IMPACT OF WATER QUALITY AND ANTIMICROBIAL RESISTANCE ON THE PATHOGENS OF FARMED FISH (*Oreochromis niloticus*) IN UASIN GISHU COUNTY, KENYA

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DECLARATION

Declaration by the Candidate

This thesis is my original work and has never been presented for the award of an academic degree in any other university and should not be copied, or reproduced in any format without written authority from the author and/or University of Eldoret.

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DEDICATION

In loving memory of my late father, Kimutai Kalya, whose values, strength, and spirit continue to inspire me every single day. To my beloved mother, Leah Kalya, your unwavering support, prayers, and sacrifices laid the foundation for my journey.

To my dear wife, Getrude, thank you for your love, patience, and steadfast encouragement throughout every step of this academic pursuit. And to my wonderful children; Kayla, Christian, and Denzel, may this achievement be a lasting reminder that with resilience, persistence and faith, you can go anywhere.

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ABSTRACT

Aquaculture is increasingly recognized as a sustainable strategy for meeting the rising global demand for protein, particularly in developing countries such as Kenya where capture fisheries are under pressure. Despite its potential, aquaculture growth is hindered by poor water quality and the emergence of microbial and parasitic infections that compromise fish health, productivity, and ultimately farmer livelihoods. This study evaluated the impact of water quality on the diversity and prevalence of microbial and parasitic organisms in cultured fish, and examined the antibiotic susceptibility of bacterial isolates from aquaculture systems in Uasin Gishu County, Kenya. A longitudinal survey was conducted from May 2023 to April 2024 across five farms and thirteen ponds. Monthly assessments of water quality parameters (temperature, pH, dissolved oxygen, turbidity, and nutrient concentrations) were performed following standard APHA protocols. Concurrently, fish samples were collected for microbial and parasitic screening. Bacteria were isolated through culture-based methods and identified morphologically and biochemically in accordance with Bergey's Manual, while parasites were identified microscopically. Antibiotic susceptibility testing employed the Kirby–Bauer disc diffusion method using commonly applied antibiotics. Statistical analyses included chi-square tests for associations between infection prevalence and host/seasonal variables, one-way ANOVA to evaluate differences in water quality parameters, and logistic regression to determine significant predictors of infection. A total of 154 bacterial isolates were recovered, with *Escherichia coli* (34.8%) and *Pseudomonas aeruginosa* (21.7%) being most prevalent. Parasitic infestations, primarily protozoans and helminths, were concentrated in gills ($p < 0.001$) and showed significant seasonal variation, with peak prevalence during warmer months. Logistic regression revealed that organ type, bacterial species, and water quality parameters were significant predictors of infection ($p < 0.05$). Poor water quality, marked by low dissolved oxygen and elevated ammonia, was strongly associated with increased pathogen load. Importantly, several bacterial isolates exhibited multi-drug resistance, raising concerns about environmental contamination and the spread of antimicrobial resistance.This study provides critical insights into the complex interactions between water quality, pathogen diversity, and fish health in aquaculture systems. It demonstrates that disease occurrence is not random but is strongly influenced by environmental conditions and farming practices. The findings highlight the need for routine water quality monitoring, improved pond management, and the adoption of biosecurity measures to reduce infection risks. Furthermore, the detection of resistant bacteria underscores the urgency of promoting responsible antibiotic use to safeguard fish health and protect public health. Overall, the study emphasizes an integrated approach that combines environmental stewardship, sustainable husbandry practices, and prudent health management to ensure the long-term viability of aquaculture in Uasin Gishu County and similar settings.

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LIST OF ABBREVIATIONS

Symbol	Meaning
AMR	Antimicrobial Resistance
ANOVA	Analysis of Variance
APHA	American Public Health Association
ASARECA	Association for Strengthening Agricultural Research in Eastern and Central Africa
BOD	Biochemical Oxygen Demand
CFU	Colony-Forming Unit
DNA	Deoxyribonucleic Acid
DO	Dissolved Oxygen
EUS	Epizootic Ulcerative Syndrome
FAO	Food and Agriculture Organization
IHNV	Infectious Hematopoietic Necrosis Virus
IPNV	Infectious Pancreatic Necrosis Virus
KHV	Koi Herpesvirus
KMFRI	Kenya Marine and Fisheries Research Institute
KNBS	Kenya National Bureau of Statistics
LDO	Luminescent Dissolved Oxygen
NADS	National Aquaculture Development Strategy
NTU	Nephelometric Turbidity Unit
OIE	World Organisation for Animal Health
PCA	Principal Component Analysis
RAS	Recirculating Aquaculture System
SRP	Soluble Reactive Phosphorus
TN	Total Nitrogen
TP	Total Phosphorus
VHSV	Viral Hemorrhagic Septicemia Virus
TSA	Tryptic Soy Agar
MI	Mean Intensity
MA	Mean Abundance

CHAPTER ONE

INTRODUCTION

1.1 Background Information

Fisheries production has undergone a transformative shift with the rapid expansion of aquaculture, one of the world's fastest-growing food production sectors in recent decades (FAO, 2022; Pradeepkiran, 2019). Aquaculture has become a vital contributor to global food security, providing an essential protein source to an increasing global human population (Allison, 2011; Edwards et al., 2019; Makori et al., 2017). With the world's human population projected to reach 10 billion by 2050, global food production must expand by up to 56% to meet demand (Allison, 2011; FAO, 2022). Aquaculture utilizes a range of technological advancements and farming systems, from simple pond farming to high-tech, intensive production systems capable of yielding up to 100 kilograms of fish per cubic meter (Ahmed et al., 2019).

Farmed fish production plays a crucial role in alleviating food insecurity and ensuring nutritional sufficiency worldwide (Makori et al., 2017; Vilane et al., 2021). In Kenya, the government has prioritized aquaculture as a key sector under its economic stimulus programs, leading to increased investment and expansion (FAO, 2021; Kasozi et al., 2024). Consequently, fish farming has evolved into both semi-intensive and intensive systems, providing significant economic benefits such as poverty alleviation, improved household incomes, and enhanced food security (KNBS, 2017; Munguti et al., 2021). However, the sector faces numerous challenges, including limited access to quality fish seed, high feed costs, water pollution, and climate change impacts (Ferreira et al., 2022; Toranzo et al., 2005). Additionally, disease outbreaks caused by endemic, emerging, and

re-emerging pathogens threaten farmed fish health and productivity, ultimately limiting access to high-value markets (Kibenge, 2019; Boyd & McNevin, 2014).

Uasin Gishu County, located in Kenya's North Rift region, has seen substantial growth in aquaculture due to government initiatives promoting fish farming (Uasin Gishu Government, 2015). Despite this growth, sustainable aquaculture can be challenged by poor water quality and the prevalence of microbial and parasitic infections, which negatively impact fish health and productivity (Dabi, 2022; Ferreira et al., 2022; Zanchett & Oliveira-Filho, 2013). Maintaining optimal water quality is crucial for fish survival and performance, as fluctuations in parameters such as dissolved oxygen, temperature, pH, and nutrient levels significantly influence disease occurrence (Dabi, 2022; Schenone et al., 2011), which negatively impacts fish growth.

Fish, like other animals, are susceptible to infections caused by bacteria, viruses, fungi, and parasites, which can lead to significant economic losses in aquaculture (Kamundia et al., 2008). Pathogenic microorganisms occur naturally in aquatic environments but can proliferate under suboptimal environmental conditions, particularly in fish farms where stressors such as overcrowding, poor nutrition, and fluctuations in water quality create a conducive environment for disease outbreaks (Jacobs & Chenia, 2007; Tacon, 2020). The introduction of new fish species, inadequate disease monitoring, and climate change further exacerbate the risks of infections in aquaculture (Naylor et al., 2021).

Several studies have highlighted the link between water quality and microbial infections in fish (Hussein et al., 2024). Elevated ammonia and nitrite levels, for example, have been associated with increased susceptibility of fish to parasitic infections (Kubečka et al., 2016). Poor water quality, characterized by high organic matter content and low dissolved oxygen levels, promotes the proliferation and virulence of bacterial pathogens

(Zhimin et al., 2021). Additionally, antimicrobial resistance (AMR) in aquaculture has emerged as a significant concern due to the misuse of antibiotics, leading to the development of resistant bacterial strains (Dayie et al., 2024; Huavas et al., 2024). The presence of drug-resistant pathogens in fish farming environments threatens both aquaculture sustainability and public health, as these pathogens may be transmitted to humans through the consumption of contaminated fish (Cabello, 2006; Souza et al., 2019).

