malapterurus* in Nigeria freshwater ecosystem as a result of low match in identification sequence with common *Malapterurus electricus* and *M. melanochir* that have earlier sequenced.

Cases of variance in species names assigned using morphological methods and DNA barcoding approach observed have been a common challenge in taxonomy for morphologically related species which can be easily resolved using detailed and combined molecular identification. Similarly, Morphology is often requiring alongside with molecular methods in identification for better and accurate results in ichthyofaunal studies. This will help to explore biodiversity research in Nigeria.

In this study, some levels of divergence were detected among few individual species collected. These species include *T. zilli*, *A. occidentalis*, *B. docmac*, *C. geripinus*, *L. coubie*, *M. senegalensis*, *M. tapirus*, *M. anguilloides* and *S. intermedius*. Deep divergence was seen between

in *S. intermedius*, *M. senegalensis* and *C. geripinus*. The intraspecific K2P distances (0.23%) of the studied species in this work was slightly higher than those reported by Ward (2009) and Knebelsberger *et al.* (2014) that gives 0.22% and 0.21% respectively. The high divergence in COI gene may reflect the adaptive effect caused by different location, distance or separations as a result of dam and requires further study.

5.3 Fish Species and Catch Abundance in Up- and Down-Stream of JHPR.

All the species recorded from up- and down-stream of Jebba reservoir have been reported by several authors to be present in Nigerian inland waters (Ita *et al.*, 1983; Ita *et al.*, 1984; 1985; Akinyemi, 1986; Idodo-Umeh, 1987; Ita, 1993; Olaosebikan and Raji, 1998; Sikoki *et al.*, 1998; Mustapha, 2010; Abiodun and Odunze, 2011; Allison and Okadi, 2013; Oguntade *et al.*, 2014; Oladipo *et al.*, 2018). The fish species richness and diversity recorded in this study presents a more comprehensive inventory of ichthyofauna of JHPR when compared with previous studies over time. The prior contribution and studies gave reference to fifty-nine (59) of fishes identified after the impoundment of the lake in year 1983 (Ita *et al.*, 1983) and 52 species recorded in 1993 (Ita, 1993). In recent time, Abiodun and Odunze (2011) carried out a survey of fish present and they recorded 51 species in 12 families and, thus, this marks the beginning of a better understanding of ichthyofaunal diversity and distribution across JHPR.

In comparison with some freshwater ecosystem in Nigeria, species diversity ($n = 83$) recorded in this work was higher compared to Asa river ($n = 21$; Omotosho, 1997), Alau Lake ($n=15$; Idowu and Eyo, 2005), Anambra basin ($n = 52$; Odo *et al.*, 2009); Oyun reservoir ($n = 18$; Mustapha, 2010); Usuma reservoir ($n = 11$; Ataguba *et al.*, 2014) and Apodu reservoir ($n = 17$; Oladipo *et al.*, 2018). The differences in the observed species diversity could be attributed to

the biotic and abiotic factors in the environment in relation to size of the river, age of the water body, locations of sampling, time frame of sampling and the combination of sampling nets (Thirumala *et al.*, 2011). This study, with its wider coverage, enabled recovery of fish species that would otherwise remain undetected if sampled within limited time frame and season.

The *Oreochromis niloticus*, *Tillapia zilli* and *Sarotherodon galileaus* species were the predominant in the family Cichlidae. Their abundance could be due to food availability such as the phytoplankton and zooplankton that aid good breeding capabilities and their adaptation to lacustrine conditions as reported by several authors. Olaniran (2003) and Mustapha (2010) revealed that *Tillapia zilli* dominated Eleiyele reservoir in Ibadan and Oyun reservoir in Offa, respectively while the *Sarotherodon galileaus* have also been reported to dominate the total catch in Oyun mini dam at the University of Ilorin and Kangimi reservoir in Kaduna (Omotosho, 1993; Balogun, 2005). The *Hemichromis fasciatus* occurrence was rare in the study site and has also been reported to be the least abundant in the family in most of the freshwater reservoirs in Nigeria (Omotosho, 1993; Balogun, 2005; Mustapha, 2010)