The impact of water quality on disease prevalence in farmed fish in Uasin Gishu County remains poorly understood, necessitating further research. Understanding the relationship between water quality parameters and the occurrence of microbial and parasitic infections is critical for developing effective disease management strategies and promoting sustainable aquaculture practices in the region.

Globally, countries such as China, Indonesia, and India dominate aquaculture production, contributing over 80% of farmed fish volumes (FAO, 2022). In Africa, Egypt and Nigeria are leaders, while Kenya is among the emerging producers. Benchmarking Kenya's production systems against these regions is important for identifying best practices. Furthermore, climate change is increasingly recognized as a compounding factor that influences both water quality and pathogen dynamics, threatening the stability of fish farming systems.

1.2 Problem Statement

Despite the rapid growth of aquaculture in Uasin Gishu County (Uasin Gishu Government, 2015), poor water quality and the presence of pathogenic parasites and microbes potentially pose significant challenges to fish production. Water quality parameters such as temperature, dissolved oxygen, pH, and nitrogenous wastes influence fish health and

disease susceptibility (FAO, 2021) if they are not optimum. However, there is limited research on how these water quality parameters impact the prevalence and distribution of microbial and parasitic infections in farmed fish systems in the region.

Microbial and parasitic infections are a major cause of fish morbidity and mortality (Jacobs & Chenia, 2007), leading to economic losses for fish farmers. Pathogenic bacteria such as *Aeromonas* spp., *Pseudomonas* spp., and *Vibrio* spp., along with parasites such as protozoans and helminths, are common in aquaculture systems (Hussein et al., 2024). The interaction between these pathogens and water quality parameters remains poorly studied in Uasin Gishu County, making it difficult to develop effective disease mitigation strategies. Therefore, the status of water quality parameters and their relationship with specific fish pathogens should be investigated to inform effective, environmentally friendly disease management practices in aquaculture systems in the region.

Furthermore, antimicrobial resistance in aquaculture has emerged as a major concern due to the excessive use of antibiotics, leading to the development of drug-resistant bacterial strains (Du et al., 2022). There is an urgent need to assess antibiotic sensitivity patterns among fish pathogens to inform responsible use of antibiotics and improve fish health management in the region.

Farmers in Uasin Gishu often rely on empirical treatments without laboratory confirmation, which increases production costs and may worsen antimicrobial resistance. Moreover, there is no systematic disease surveillance framework in the county, leading to under-reporting of outbreaks. The lack of reliable diagnostic and epidemiological data has made it difficult for policymakers and stakeholders to design targeted intervention strategies.

1.3 Justification and Significance of the Study

Despite the known risks, there is limited data on the diversity and occurrence of bacterial and parasitic pathogens in aquaculture systems in Uasin Gishu County. Most local studies have focused broadly on production constraints or water quality, with few specifically addressing pathogen identification and distribution. As such, farmers often lack access to accurate diagnostic information, which hinders the implementation of timely and targeted disease management strategies.

The findings of this study will provide valuable insights into the relationship between water quality parameters and disease prevalence in farmed fish. This knowledge will be instrumental in guiding policy decisions, improving farm management practices, and promoting sustainable aquaculture. Additionally, assessing antibiotic resistance patterns in fish pathogens will inform strategies for responsible antibiotic use, thereby mitigating the risks associated with antimicrobial resistance.

By addressing these challenges, this research will support the development of evidence-based interventions for sustainable aquaculture in Uasin Gishu County and beyond, benefiting both farmers and consumers.

The results of this study will also contribute to national strategies such as the Blue Economy framework and Kenya's Vision 2030, which emphasize sustainable exploitation of aquatic resources. At the community level, healthier fish farming systems will enhance household nutrition and incomes, particularly for youth and women engaged in small-scale aquaculture. Regionally, this research will create a model that can be replicated in other counties with similar ecological conditions, thereby scaling the benefits beyond Uasin Gishu.

1.4 Objectives

1.4.1 Broad Objective

To evaluate the impact of water quality on diversity and prevalence of bacteria and parasites, and to investigate antimicrobial resistance of farmed fish pathogens in Uasin Gishu County, Kenya.

1.4.2 Specific Objectives

1. To assess the diversity of bacteria and parasites in fish in selected fish farms in Uasin Gishu County
2. To determine the water quality status in randomly selected fish farms in Uasin Gishu County
3. To evaluate the influence of water quality on the infestation of fish by diverse bacteria and parasites
4. To assess the antimicrobial resistance of fish pathogens isolated from farmed fish in Uasin Gishu County to commonly used antibiotics

1.5 Research Questions

1. Is there significant diversity of bacteria and parasites in fish from randomly selected farms in Uasin Gishu County?
2. Do water quality parameters in selected fish farms in Uasin Gishu County significantly vary across different locations and compared to expected standard ranges?
3. Does water quality have a significant influence on bacteria and parasites infestations in farmed fish in Uasin Gishu County?

4. Are the fish pathogens isolated from farmed fish in Uasin Gishu County sensitive to commonly used antibiotics?

CHAPTER TWO

LITERATURE REVIEW

2.1 Overview of Aquaculture Production

Aquaculture has become one of the fastest-growing food-producing sectors worldwide, outpacing capture fisheries over the past three decades (FAO, 2021; Tacon & Metian, 2015). In Asia, particularly in China, India, Vietnam, and Bangladesh, aquaculture contributes more than 60% of fish consumed domestically (Amed & Lorica, 2002; FAO, 2022). This dominance is attributed to heavy government investment in infrastructure, improved hatcheries, and feed industries. Europe and North America have focused on intensive production systems such as recirculating aquaculture systems (RAS) and cage culture, supported by strong regulatory frameworks to ensure environmental sustainability (Bostock et al., 2010; Ebeling & Timmons, 2012). Africa, though lagging behind Asia, has demonstrated rapid growth in countries such as Egypt (the largest tilapia producer outside Asia), Nigeria, and Ghana, where aquaculture now forms a critical component of national food security policies (Obiero et al., 2019; Njiru et al., 2021; Elsayad et al., 2024). In comparison, Kenya's aquaculture industry is at an intermediate stage, with high potential for expansion due to abundant freshwater resources and increasing market demand for fish products (Opiyo et al., 2018).

Fisheries play a vital role in supporting food security and livelihoods, while also serving as a key source of income and social development in developing countries (Stankus, 2021). Recently, the sector has gained significant attention and is experiencing rapid growth, largely driven by the expansion of aquaculture (Kubečka et al., 2016). Advances in technology and rising demand for fish as a major source of animal protein

are key factors behind this growth. As the industry expands, farming methods have become more intensive to increase production (Rico et al., 2012). In 2014, aquaculture contributed 44% to global fish production, amounting to 74 million tons of fish valued at USD 160 billion. Nearly all fish produced through aquaculture is intended for human consumption.

Aquaculture was first introduced in Kenya by the colonial government in the 1920s (Van Someren, 1960). It began with static water pond culture of native tilapiines, followed by Common carp and African catfish. Between the 1940s and 1960s, aquaculture was promoted as a sustainable food production method, aimed at improving rural nutrition, generating supplementary income, and creating employment (Adeleke et al., 2020). Early efforts were focused on basic research to develop practical technologies for the culture of indigenous species (Brummett et al., 2008).

The colonial government established Sagana and Kiganjo fish farms in 1948 for warm water species (tilapia) and cold water species (trout), respectively. After independence, Kenya's government created the Fisheries Department within the Ministry of Agriculture to lead fisheries development. The department promoted the "Eat More Fish Campaigns" of the 1960s, resulting in rapid growth of rural pond fish farming, particularly in Nyanza and Western Provinces, which had over 30,000 fish ponds by the early 1970s (Zonneveld et al., 1988). However, many of these ponds were later abandoned (Charo-Karisa & Gichuri, 2010; Opiyo et al., 2018). Between 1970 and 2006, aquaculture production fluctuated between 1,000 and 4,000 MT. By 2007, 4,742 farmers produced 4,250 MT of fish from 7,477 ponds covering 217 hectares, 301 dams and reservoirs (497 hectares), and 248 tanks and raceways (Omasaki & Ngeno, 2024).