The Mochokidae presents a large numbers of species with *Brysynodontis bensoda*, *Hemisynodontis membranaceus*, *Synodontis budgetti*, *S. schall* and *S. gambiansis* dominating the family. They have been known to be present in high abundance in the lower River Niger basin (Oyewo, 2005; Iyaji, 2015; Atila *et al.*, 2016; Abiodun and John, 2017). This family has been known to have high ability to forage and utilize wide varieties of food resources presents in their environment and have high species diversity recording over two hundred species in the world and about twenty eight species in Nigeria freshwater ecosystem (Welcomme, 1976; Olaosebikan and Raji, 1998; Idodo-Umeh, 2003). This may account for their high species diversity.

Heperopisus bebe, *M. rume*, *M. anguilloides*, and *Mormyrops deliciosus* were the species that are moderately in abundance in the family Mormyridae. They have been known to have high diversity in numerical point of view in riverine habitats of West Africa associated with turbid and moderately low DO (Harder, 2000). This catch abundance in this study could be as a result of their predatory feeding habit on aquatic insects, smaller crustaceans and worms, adapted for life in and near rapids of smaller streams or swamps (Lowe- McConnell, 1987; Roberts and Stewart, 1976).

Gymnarchus niloticus, the only species in family Gymnarcidae and endemic to Africa show low abundance throughout the sampling period. The species were only found at the upstream. The only reason that could be adduced for its low population might be over fishing due to its commercially important species, having its flesh oily with a strong flavor which is greatly relished in most of the African countries (Sagua, 1983; Holden and Reed, 1972). Conservation measures and awareness is requiring in the catchment area on the killing of broodfishes and juveniles of the fish species.

Characidae shows high abundance in the study area having genus *Hydrocynus* dominating the group. The abundance of the species contributed significantly to the fisheries of the area as it was caught in substantial number throughout the period of sampling. The Characids have been reported to be a diverse group widespread in tropical water and occur throughout African waters (Bruton and Kok, 1981; Teugels *et al.*, 1992). The Characids group of fishes widely distributed in Nigerian inland waters except the Cross River (Paugy, 2002; Olaosebikan and Raji, 2003). It has high occurrence and abundance in some Nigeria waters having been reported to dominate the catch in Anambra river basin, Nigeria (Odo *et al.*, 2009) and reported to be present in Apodu reservoir, Malete, Kwara State (Oladipo *et al.*, 2018).

The total percentage catch abundance of the family Characidae was also similar to report of Ataguba *et al.* (2014) in Gubi Dam, Bauchi State; Oguta Lake, Southeast Nigeria (Adaka *et al.*, 2016) and many others in Northern Nigeria waters (Ita, 1993; Olaosebikan and Raji, 1998; Mustapha, 2010; Oladipo *et al.*, 2018). Mady-Goma *et al.* (2016) similarly reported 12% abundance in tributary of Alima River in Congo. The abundance reported was due to the ability of the fish species to thrive well in lacustrine and riverine conditions (Saliu, 2002), and has been reported to utilize different food resources that may be available in its environment being a planktivore, entomophagous, detritivore, and piscivorous species (Fagade, 1983; Bell-Cross and Minshull, 1988; Victor and Brown, 1990; Hanna and Scheimer, 1993; L  v  que, 1995).

Distichodus rostratus was found almost throughout the sampling period of the year. The species could be said to be fairly abundant in the sampling area especially at the upstream. This could be due to the presence of food source and its ability to withstand averagely high volume of water. The species is very important in commercial fishing due to its size and flesh. The family was caught at a significantly higher rate in the dry season than in the wet season and also have been reported in large rivers in Nigeria having similar abundance and occurrence (references???). The trophic ecology of commercially important fishes in the Cross River, Nigeria shows the availability of this species having its food to comprise of insect, detritus and annelids worms (Offem *et al.*, 2009). The total catch percentage recorded in this work is in line with the percentage recorded by Odo *et al.* (2009) in Anambra river basin, Nigeria.

Citharinus species are among the major economic fish exploitable in River Niger, Jebba, Nigeria as they feed chiefly on insect larvae, plankton and aquatic plants. The species have deep, flattened bodies that earn them the popular name 'moon fish' (Olaosebikan and Raji, 1998; Idodo-Umeh, 2003). They are highly priced due to size and flesh quality, most times in smoked-dried

form because they die-off immediately, when removed from the habitat (Uneke, 2015). *Citharinus citharus* in the study area show high abundance through the period of survey as a result of adaptations to the microphagous and planktivorous feeding habitats associated with lacustrine environment (Arawomo, 2006). This is similar to the report of the species occurrence in Njoboliyo Lake, Adamawa State and Anambra river basin, Nigeria (Odo *et al.*, 2009; Amos and Linus, 2017).

The *Labeo senegalensis*, *L. coubie* and *Barbus occidentalis* dominated the total catch of the family Cyprinidae. The fluctuation in the monthly and site catch could be associated with variations in the water volume as a result of dam operation and management, physico-chemical conditions of the reservoir and food supply. The species reported in this work have been known to be highly endemic in Nigeria freshwaters as recorded in Agbokim Waterfalls, Nigeria (Ikpi *et al.*, 2012), *Labeo ogunensis* in Asejire Lake Southwestern Nigeria (Ayoade, 2011), *Barbus callipterus* in Kangimi Reservoir, Kaduna, Nigeria (Balogun, 2005), *Labeo coubie* and *Barbus Occidentalis* in Oyun reservoir, Kwara State (Mustapha, 2010). Similar abundance of the dominant species of the group were also noticed in Gubi Dam of Bauchi State, Anambra river basin, Usuma reservoir in Bwari of FCT, Ntak Inyang stream of Ikpa river and Oyun reservoir of Kwara State. (Odo *et al.*, 2009; Onuoha *et al.*, 2010; Dan-kishiya *et al.*, 2013; Ataguba *et al.*, 2014; Mustapha, 2009). *Garra waterloti* an endemic and rare species in this group encountered during the sampling period need further research attention and conservation as it was only encountered once with just one sample.

The *Lates niloticus* (Linnaeus, 1762) popularly known as the Nile perch is the only species known in family Centropomidae in Nigeria. It is widely spread in Africa large rivers including Niger, Volta, Nile and Lakes such as Chad, Kainji, Jebba, Albert e.t.c (Paugy *et al.*,

2003; Simon *et al.*, 2009). It is of great commercial importance to the people of Jebba due to the size, flesh quality and the abundance. The abundance of this species may be explained in relation to its biology inhabiting deep water with juveniles found in shallow water, as well as presence of abundant food such as fishes on which they feed especially the clupeids and *Alestes* (Reed *et al.*, 1967; Froese and Pauly, 2010). The smaller one likewise feed on arthropods such as crustaceans and insects and also being planktivorous in nature (Bailey, 1994). In addition, the abundance and size could also be justified through the growth pattern and condition factor of *Lates niloticus* in the study area (Oladipo *et al.*, 2018b). Similar record in abundance and condition were reported in the Pendjari River, West Africa (Simon *et al.*, 2009), but in contrast, report from Anambra river basin, Nigeria showed the species to have few number present (Odo *et al.*, 2009).

This family Bagridae is a group of fishes widely spread in West African countries (Bailey, 1969; Daget and Durand, 1981). Olaosebikan and Raji (1998) describe *Bagrus* fishes as common and of high economic importance in upper and lower Niger River. They are of economic importance due to their marketable size, good taste, quality flesh and acceptability by common people (Boulenger, 1907; Idodo-Umeh, 2003). The three species encountered in this study have been reported in Kainji Lake, Jebba Lake and Asejire Lake known to be wide spread in lakes, swamps and rivers (Idodo-Umeh, 1988; Ita, 1993; Olaosebikan and Raji, 1998). Despite the widespread and abundance that have been reported over years, the moderately low abundance of this present work may be related to nature of the habitat and behavior of the fish. *Bagrus* is known to associate with rocky bottom and coarse substrate in both shallow and deep water (Lock, 1982; Witte and Winter, 1995). They are benthic omnivorous feeder even on bottom deposit as described by many authors (Reed *et al.*, 1967; Holden and Reed, 1972; Ipinjolu *et al.*, 1988). The present abundance of *Bagrus bayad* in up and down-stream of Jebba Lake is higher