The aquaculture industry in Kenya has experienced significant growth over the past few

decades, transforming into a vital component of the country's food security and economic development strategies. Historically, fish farming in Kenya began in the early 20th century but gained substantial momentum in the late 1990s and early 2000s, driven by the need to supplement declining wild fish stocks and to improve rural livelihoods (Stankus, 2021). Government initiatives have played a crucial role in promoting aquaculture. Programs such as the Economic Stimulus Program (ESP), launched in 2009, aimed to enhance fish farming by providing funds for the construction of fish ponds, provision of inputs, and technical support to farmers (Keyombe et al., 2021). These efforts have led to a significant increase in aquaculture production, particularly in regions such as Uasin Gishu County, where favorable climatic conditions and water resources support fish farming activities (Uasin Gishu Government, 2015).

According to (Njiru et al., 2021), significant growth in the aquaculture sector began in the early 2000s, driven by increasing recognition of its potential to enhance food security and economic development. The turning point came with the launch of the Economic Stimulus Program (ESP) in 2009, which aimed to boost aquaculture production as part of a broader strategy to stimulate economic growth (Onyango et al., 2024). The ESP provided substantial investments for the construction of fish ponds, provision of inputs such as fingerlings and feed, and capacity-building initiatives. The government's commitment in promoting aquaculture was further demonstrated through policies and strategic plans, such as the National Aquaculture Development Strategy (2009-2013) and the Aquaculture Business Development Program (ABDP), which aimed to create a conducive environment for the growth of the sector (Tacon, 2020). These efforts led to a rapid increase in the number of fish farmers and the total area under aquaculture.

Today, aquaculture is a vital component of Kenya's agricultural sector. The industry has

grown from a subsistence activity to a commercial enterprise, contributing significantly to the country's fish production. According to the Kenya Marine and Fisheries Research Institute (KMFRI), aquaculture production reached approximately 24,000 metric tons in 2019, representing a substantial increase from previous years (Keyombe et al., 2021). The sector has also seen increased diversification, with the introduction of high-value species such as ornamental fish and prawns. Innovations in production systems, such as integrated aquaculture-agriculture (IAA) systems and recirculating aquaculture systems (RAS), have further contributed to the sector's growth and sustainability (Ebeling & Timmons, 2012).

2.1.1 Role of Government Initiatives in Promoting Aquaculture

The Kenyan government has played a pivotal role in the promotion and development of the aquaculture sector through various initiatives and policies. These efforts have been instrumental in transforming aquaculture from a subsistence activity to a commercially viable industry, contributing significantly to food security, economic development, and boosting rural livelihoods (Keyombe et al., 2021).

The role of government initiatives in aquaculture extends beyond direct financial investment. Governments also provide indirect support through subsidies, credit facilities, and extension services that improve farmers' technical knowledge (Munguti et al., 2024; FAO, 2018). In Kenya, these interventions have not only facilitated increased fish production but also promoted gender inclusion, with women and youth increasingly participating in fish farming (Opiyo et al., 2018; Njiru et al., 2021). Globally, similar programs have succeeded in Asia, such as India's Blue Revolution initiative (Kumar et al., 2022), and in Africa, such as Nigeria's Presidential Initiative on Fisheries and Aquaculture Development (Olapade, 2020). Kenya's alignment with continental poli-

cies such as the African Union's Policy Framework and Reform Strategy for Fisheries and Aquaculture (PFRS) underscores its recognition of aquaculture as a driver of rural development, employment, and foreign exchange earnings (Keyombe et al., 2021).

2.1.2 Economic Stimulus Program (ESP)

One of the most significant government initiatives in recent years was the Economic Stimulus Program (ESP) launched in 2009. The ESP aimed to revitalize the economy following the global financial crisis, with aquaculture identified as a key sector for investment. The program allocated substantial funds for the construction of fish ponds, provision of inputs such as fingerlings and feed, and capacity-building initiatives for fish farmers (Orina et al., 2021). The ESP led to the establishment of thousands of new fish ponds across the country, significantly increasing aquaculture production and farmer participation.

2.1.3 National Aquaculture Development Strategy (NADS)

The National Aquaculture Development Strategy (NADS) for 2009-2013 outlined the government's vision for the sector and set clear targets for increasing aquaculture production. The strategy emphasized the need for; Infrastructure Development, Research and Development and Capacity Building (FAO, 2022).

2.1.4 Aquaculture Business Development Program (ABDP)

Building on the successes of earlier initiatives, the Aquaculture Business Development Program (ABDP) was launched to further enhance the commercial viability of the sector. The ABDP focuses on; improving market infrastructure and linking fish farmers to local and international markets to ensure better prices for their produce, facilitating access to credit and insurance for fish farmers to enable them to invest in and expand their opera-

tions and promoting environmentally sustainable aquaculture practices to minimize the sector's ecological footprint and ensure long-term productivity (FAO, 2022).

2.1.5 Regulatory Framework and Policy Support

The Kenyan government has also developed a robust regulatory framework to support the aquaculture sector. Key policies and regulations include; The Fisheries Management and Development Act (Republic of Kenya, 2016) provides a comprehensive framework for the management and development of fisheries and aquaculture in Kenya which includes provisions for licensing, monitoring, and enforcing compliance with best practices, Aquaculture Policy (Kenya Fisheries Service, 2025) which outlines the government's commitment to developing the sector through investment in infrastructure, research, and capacity building. It also emphasizes the importance of sustainable practices and the conservation of aquatic ecosystems (Obiero et al., 2021).

2.1.6 Research and Extension Services

The government, through institutions such as the Kenya Marine and Fisheries Research Institute (KMFRI) and various universities, has invested in research to address key challenges facing the aquaculture sector. Research areas include fish breeding, disease management, water quality control, and the development of cost-effective and nutritious fish feeds (Jahangiri et al., 2021). Extension services have also been crucial in disseminating research findings and providing technical support to fish farmers (Orina et al., 2021).

2.1.7 Collaboration with International Organizations

Kenya has benefited from partnerships with international organizations such as the Food and Agriculture Organization (FAO), the World Bank, and various non-governmental organizations (NGOs). These collaborations have provided additional funding, techni-

cal expertise, and capacity-building support, further enhancing the development of the aquaculture sector (FAO, 2022).

Production systems in Kenya reflect the socio-economic and environmental diversity of the country. Extensive systems remain important for resource-poor farmers, yet they yield low outputs (FAO, 2021; Munguti et al., 2021). Semi-intensive systems dominate due to their balance between input costs and yields, making them more suitable for smallholder farmers (Opiyo et al., 2018; Njiru et al., 2021). Intensive systems such as cage farming and recirculating aquaculture systems (RAS) are emerging but face constraints of high initial investment, energy requirements, and the need for skilled management (Ebeling & Timmons, 2012; Obiero et al., 2019). Comparative studies have shown that a hectare of semi-intensive ponds in Kisii County can produce up to 2,500 kg annually, while similar farms in Uasin Gishu under intensive systems can produce over 15,000 kg per hectare (Aura et al., 2018). These systems also present environmental challenges, including nutrient loading in water bodies, effluent discharge, and biosecurity risks (Boyd & Tucker, 2014; Rico et al., 2012). Introducing biofloc technology and integrated aquaculture–agriculture (IAA) systems offers new opportunities for enhancing productivity while maintaining sustainability (Avnimelech, 2009; FAO, 2022).

2.1.8 Aquaculture Production Systems in Kenya

Kenya's aquaculture production systems comprise primarily extensive and semi-intensive systems, with a relatively small proportion of intensive systems. While most fish farming occurs at the subsistence level, some farmers are transitioning to commercial intensive aquaculture, earning as much as US$11,000 per hectare annually (Aura et al., 2018). Over 90% of fish farmers practice semi-intensive systems, while only about 3% engage

in intensive farming, mainly due to the high cost of electricity and the limited availability of affordable, high-quality feeds (FAO, 2021). In semi-intensive systems, ponds are fertilized using manure from cattle, sheep, poultry, or rabbits, and supplemented with cereal bran (wheat, rice, maize) or low-protein formulated feeds (Munguti et al., 2021). Additionally, aquaculture in Kenya is often integrated with crop and livestock production, such as vegetables, bananas, goats, cattle, and chickens. Crop farming is typically subsistence-based, while livestock farming is commercial, particularly for milk and meat production (Kyule-Muendo et al., 2022; Orina et al., 2021).