than what was recorded in Anambra river basin and Ikwori Lake, South-Eastern Nigeria (Odo *et al.*, 2008; Offem *et al.*, 2011). Whereas the family abundance was in line with what was recorded in Lake Alau, Maiduguri in the North East zone of Nigeria (Idowu and Eyo, 2005).

The family Clariidae represented by *Claris angularis* and *C. gariepinus* were generally low in abundance and rarely encountered. The low abundance could be as a result of River Niger being a very large River whereas they are bottom dwellers and do most of their feeding there being a benthopelagic. This could account for the low catch observed in this study (FAO 2011). This species is of major economic importance all over its range and it is an important aquaculture species almost everywhere in Nigeria. Oladipo *et al.*, 2018 and Agali and Edema (2016) report on high abundance of *Clarias* in the studied water body which is in contrast with the present work because of small water body that favors their existence compares to River Niger.

The Malapteruridae have been known to be widely distributed in West Africa and Nigeria in particular. They are benthopelagic and non-migratory species with a strong electric discharge to stun its prey of small fishes. Commonly found offshore in open waters and breeds in September to November. The population trend was not yet known but most of the river that they have been reported shows low abundance similar to present record (Odo *et al.*, 2008; Offem *et al.*, 2011; Olaosebikan and Lalèyè, 2010). This could be as a result of the ecology and nature of *Malapterurus* being found in turbid water that brings less visibility in standing water coupled with fewer hours used for feeding that do not correspond with fish harvest period (Sagua, 2006). However, high occurrence have been reported in lake Alau by Idowu and Eyo, (2005).

The family Schilbeidae generally has moderately high abundance being represented by *Parailia pelucida*, *Schilbe mystus*, *S. uranoscopus*, and *S. intermedius*. *S. intermedius* dominated

the catch in up and down-stream of Jebba Lake. The occurrence of this species has been recorded in River Niger and other river in Northern part of the country. This occurrence of *S. mystus* in this present work is similar to observation made by Olatunde (1977) and Mustapha, (2009) in Kainji Lake and Oyun reservoir respectively. Contrasting report was seen in Omotosho (1993) and Araoye (1997) which showed the species to be rare with low population density in in Oyun mini dam at the University of Ilorin and Asa reservoir respectively. Ipinmoroti (2013), reported Schilbeidae as a carnivore with relatively high abundance in Lake Asejire and Asiwaju (2011) reported only *S. mystus* in Ogun estuary with high abundance. In Lake Kalgwai Jigawa State, this group was being represented by *Schilbe mystus* and *S. senegalensis* with low abundance (Solomon *et al.*, 2017).

The family Claroteidae were represented by three general dominated by genus *Achenoglanis*. Significant difference was seen between the up and down-stream with high abundance at the upstream. The reason could be that there is availability of plenty of food at the upstream as *Auchenoglanis occidentalis* has been known to feed on broad spectrum of food ranging from phytoplankton, insects, sand, plant materials, crustacean, fish, protozoa and phytoplankton (Chukwuemeka *et al.*, 2019; Meye, J. A. and Ikomi, 2010). The peak occurrences were noticed at the early period of the rainy season. Sometimes, this family was grouped with family Bagridae even after the taxonomy has been separated as seen in report of Odo *et al.* (2008). The catch abundance of family Bagridae in this work is similar to report obtained in Lake Asejire; Anambra river basin, and Oguta Lake, Nigeria (Onuoha *et al.*, 2010; Ipinmoroti, 2013; Adaka *et al.* 2016). In genus *Achenoglanis*, the abundance and occurrence of the species in this family is in contrast with report of Solomon *et al.* (2017) in Lake Kalgwai Jigawa State which recorded low abundance of *Achenoglanis occidentalis*. The abundance of *Auchenoglaris*

occidentalis, *Chrysichthys nigrodigitatus* and *Chrysichthys walkeri* in Warri River of Niger Delta, Nigeria was higher than what was reported in this present work (Aghoghovwia *et al.*, 2014).