2.1.9 Extensive Fish Farming

Extensive fish farming primarily takes place in dams and water reservoirs, where fish rely on the natural productivity of the water without the addition of artificial feeds. The main species cultivated in this system are *Oreochromis niloticus* (Nile tilapia) and *Clarias gariepinus* (African catfish), which are often stocked to control mosquito populations in dams that are primarily used for livestock watering. These dams are predominantly located in the Central and Rift Valley regions. Production in extensive systems ranges from 500 to 1,500 kg per hectare annually, contributing approximately 10% of the total farmed fish in Kenya (Aura et al., 2018; Pradeepkiran, 2019). Extensive fish farming is a low-input system, making it particularly suitable for resource-limited farmers; however, it remains underdeveloped due to challenges such as poor water quality management and reliance on natural food productivity (Hussein et al., 2024; Njiru et al., 2021).

2.1.10 Semi-Intensive Systems

Semi-intensive aquaculture systems dominate fish farming in Kenya and are used primarily to rear *O. niloticus* and *C. gariepinus*, either in monoculture or polyculture se-

tups. These systems include earthen, lined, and concrete ponds that are fertilized with organic manures such as cow dung, sheep, poultry, or rabbit manure (Munguti et al., 2012). Supplementary feeding includes farm-formulated feeds or those purchased from cottage industries, while cereal brans are also utilized to enhance pond productivity. Production levels range from 1,000 to 2,500 kg per hectare annually (Ngugi et al., 2007). This system is popular due to its lower input costs, especially for feed.

2.1.11 Intensive Systems

2.1.11.1 Raceways

Raceway systems are primarily employed for the production of *Oncorhynchus mykiss* (rainbow trout), especially in the Mount Kenya region. There are approximately six commercial trout farms operating in this area, with annual yields ranging from 10,000 to 80,000 kg per hectare. One significant challenge in these systems is the high cost of high-quality feed, which is often imported. This factor limits the number of farmers who can sustain such intensive operations. Many farms, like Trout Masters, have sought to mitigate this by producing their own feed, though they still rely on imported feeds to ensure optimal growth results (FAO, 2017). Additionally, water availability is critical, with farms needing continuous access to high-quality water to maintain production. Trout farms often import rainbow trout eggs from countries such as the U.S., Denmark, and South Africa to sustain their operations (FAO, 2017; Mbugua, 2008; Ogello et al., 2013).

2.1.11.2 Recirculating Aquaculture Systems (RAS)

Recirculating aquaculture systems (RAS) in Kenya are primarily tank-based setups used for culturing *O. niloticus* (Nile tilapia) and Clarias gariepinus (African catfish). In these systems, fish are raised at high stocking densities, ranging from 5 to 20 fish per cubic meter, under controlled environments, either indoors or in greenhouses. As of 2016, there were eight operational RAS farms in Kenya, capable of producing up to 200 tonnes per hectare annually (Kenya Fisheries Service, 2025). Despite the efficiency of these systems, their adoption remains low due to the high initial capital investment required for infrastructure such as tanks, greenhouses, and the significant costs associated with electricity to maintain water quality and recirculation (Ogello et al., 2013; Kenya Fisheries Service, 2025).

2.1.11.3 Cage Farming

Recent studies have shown that cage farming in Lake Victoria not only provides food security but also contributes significantly to household income in riparian communities (Njiru et al., 2021). Despite this, environmental concerns such as eutrophication, nutrient loading, and conflicts with wild capture fisheries have been raised (Aura et al., 2018). Policy interventions are therefore required to balance production growth with ecosystem protection. Experiences from Asia (China, Vietnam) demonstrate that strict regulation of cage numbers, spatial zoning, and coordinated farmer associations can mitigate these challenges (FAO, 2021).

Cage farming is rapidly growing in Lake Victoria, with Siaya County having the largest number of cages. Intensive cage culture began in 2013 after successful trials at Dunga

Beach in Kisumu County, led by the Kenya Marine and Fisheries Research Institute (KMFRI) and the Dunga Beach Cooperative Society under the ASARECA project (Aura et al., 2018; Njiru et al., 2021). Cage farming is now practiced in five riparian counties: Migori, Siaya, Homabay, Busia, and Kisumu. Stocking densities in cages range from 60 to 250 fish per cubic meter, with cage sizes varying from 8 to 125 cubic meters. The number of cages increased from 1,663 in 2016 to 3,398 in 2017 (Aura et al., 2018). This system has significant potential to boost aquaculture production and support economic growth in the Lake Victoria region (Aura et al., 2024).

2.2 Culture Ponds

Culture ponds remain the backbone of aquaculture in Kenya. Modern pond management includes lining ponds with plastic or concrete to minimize seepage, adopting aeration technologies, and mechanizing feeding practices (Boyd & Tucker, 2012; FAO, 2021). Pond-based aquaculture provides opportunities for integrating fish with crop irrigation and livestock production, enhancing household food security (Munguti et al., 2024). However, challenges such as predation, water scarcity during dry seasons, and siltation remain prevalent (Njiru et al., 2021). Studies in Kisumu and Busia counties have demonstrated that proper pond preparation, including liming, fertilization, and regulated stocking density, can double yields (Opiyo et al., 2018; DeBruyn, 2022). Economically, ponds provide accessible entry points for smallholder farmers, but commercial-scale pond farming requires reliable access to inputs and markets (Obiero et al., 2019). Socio-economic studies reveal that pond aquaculture enhances rural household resilience by providing both direct nutrition and income from surplus sales (Obwanga et al., 2020; Njiru et al., 2021). In Kisumu, households practicing aquaculture alongside crop farming reported a 35% increase in annual household income compared to non-farming

households (KMFRI, 2019). However, challenges such as limited access to quality fingerlings and feeds, and poor post-harvest handling, reduce profitability (Opiyo et al., 2018). Government-subsidized hatcheries and private-sector investments in feed mills are essential to address these gaps (FAO, 2022; Aura et al., 2018).

Ponds are widely used by smallholder farmers, with farm sizes ranging from one to 60 ponds. Farmers are categorized as small-, medium-, or large-scale operators based on pond surface area. Large-scale farmers have pond areas of 4,000 to 80,000 square meters, while medium-scale operators have 601 to 3,999 square meters, and small-scale farmers (Fewer than five ponds) have 30 to 500 square meters (Obwanga et al., 2020). A common stocking rate in Kenyan ponds is three fish per square meter, yielding approximately 1 kg per square meter, with weight gains of 1.5 to 2.0 grams per day in well-managed systems. Higher stocking densities of up to six fish per square meter can yield 3 kg per square meter (FAO, 2017). Manures such as cow dung, sheep, poultry, and rabbit manure are commonly used to enhance natural food production in the ponds, although this practice may introduce pathogens into the system (Little & Edwards, 2003; Mbugua, 2008; Mente et al., 2011). Fish typically reach a weight of 250 to 300 grams within six months, depending on water temperature, feed quality, and management practices (Adeleke et al., 2020).

2.3 Culture Species

In Kenya, the key aquaculture species include Nile tilapia (*Oreochromis niloticus*), African catfish (*Clarias gariepinus*), and common carp (*Cyprinus carpio*). Tilapia is the most widely farmed species due to its fast growth, adaptability to various environmental conditions, and high market demand (Ngugi et al., 2007). Nile tilapia accounts for approximately 75% of the total cultured fish, followed by African catfish at 18%.

These species thrive in most aquatic ecosystems across the country and are highly preferred by consumers both locally and regionally (Kasozi et al., 2024). Common carp (*Cyprinus carpio*) and Rainbow trout (*Oncorhynchus mykiss*) contribute 4% and 1% of farmed fish, respectively. Both species were introduced during the colonial period (Opiyo et al., 2018).

Nile tilapia and African catfish are highly adaptable and can be cultured in various freshwater systems, including ponds, tanks, and cages. In contrast, Rainbow trout is more limited in distribution, as it requires cold water conditions, found mainly in the high-altitude areas of Mount Kenya, where water temperatures do not exceed 19°C (Omweno & Omondi, 2024).