The *Arius heudeloti* and *Arius gigas* species were both encountered and found to be of economic importance but with low abundance during the period of survey. The two species encountered in this work have also been reported having low abundance in Uta Ewa Creek, Niger Delta Region, Nigeria by Akpan (2013). The occurrence was not specific to certain period of month or season and this called for the conservation to ensure sustainability of the species. *Arius gigas* have also been reported in many rivers system in Nigeria (Aghoghovwia *et al.*, 2015). Moderate abundance of it was reported to be in Agorin and Yoyayan Coastal waters in Badagry, Lagos State and high abundance in Warri River, Niger Delta, Nigeria (Whenu *et al.*, 2017).

Tetraodon lineatus, *Protopterus annectans*, *Heterotis niloticus*, *Dasyatis garouaensis*, *Polypterus senegalus senegalus* and *Laeviscutella dekimpel* were only available at a few times at downstream except *Tetraodon lineatus* which was available at the upstream. The reason that could be adduced for its low population and occurrence is that the species were known to be rare why some are threatened (Olaosebikan and Bankole, 1998; Idodo-Umeh, 2003). This could have been caused by overfishing, poor reproduction or disturbance of the species range. Same report was given for *Heterotis niloticus* in Oyun reservoir, Offa Kwara State and Oguta Lake, Southeast Nigeria (Mustapha, 2009; Adaka *et al.*, 2016). Likewise with *Dasyatis garouaensis* and *Polypterus senegalus senegalus* in Water Bodies in Asaba Metropolis, Delta State, Nigeria and low brackish open Lagoon in South-western Nigeria (Emmanuel and Osibona, 2013; Ayamre and Ekelemu, 2016).

5.4 Seasonal Diversity Indexes of Fish Species in Up- and Down-stream of JHPR

The measurement of the species richness can be done using the Margalef index which can be affected by the individual species dominance (Magurran, 2004). The highest species richness was found in the downstream during the rainy season than the dry season. The richness at the upstream presented a moderately lower species richness index showing that all sampling sites have high level of fish species richness. This implies that the environmental factors favour the fish species catching ability which was influenced by the water level, turbidity and DO level as presented in this research. The species richness at the upstream presented a moderately lower species index similar to previous reports (Ita, 1993; Abiodun and Odunze, 2011).

Generally, the species diversity and dominance were also affected by the level of distribution of species and this work show moderate distribution of the fish species composition (Pielou, 1966; Clarke and Warwick, 2001). Number of species and abundance of each of the species brings about the evenness and is inversely proportional to dominance, which implies that the level of dominance decrease with increase in evenness index. The observation made on species dominance was lower compared to report in Eko-Ende and Owalla reservoirs, southwest Nigeria (Taiwo, 2010), Majidun Creek, Lagos, Nigeria (Lawson *et al.*, 2013), coastal waters of Ondo State, Nigeria (Bolarinwa *et al.*, 2015). Likewise, Ramakkal Lake, Pechiparai reservoir and Vaigai reservoir have some level of single species dominance (Mohan *et al.*, 2009; Dhanasekaran *et al.*, 2017; Mogalekar, 2015). In contrast, lower ranges were observed in Meghadrigedda, Dhaura and Baigul reservoirs (Mishra *et al.*, 2010; Sharmila and Shameem 2017). This was influenced by the type and numbers of combined gears used.

The evenness index ranges from 0-1 and the observed index both at up and down stream ranged from 0.59 to 0.67. This shows moderate distribution of the fish species composition

(Pielou, 1966). Number of species and abundance of each of the species brings about the evenness and is inversely proportional to dominance that is the level of dominance decrease with increase in evenness index. The observation made was lower compared to report in Ramakkal Lake, Pechiparai reservoir and Vaigai reservoir (Mohan *et al.*, 2009; Dhanasekaran *et al.*, 2017; Mogalekar, 2015). In contrast, lower ranges were observed in Meghadrigedda, Dhaura and Baigul reservoirs (Mishra *et al.*, 2010; Sharmila and Shameem 2017).

5.5 Relationship between Fish Species and Physico-chemical Parameters in Up and Down-Stream of JHPR

The factor analysis explains how the physico-chemical parameters variations influencing the abundance, distribution and diversity of fish families. The arrow in factor analysis bi-plot shows the direction of maximum change of the factor physico-chemical parameters and the fish family abundance. The phosphate, COD, chloride, hardness, BOD, TS and ions formed a positive relationship with Mochokidae, Gymnarcidae and Distichodontidae whereas the DO, TDS, TS, TSS, turbidity, hydrogen carbonate and temperature had positive influence on the remaining fish family abundance. The effects of the physico-chemical parameters on species distribution and composition have been explained and similar to findings obtained in other studies conducted in Nigeria and other tropical streams (Araoye, 1999; Omotosho, 1998; Mustapha, 2010; Oladipo *et al.*, 2018). The family Mormyridae, Gymnarcidae, Characidae, Distichodontidae, Bagridae, Malapteruridae and Schilbedae abundance were determined by the level of turbidity with high level of DO showing correlation with abundance of all the fish family except Claroteidae, Mochokidae, Centropomidae, Cichlidae and Tetraodontidae. The relationship of the physico-chemical parameters, species abundance, distribution and richness of this present work were similar to the previous works which showed that abundance depends on the

temperature, pH, TDS, turbidity, hardness and nutrient due to greater heterogeneity (Akinbuwa, 1999; Imevbore, 1975; Egborge, 1981, Angermeier and Schlosser, 1989; Barrella and Petrere Jr., 1994; Araújo-Lima *et al.*, 1999; Uieda and Barretto, 1999; Mendonça *et al.*, 2005).

All physico-chemical parameters showed a strong relationship with each other except turbidity and chloride that shows a distance in respect to the association formed. The turbidity was strongly correlated with the rainy season with Schilbeidae, Cyprinidae, Mormyridae and Bagridae in high abundance as the parameters increased. The extraction of different assemblage gotten through the physico-chemical measurement and fish abundance through the ordination method helps in niche separation among fish family (ter Braak and Verdonschot, 1995; Ramette, 2007). The positive influence of physico-chemical parameters on the fish family abundance is determined by the position of each vector with the length determining the rate of change in seasons and locations. The ordinal pattern gradient of the parameters tends towards the upstream at both seasons. This suggests that Cichlidae, Claroteidae, Citharinidae, Centropomidae, and Distichodontidae have optimum abundance at the upstream during dry season; the Bagridae, Schilbeidae and Tetraodontidae, with optimum abundance in rainy season at the upstream; Mormyridae and Cyprinidae at the downstream during rainy season while Mochokidae and Characidae show high abundance during dry season at the downstream.

5.6 Summary of Findings, Conclusion, Contribution to Knowledge and Recommendations

5.6.1 Summary of Findings

Lack of adequate information on the morphological and molecular identification has limited knowledge on the diversity, distribution and abundance of freshwater fishes from up- and down-stream of Jebba HEP Reservoir in North Central Nigeria. Most studies in this area have focused only on the morphological identification and upstream section of the dam. To date, limited comprehensive information on the diversity and distribution of freshwater fishes of this aquatic ecosystem is still lacking. Today, there is increasing threats to aquatic ecosystem due to increased human activities in the dam. Thus, there is need for an exhaustive inventory and documentation of the ichthyofaunal diversity of both up- and down-stream sections of the reservoir. Therefore an exhaustive study was conducted to study the physico-chemical parameters and an inventory of the fish diversity of Jebba HEP reservoir. A total of 9605 freshwater fish belonging to 83 species, 43 genera, 24 families and 11 orders were recorded and identified morphologically. Sixty-one species were common to both dry and rainy season with sixty-two species caught in dry season and eighty-two species during rainy season. The total species of eighty was capture at the downstream higher than upstream of sixty-eight species with family Cichlidae and Mochokidae dominating the upstream and downstream respectively. The fish diversity and richness recorded at both site were relatively higher and well distributed. One hundred and seventy (170) specimens from 55 different species, belonging to 33 generals in 23 families were molecularly identified using DNA barcode (CO1) to confirm the identity of the sampled species. All the successful sample sequences show levels of genetic distinctive in intra- and interspecific taxonomical hierarchy; this confirms the use of DNA barcoding as an effective