Small-scale production of ornamental fish is also practiced, with species like Koi carp (*Cyprinus rubrofuscus*), Goldfish (*Carassius auratus*), and Swordtail (*Xiphophorus hellerii*) produced primarily for the regional market (Nyonje et al., 2018). Recent efforts by the Kenya Marine and Fisheries Research Institute (KMFRI) have focused on culturing indigenous species such as African carp (*Labeo victorianus*), *Oreochromis jipe*, and *Oreochromis niloticus baringoensis*. Additionally, domestication and breeding trials for the African lungfish (*Protopterus aethiopicus*) are ongoing (DeBruyn, 2022).

Beyond tilapia, catfish, carp, and trout, aquaculture in Kenya is gradually diversifying to include high-value species such as prawns, ornamental fish, and indigenous cichlids (Obiero et al., 2019). Nile tilapia (*Oreochromis niloticus*), making up over 70% of farmed fish, is favored due to its rapid growth, adaptability to different culture systems, and strong consumer preference (Njiru et al., 2021; Elsayad et al., 2024). Catfish farming is gaining ground in urban markets due to its high protein content, relatively short grow-out period, and resistance to disease (Opiyo et al., 2018; Munguti et al., 2024).

Common carp (*Cyprinus carpio*), while less popular among Kenyan consumers, plays a crucial role in polyculture systems where it enhances pond productivity by feeding on benthic organisms and contributing to nutrient recycling.

Rainbow trout (*Oncorhynchus mykiss*) farming remains niche, targeting high-value tourist and hotel markets in Mount Kenya, the Aberdares, and the Rift Valley, where cold-water conditions are favorable (Jahangiri et al., 2021); KMFRI, 2019). Emerging interest in indigenous species such as *Labeo victorianus* (commonly known as "ningu") demonstrates growing awareness of biodiversity conservation and the need to promote native species in aquaculture practices (Aura et al., 2018). Market studies reveal that Nile tilapia and African catfish together account for over 90% of farmed fish consumed domestically (Njiru et al., 2021). Catfish, being highly resilient, has been identified as a candidate species for scaling aquaculture in arid and semi-arid regions of Kenya where water scarcity limits tilapia production (Opiyo et al., 2018). Ornamental fish farming is increasingly gaining traction in urban centers such as Nairobi and Mombasa, tapping into regional and international aquarium markets (Nyonje et al., 2018; FAO, 2022).

2.4 Water Quality Parameters and Fish Health

Aquaculture has seen a significant shift from extensive methods to more intensive and semi-intensive systems, aiming for higher production outputs. However, intensification often brings an increased risk of diseases, which can lead to substantial losses, especially for new farmers. While diseases are a significant limiting factor in fish production, most pathogens are naturally present in aquatic systems and only become problematic when environmental conditions or husbandry practices deteriorate. Fluctuations in water quality are a key stressor that can trigger disease outbreaks and compromise fish health (Boyd & Tucker, 2014; Conte, 2004; Jobling, 2012).

Several studies have emphasized the impact of poor water quality on disease prevalence in fish farms. (Svobodova et al., 1993) highlighted that water quality is a fundamental determinant of fish health, directly influencing feed efficiency, growth, and survival. Furthermore, (Ngugi et al., 2007) noted that fluctuations in water quality parameters such as dissolved oxygen, pH, and ammonia can exacerbate stress, reduce disease resistance, and result in high mortality rates in farmed fish.

(Abdelrhman et al., 2022) found that approximately 90% of fish diseases in controlled aquaculture environments are linked to improper husbandry practices and inadequate biosecurity measures. Poor management of water quality parameters often leads to stress, making fish more susceptible to infections by parasites, bacteria, and viruses (Boyd & Tucker, 2014; Dhawan & Kaur, 2002; Jobling, 2012). (Dhawan & Kaur, 2002) also observed that chemical imbalances in water, such as elevated ammonia levels, impair the physiological functions of fish, including osmoregulation and respiration, further increasing the risk of disease outbreaks.

Water quality remains a central determinant of aquaculture productivity. Technologies such as automated sensors and mobile phone-based monitoring tools are being introduced to allow farmers to track dissolved oxygen, temperature, and pH in real time (Ebeling & Timmons, 2012). Climate change poses additional risks, as rising temperatures may increase susceptibility to fish diseases (Boyd & Tucker, 2014). Comparisons between farms in Lake Victoria and recirculating aquaculture systems (RAS) in Nairobi show stark differences in management: while open systems struggle with algal blooms, pollution, and dissolved oxygen fluctuations, controlled RAS systems achieve higher survival rates due to stable water quality parameters (Ogello et al., 2013; Njiru et al., 2021). Future management strategies must emphasize eco-friendly biofilters, renewable

energy–powered aeration, and farmer training on disease prevention to reduce reliance on antibiotics (Boyd et al., 2020; Rico et al., 2012).

Climate variability is emerging as a critical factor affecting water quality in Kenya's aquaculture. Rising temperatures accelerate algal blooms and oxygen depletion, particularly in open pond and cage systems (Boyd, 2019). In contrast, controlled RAS farms around Nairobi mitigate these risks, though at higher energy costs (Ogello et al., 2013). International comparisons show that climate-smart aquaculture practices, such as biofloc systems in India and integrated multi-trophic aquaculture (IMTA) in Norway, could be adapted in Kenya to improve resilience (Avnimelech, 2009; FAO, 2021).

2.4.1 Importance of Water Quality in Aquaculture

Water quality is fundamental to the health, growth, and survival of fish in aquaculture systems. The physical, chemical, and biological characteristics of water directly influence vital processes such as metabolism, immune response, and feed utilization efficiency in fish. (Boyd, 2017) emphasized that water quality is the most critical factor limiting fish production in aquaculture. Poor water quality can lead to stress, which compromises fish immunity, reduces resistance to diseases, and negatively affects fish overall health.

Maintaining optimal water quality is essential for achieving high production and ensuring fish welfare. (Svobodova et al., 1993) noted that optimal water conditions significantly improve feed conversion efficiency, growth rates, and fish survival. Critical water quality parameters that require constant monitoring include dissolved oxygen (DO), temperature, pH, ammonia levels, and alkalinity. These parameters not only influence fish physiology but also affect microbial dynamics and waste decomposition in aquatic

systems (Omweno & Omondi, 2024).

(Conte, 2004) highlighted that fluctuations in water quality, especially in intensive aquaculture systems, are a major cause of stress for fish, leading to increased vulnerability to pathogens and parasites. (Dhawan & Kaur, 2002) also reported that poor water quality management, such as high ammonia concentrations and low DO levels, can result in respiratory problems, impaired growth, and increased mortality rates of fish. Ensuring optimal water quality conditions not only improves fish health but also enhances overall farm profitability by reducing disease outbreaks and mortality.

In addition, (Boyd & Tucker, 2014) emphasized that different fish species have unique tolerance limits for water quality parameters. For instance, Nile tilapia thrive in water with DO levels above 3 mg/L, a temperature range between 20 - 35°C, and a pH range of 6.5 - 9.0. Failure to maintain these optimal conditions can result in reduced growth and survival, as well as increased susceptibility to diseases.

2.4.2 Common Water Quality Parameters and Their Effects in Aquaculture

2.4.2.1 Dissolved Oxygen (DO)

Dissolved oxygen (DO) is vital for fish respiration, metabolism, and overall health. Adequate DO levels are necessary for maintaining fish health, with most species requiring concentrations above 3 mg/L. Low DO can cause hypoxia, stress, and increased disease susceptibility (Boyd & Tucker, 2012; Ngugi et al., 2007) Oxygen depletion is often exacerbated by overfeeding, high stocking densities, and organic waste accumulation (Rahat et al., 2022). Hypoxic conditions force fish to the water surface, making them more susceptible to pathogens (Boyd & Tucker, 2014).

2.4.2.2 Temperature

Temperature affects metabolic rates, immune responses, and growth rates in fish. Different species have specific thermal ranges; for instance, Nile tilapia thrive at temperatures between 20°C and 35°C (Boyd & Tucker, 2014). Temperatures outside this range can cause stress, reduced growth, and increased disease risk (Oliveira et al., 2024). Sudden fluctuations in temperature can destabilize fish physiology and lead to higher mortality rates. For example, cold-water species, like trout, require lower temperatures to thrive (Thompson et al., 2024).