tool in accurate fish identification. Additionally, this study recorded molecularly unidentified species –*Ctenopoma* sp, *Malapterurus* sp, *Dasyatis* sp and *Protopterus* sp. in Nigeria freshwater ecosystem and more research is needed on the molecular identification and genetic diversity in the genus *Oreochromis* and *Sarotherodon*. This work also presents the first sequence of *Ctenopoma* sp, *Polypterus senegalus* to be generated from Nigeria and *Dasyatis garouaensis* (Smooth Freshwater Stingray) in the world freshwater ecosystem to Genbank. Thus, this study marks the beginning of a better understanding of ichthyofauna of up- and down-stream of JHPR. This study was done to serve as a valuable resource in guiding future studies on Nigerian freshwater fish species identification and diversity.

5.6.2 Conclusion

In other to assess the ecology, abundance and fish diversity in up- and down-stream of Jebba reservoir, this present investigation was carried out to study the morphological and molecular systematics of the fish to identify the present species from this area and the physico-chemical parameters, for proper management and ensure it sustainability. DNA barcode (CO1 gene) was used as a molecular systematics tool to confirm the species identity. The monthly results of physico-chemical parameters used to assess the water quality such as pH, dissolved oxygen, water temperature, conductivity, TDS, hardness, nitrate, phosphate and others were within the limit by federal ministry of environment and the present fish biodiversity status of up- and down-stream of Jebba reservoir, gives eighty-three species higher than the number that have been recorded in the literature with higher species richness and diversity at the downstream in raining season. The use of DNA barcoding efficiency was also confirmed by verifying the species identification as most of the barcode species correspond with the morphological identified species.

This study concluded that the morphological and molecular methods used for fish species identification in this study reveals JHPR harbours high diversity of fish species which was influenced by seasonal variations in turbidity, DO, COD and nitrate concentrations.

5.6.3 Contribution to Knowledge

The present assessment of fish fauna diversity in up and down-stream of Jebba reservoir being supported with DNA barcode for proper species identification have contributed to documentation and catalogue of fish diversity in this area that could be of help with regard to conservation and management. This work also present the first study that use combined morphological and molecular identification for fish diversity study in Nigeria. Likewise, unreported species sequences of *Malapterurus* sp and *Dasyatis garouaensis* were generated for the first time in the Genbank and the sequences of *Ctenopoma* sp and *Polypterus senegalus senegalus* were also reported from Nigeria for the first time. The data generated will be a good data that will be useful for proper monitoring, effective planning in conservation of fish and fisheries in Nigeria freshwater ecosystems.

5.6.4 Recommendation

DNA barcodes should be used to complement morphological identification method in fishery ecology and management, most especially for fish species that are yet to be identified and which shows close resemblance to each other in order to avoid taxonomic conflict. This will help in proper biodiversity monitoring and assessment studies.

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APPENDIX

Plate of some fish species encountered during the sampling period



Citharus citharus



Mormyrops



Hemisynodontis



Branchynodontis



Distichodus encyphalus



Tetraodon



Clarotes



Barbus



Latis niloticus



Achenoglanis bisculatus



Malapterurus sp



Malapterurus electricus



Brycinus



Schilbe



Clarotes



Arius gigas



Heperopsis



Mormyrops



Hydrocynus forskalis



Hydrocynus vittatus



Labeo parvus



Garra waterlotii



Bagrus



Oreochromis niloticus



Oreochromis aureus



Sarotherodon



Hemichromis



Protopterurus



Distichodus rostratus

Pictures of fishing activities and sampling sites