2.4.2.3 pH and Alkalinity

The pH level of water affects nutrient availability, fish physiology, and the toxicity of compounds like ammonia. Most freshwater species, including Nile tilapia, prefer pH levels between 6.5 and 9.0 (Boyd & Tucker, 2014; Ngugi et al., 2007). Alkalinity helps buffer pH changes and should be maintained at or above 40 mg/L (Kasper et al., 2022). Extreme pH levels can disrupt osmoregulation, reduce oxygen uptake, and increase stress, making fish more vulnerable to diseases (Boyd, 2017).

2.4.2.4 Ammonia

Ammonia, a byproduct of organic matter decomposition, is toxic to fish, particularly in its un-ionized form (NH_3). High pH and temperature levels exacerbate ammonia toxicity, and concentrations should be kept below 0.5 mg/L to prevent gill damage and respiratory distress (Colt, 2006; Reed et al., 2009). Chronic exposure to high ammonia levels can lead to slow growth and increased mortality (Dalsgaard et al., 2013). Effective

waste management and filtration are critical to controlling ammonia levels (Elsayad et al., 2024).

2.4.2.5 Nitrite and Nitrate

Nitrite (NO_2^-) and nitrate (NO_3^-) are intermediate and final products of the nitrogen cycle. Nitrite toxicity can lead to "brown blood disease," and levels should be kept below 0.1 mg/L. Nitrate, though less toxic, can still be harmful at concentrations above 50 mg/L, impacting fish growth and reproduction (Rabalais & Baustian, 2020). Effective filtration and regular water exchanges are essential for managing these compounds (Boyd & Tucker, 2014).

2.4.2.6 Hardness

Water hardness, measured by calcium and magnesium concentrations, is important for fish osmoregulation and health. Adequate hardness levels (50-200 mg/L $CaCO_3$) are necessary for stable and healthy aquaculture conditions (Boyd & Tucker, 2014). Soft water can lead to stress and ion loss in fish, affecting their health and growth (Bhatnagar & Devi, 2013; Elsayad et al., 2024).

2.4.2.7 Carbon Dioxide (CO_2)

Excess CO_2 in aquaculture systems can lead to respiratory stress in fish by reducing their ability to absorb oxygen. Elevated CO_2 levels (above 15 mg/L) can cause hypercapnia and acidosis, negatively impacting fish health and growth (Colt, 2006). Proper aeration and CO_2 management are crucial in intensive systems (Zheng et al., 2023).

2.4.2.8 Salinity

Salinity is a critical parameter for brackish and marine species. Changes in salinity affect osmotic regulation and can lead to stress if not managed properly. Freshwater species like Nile tilapia prefer salinity levels below 5 ppt, while marine species thrive at higher salinities (Wood et al., 1984). Sudden changes in salinity can cause osmotic stress and increase disease susceptibility (Boyd, 2017).

2.4.3 Causes of Water Quality Deterioration

2.4.3.1 Poor Pond Management Practices

Improper pond management is a significant factor contributing to water quality deterioration. Over-application of fertilizers, manures, and feed can lead to excessive nutrient loading in the water. This excess organic matter decomposes, consuming oxygen and producing harmful by-products like ammonia and hydrogen sulfide (Boyd et al., 2020; Liti et al., 2005). These by-products can create an environment conducive to pathogen proliferation and stress the fish. Inefficient waste removal practices exacerbate these issues, leading to rapid declines in water quality (Boyd & Tucker, 2014; Chen et al., 2022).

2.4.3.2 Effects of Intensification of Aquaculture on Water Quality

The shift towards more intensive aquaculture systems has heightened concerns regarding water quality. High stocking densities typical of intensive systems lead to increased organic waste, which in turn raises the biochemical oxygen demand (BOD) of the water. Elevated BOD can reduce dissolved oxygen (DO) levels, making the water unsuitable

for fish survival (Kasozi et al., 2024). Intensive systems require diligent monitoring and management of water quality parameters to maintain optimal conditions and minimize stress on fish (Sherif et al., 2021; Cheng et al., 2025).

2.4.3.3 Impact of Poor Water Quality on Fish Health

Poor water quality directly impacts fish health by inducing stress and weakening the immune system. (Jobling, 2012) found that while fish with latent infections can generally maintain health under optimal conditions, suboptimal water quality can trigger the expression of diseases, leading to increased mortality rates. Chemical imbalances, such as high ammonia levels, can damage gill tissues, impair respiration, and disrupt normal physiological functions (Boyd & Tucker, 2012; Colt, 2006). Poor water quality can also compromise the protective barrier of fish skin, facilitating parasite invasions (Aly et al., 2024).

Stress caused by hypoxia, extreme pH levels, or fluctuating temperatures increases cortisol production, which suppresses immunity and makes fish more susceptible to bacterial, viral, and parasitic infections. Prolonged exposure to poor water quality also reduces feed conversion efficiency, stunts growth, and increases deformities in farmed fish (Ebeling & Timmons, 2012). Furthermore, oxygen depletion and eutrophication in cage systems have been linked to outbreaks of *Aeromonas* spp. and *Flavobacterium columnare* (Rendueles & Ghigo, 2015). This shows that poor water quality is both a direct stressor and an indirect facilitator of disease outbreaks.

2.4.4 Mitigation Strategies for Water Quality Management

To enhance good water quality and prevent fish diseases, the following strategies should be implemented:

2.4.4.1 Regular Monitoring

Continuously monitor key water quality parameters, including DO, temperature, pH, and ammonia levels, to ensure they remain within optimal ranges (Elsayad et al., 2024; Ahmed et al., 2018). Digital tools such as handheld water meters, automated sensors, and mobile phone apps are now being tested in Kenya and Nigeria to give farmers real-time alerts. These technologies have reduced mortality by up to 25% and improved productivity (Action, 2020; FAO, 2022).

2.4.4.2 Optimal Stocking Densities

Maintain appropriate stocking densities to prevent excessive organic waste accumulation, which can degrade water quality (Oliveira et al., 2024; Sherif et al., 2021). Overstocking has been linked to higher aggression, oxygen depletion, and stress among fish. Studies in Egypt showed that reducing stocking density by 20% improved growth rates by 15% and reduced mortality (Elsayad et al., 2024).

2.4.4.3 Pond Cleaning

Regularly remove excess organic matter and waste from ponds to prevent nutrient overload and maintain water quality (Huicab-Pech et al., 2016). Best practices include drying and liming ponds between cycles, adjusting feeding rates to avoid waste, and using

integrated aquaculture–agriculture (IAA) systems where pond effluents fertilize crops rather than pollute natural water bodies (Munguti et al., 2021).

2.4.4.4 Aeration

Use aeration devices to enhance DO levels in the water, particularly in intensive systems where high stocking densities and waste production can lead to oxygen depletion (Chen et al., 2022). Solar-powered aeration systems are being piloted in Kenya to reduce energy costs while maintaining oxygen levels (Njiru et al., 2021). Proper aeration not only improves DO but also minimizes ammonia buildup and improves feed efficiency (DeBruyn, 2022).

2.4.4.5 Biosecurity Measures

The threat of fish diseases is universal across aquaculture systems. Kenya's aquaculture sector faces bacterial infections such as *Aeromonas hydrophila* (causing Aeromoniasis) and viral threats like Tilapia Lake Virus (TiLV) (Opiyo et al., 2018). Comparative studies reveal that similar pathogens in Asia have caused multimillion-dollar losses, emphasizing the importance of preventive approaches (Jansen et al., 2019). Global best practices recommend a biosecurity framework involving quarantine of broodstock, vaccination programs, and real-time disease surveillance (Subasinghe & Chief, 2016; Kamau et al., 2020). Kenya has yet to adopt fish vaccines on a large scale, but pilot projects by KMFRI and Egerton University are ongoing (Njiru et al., 2021). Antimicrobial resistance (AMR) remains a concern; misuse of antibiotics could threaten both aquaculture and public health (Rico et al., 2012). Alternative approaches such as probiotics, herbal treatments, and selective breeding for disease-resistant strains are promising areas of

research (Hasan et al., 2023).

The socio-economic cost of fish disease outbreaks in Kenya is under-researched. However, extrapolations from similar outbreaks in Uganda and Nigeria suggest losses ranging between 10–15% of annual farm output. Recent cases of Tilapia Lake Virus (TiLV) in East Africa highlight the urgent need for surveillance systems (Njiru et al., 2021). Global experiences in Chile's salmon industry emphasize the necessity of vaccination, strict biosecurity, and coordinated disease monitoring strategies to safeguard the industry. Implement robust biosecurity practices to prevent the introduction and spread of pathogens, which can exacerbate water quality issues and impact fish health (Elsayad et al., 2024; Huicab-Pech et al., 2016).

2.5 Pathogenic Parasites and Microbes in Aquaculture

Fish are susceptible to a broad spectrum of diseases, similar to other animals, which can be categorized into diseases caused by external agents and internal disorders. External pathogens include viruses, bacteria, fungi, and parasites, while internal issues involve organic and degenerative conditions (Mwangi et al., 2024). Infestations by pathogenic bacteria, viruses, parasites, and fungi, can lead to high mortality rates, economic losses, and compromised product quality (Akter et al., 2023). Common symptoms associated with these infections include weight loss, reproductive impairment, blindness, abnormal behavior, epithelial lesions, and gill deformities (Aloo, 2002; Kamundia et al., 2008). These health issues can result in significant economic losses for the fish farming industry, making them critical factors in production decline (Singh et al., 2024; Yadav et al., 2023).

2.5.1 Bacterial Diseases

Bacterial infections are a significant concern in aquaculture, with various pathogens causing severe diseases that can impact fish health and farm productivity. These bacteria, typically saprophytic in nature, become pathogenic under conditions where fish are physiologically stressed, nutritionally imbalanced, or exposed to other stressors such as poor water quality and overstocking (Sandeep et al., 2022). Such stress factors create an environment conducive to opportunistic bacterial infections, which are particularly problematic in fish at various life stages, including eggs, fry, and fingerlings, often resulting in high mortality rates (Kumar et al., 2024; Cheng et al., 2025).

Bacterial infections are among the leading causes of economic losses in aquaculture worldwide, accounting for nearly 50% of disease-related mortalities in freshwater production systems (Austin & Austin, 2012). In Kenya, bacterial diseases have been reported in farmed tilapia and catfish, with outbreaks often linked to poorly managed ponds and cage systems (Opiyo et al., 2018). The misuse of antibiotics to treat bacterial infections is also a concern, as it contributes to the rise of antimicrobial resistance (AMR), posing risks to fish health, farm productivity, and public health (Rico et al., 2012; Sardar et al., 2025). This underscores the need for integrated health management strategies that focus on prevention rather than treatment.

One notable example is Ulcerative Disease Syndrome (EUS), which has been particularly devastating in Southeast Asia. EUS outbreaks have led to significant economic losses, with estimated damages of approximately USD 10 million in Thailand and over USD 3 million in Bangladesh (Singh et al., 2024; Thakur et al., 2023). This underscores the critical need for effective management and control strategies to mitigate the impact

of bacterial diseases in aquaculture systems. Although EUS has not been widely documented in Kenya, there is evidence that climate variability, increased intensification, and cross-border fish trade could increase the risk of its introduction (Njiru et al., 2021). Strengthening national fish health surveillance systems, laboratory capacity, and farmer training in early disease recognition are essential to prevent future outbreaks.

2.5.1.1 *Aeromonas* spp.

Aeromonas hydrophila is a prominent pathogen in freshwater fish, responsible for causing hemorrhagic septicemia and ulcerative conditions. Infections with this bacterium lead to severe skin ulcers, internal hemorrhages, and extensive organ damage. The disease is exacerbated by poor water quality and high stocking densities (Austin & Austin, 2012; Stankus, 2021; Yan et al., 2023). Field studies in East Africa have confirmed outbreaks of Aeromonas infections in tilapia and African catfish farms, often associated with poor pond management and elevated organic matter (Opiyo et al., 2018). Preventive measures include good water quality management, use of probiotics, and selective breeding for disease resistance.

2.5.1.2 *Flavobacterium columnare*

This bacterium is the causative agent of columnaris disease, which is characterized by gill necrosis, skin lesions, and fin erosion. Factors such as poor water quality and high fish density increase the likelihood of outbreaks (Declercq et al., 2013; Thompson et al., 2024). Columnaris disease is particularly devastating in fingerlings and fry, where mortality can exceed 70% in uncontrolled outbreaks. In Kenya, *Flavobacterium* spp. have been isolated in hatcheries, raising concern about the biosecurity of seed production

systems (Njiru et al., 2021).

2.5.1.3 *Vibrio* spp.

Vibrio anguillarum and *Vibrio vulnificus* are major pathogens in marine and brackish water fish, causing vibriosis. Symptoms include hemorrhagic septicemia and skin lesions. Vibrio infections are often associated with environmental stress and poor husbandry practices (Mohamed et al., 2025; Toranzo et al., 2005). While vibriosis is more common in marine aquaculture systems, concerns have been raised about its potential spread through ballast water and regional fish trade. Preventive measures include vaccination, use of immunostimulants, and strict regulation of aquaculture effluents (Subasinghe & Chief, 2016). Streptococcosis is one of the most important bacterial diseases in tilapia aquaculture globally, with outbreaks reported in Asia, the Middle East, and parts of Africa. Losses are estimated to exceed USD 150 million annually in intensive tilapia farms (Amhed et al., 2022). Although not yet widely reported in Kenya, increased intensification and warming water temperatures could make local systems vulnerable. This highlights the importance of proactive monitoring and potential adoption of vaccines currently in use in other regions.

2.5.1.4 *Streptococcus iniae*

This bacterium causes streptococcosis, which is marked by erratic swimming, exophthalmia, and hemorrhages in various fish species. It often affects fish under stress or poor environmental conditions (Agnew & Barnes, 2007; Uma, 2025).

Bacterial diseases such as Ulcerative Disease Syndrome (EUS) and motile aeromon-

Table 2.1: Common Bacterial Diseases in Aquaculture (Haenen, 2017)

Disease Condition	Symptoms	Pathogens Involved
Columnaris Disease	Hemorrhagic and ulcerative lesions on fins, head, back.	*Flavobacterium columnare*
Tail and Fin Rot	Erosions, discoloration, and disintegration of fins and tails.	*Aeromonas hydrophila*, *Pseudomonas* spp.
Bacterial Gill Disease	Gasping, lethargy, discolored gills, secondary fungal infection.	*Flavobacterium branchiophilum*, *Cytophaga* spp.
Aeromoniasis	Hemorrhagic and ulcerative lesions on skin, fins, head.	*Aeromonas hydrophila*, *A. veronii* bv. *sobria*
Edwardsiellosis	Ulcerative abscesses in internal organs, hemorrhagic ulcers on skin.	*Edwardsiella tarda*
Vibriosis	Ulcerative abscesses, hemorrhagic ulcers on skin and internal organs.	*Vibrio anguillarum*, *V. parahaemolyticus*
Eye Disease	Cataracts, corneal damage, eyeball putrefaction.	*Aeromonas liquefaciens*, *Staphylococcus aureus*
Pseudomoniasis	Hemorrhagic lesions on skin, fins, tail.	*Pseudomonas* spp.
Enteric Red Mouth Disease	Hemorrhagic lesions around mouth, fins, tail, and internal hemorrhages.	*Yersinia ruckeri*

ads septicaemia are particularly impactful in aquaculture, especially in Southeast Asia, where they have caused significant economic losses (Kalaria et al., 2024; Mohanty & Sahoo, 2007). Effective management of these diseases involves maintaining optimal water quality, implementing robust biosecurity measures, and regular health monitoring.

EUS, caused by a combination of fungal and bacterial pathogens, has been responsible for mass mortalities in freshwater fish such as carp and catfish, leading to trade restrictions in several Asian countries (Thakur et al., 2023). Motile aeromonads septicaemia, primarily caused by *A. hydrophila*, remains one of the most common bacterial diseases in freshwater aquaculture worldwide, characterized by hemorrhagic lesions, fin rot, and internal organ damage (Austin & Austin, 2012). Both diseases are often triggered by

environmental stressors such as poor water quality, overcrowding, and sudden temperature fluctuations, underscoring the strong link between farm management practices and disease outbreaks (Opiyo et al., 2018; Njiru et al., 2021). Preventive strategies that have proven effective include the use of probiotics, vaccination trials, and selective breeding of resistant fish strains (Abbas et al., 2023). In Kenya, while large-scale EUS outbreaks have not been documented, cases of bacterial infections linked to *Aeromonas* spp. have been reported in tilapia and catfish farms, highlighting the need for early detection systems and farmer training in fish health management (Obwanga et al., 2020).

2.5.2 Viral Diseases

Viral infections can cause devastating outbreaks in aquaculture, leading to high mortality rates. Unlike bacterial diseases, viral infections often have no effective treatment, making prevention, strict biosecurity, and early detection the most important control measures (Abwao et al., 2023). The rapid intensification of aquaculture, coupled with global fish trade and climate variability, has increased the risk of viral pathogens spreading across regions. In Kenya, viral diseases remain under-reported due to limited diagnostic capacity, but the growing adoption of intensive cage culture and recirculating aquaculture systems raises concern about their possible emergence (Njiru et al., 2021). Pilot studies by KMFRI and regional laboratories have emphasized the urgent need for viral surveillance programs and farmer sensitization on quarantine measures.

2.5.2.1 Infectious Hematopoietic Necrosis Virus (IHNV)

This virus primarily affects salmonids, causing anemia, hemorrhages, and high juvenile mortality rates. IHNV outbreaks can result in significant economic losses (Wolf

& Wolfe, 2005). IHNV has historically been one of the most destructive viral diseases in salmonid hatcheries in North America and Europe, with some outbreaks leading to losses exceeding 90% of stocked fry (Kumar et al., 2024). Transmission occurs both horizontally through water and vertically via infected gametes, making broodstock screening critical for prevention. While Kenya does not culture salmonids at scale, small-scale trout farms in the Rift Valley could be vulnerable if biosecurity measures are not strengthened.

2.5.2.2 Infectious Pancreatic Necrosis Virus (IPNV)

IPNV affects a wide range of fish species, including salmonids, leading to necrosis of the pancreas and other organs. Symptoms include abdominal distension and hemorrhages (Dopazo, 2020; Reno, 2001). Outbreaks of IPNV are particularly severe in young fish, where mortality rates range between 10% and 90% depending on environmental stress factors (Bandyopadhyay, 2022). The virus is highly resistant, persisting in water and equipment for long periods, which complicates eradication efforts. Globally, selective breeding of resistant strains and vaccination have reduced IPNV prevalence, providing lessons that Kenya could adopt as it expands its aquaculture sector.

2.5.2.3 Koi Herpesvirus (KHV)

KHV is known for causing high mortality in koi and common carp. It leads to gill necrosis and erratic swimming behavior, with severe outbreaks in crowded conditions (Haenen, 2017; Fijan, 1972). KHV has spread rapidly worldwide since its first detection in the 1990s, and it remains a serious threat to ornamental and food carp production (Haenen, 2017). Mortality rates can exceed 80%, especially in poorly managed systems

(Sing et al., 2025). In Kenya, the growing interest in ornamental fish farming in Nairobi and Mombasa poses a potential biosecurity risk if imported broodstock are not properly screened (Nyonje et al., 2018; Njiru et al., 2021). Lessons from Japan and Israel, where strict quarantine protocols have reduced KHV outbreaks, highlight the importance of strong national regulatory frameworks.

2.5.2.4 Viral Hemorrhagic Septicemia Virus (VHSV)

VHSV affects various fish species, causing viral hemorrhagic septicemia characterized by hemorrhages, ascites, and high mortality rates (Mugimba et al., 2021). VHSV has been reported in more than 80 marine and freshwater fish species globally (Awuor et al., 2021). It poses a significant risk to both wild and farmed fish populations, with potential ecological as well as economic impacts. Although not yet detected in Kenya, regional studies have suggested that climate variability and increasing aquaculture intensification could facilitate its emergence. Preventive measures include strict control of live fish movement, improved diagnostic capacity, and investment in regional reference laboratories (FAO, 2021).

2.5.3 Parasitic Diseases

Parasitic infestations pose significant challenges to fish production systems, particularly in freshwater aquaculture, where they have become a major concern. Parasitic diseases can severely impact fish health, growth, and overall productivity, leading to considerable economic losses in aquaculture operations (Abbas et al., 2023; Mohanty & Sahoo, 2007).

Parasitic organisms, including protozoan ciliates, monogenetic trematodes, and crus-

tacean ectoparasites, multiply rapidly under favorable conditions, causing extensive damage to their hosts. Notable protozoan parasites include *Ichthyophthirius multifiliis*, which causes "white spot" or "ich" disease in freshwater fish, leading to severe irritation and respiratory distress (Walker & Mohan, 2009). *Trichodina spp.* are also significant, as they damage fish gills and skin by feeding on dead tissue, necessitating frequent chemical treatments for control (Bacharach et al., 2016; Lian et al., 2023). Monogenetic trematodes such as *Dactylogyrus spp.* (gill flukes) and *Gyrodactylus spp.* (skin flukes) are prevalent in freshwater systems. These parasites cause irritation and destruction of gill tissues, impairing respiration and overall health (Ferreira et al., 2022; Sandeep et al., 2022). The economic impact of these parasites is significant, with reports indicating substantial losses in aquaculture productivity due to their presence (Mohanty & Sahoo, 2007; Shigoley et al., 2024).

Crustacean ectoparasites, such as Argulus spp., commonly known as freshwater fish lice, also cause severe damage. Argulosis can lead to dermal ulceration, osmotic imbalance, and increased susceptibility to secondary infections, although mass mortality rates are relatively low (Monir et al., 2015; Thakur et al., 2023). The intensity of infestation by these parasites is often influenced by seasonal changes, which affect host physiology and ecology, further complicating management efforts (Abbas et al., 2023; Mukherjee, 2002).

Parasitic infections not only reduce fish survival but also lower feed conversion efficiency and overall growth rates, which significantly reduces farm profitability. Outbreaks of parasites in poorly managed ponds and cages have been associated with secondary bacterial and fungal infections, amplifying losses. In Kenya, *Trichodina* spp. and *Dactylogyrus* spp. have been reported in tilapia hatcheries, highlighting the urgent

need for better hatchery biosecurity (Opiyo et al., 2018; Njiru et al., 2021). Management strategies include regular pond drying and liming, controlled stocking densities, use of salt and formalin baths, and introduction of biological control methods such as cleaner fish. Climate change, by altering water temperatures and rainfall patterns, is also predicted to intensify parasite prevalence, necessitating adaptive management approaches in African aquaculture systems.

2.5.3.1 *Ichthyophthirius multifiliis*

Commonly known as "ich" or "white spot disease," this protozoan parasite affects freshwater fish, causing white cysts on the skin and gills. It leads to respiratory distress and high mortality (Ahmad, 2024a; Dickerson, 2006). Ich is regarded as one of the most economically important parasites in global freshwater aquaculture, with outbreaks capable of wiping out entire production cycles if untreated. It spreads rapidly in overcrowded ponds and recirculating aquaculture systems (RAS), especially under stress conditions such as low dissolved oxygen. Treatment methods include salt baths, formalin, and potassium permanganate applications, though prevention through biosecurity remains more sustainable.

2.5.3.2 *Cryptocaryon irritans*

Marine ich affects marine fish, causing white cysts, skin irritation, and respiratory distress. This parasite can be particularly devastating in densely stocked marine systems (Colorni & Burgess, 1997; Hossain et al., 2024). Outbreaks of Cryptocaryon are especially problematic in ornamental marine fish trade, where international transport of infected fish has accelerated its spread. Mortality rates can exceed 50% in severe cases,

and repeated outbreaks reduce market value of cultured fish (Yan et al., 2023). Quarantine of new stock and ultraviolet sterilization of water are widely recommended preventive measures.

2.5.3.3 Lernaea

spp. Known as anchor worms, these crustacean parasites attach to the skin and gills of fish, causing tissue damage and secondary infections (Ahmad, 2024b). Infestations by *Lernaea* spp. cause hemorrhages and deep ulcers, often serving as entry points for bacterial pathogens like *Aeromonas* spp. (Alhaji et al., 2024). They are particularly difficult to eradicate because of their burrowing life cycle. Control methods include chemical treatments (e.g., organophosphates) and breaking the life cycle by managing intermediate hosts.

2.5.3.4 *Gyrodactylus* spp.

Monogenean parasites that affect the skin and gills, leading to gyrodactylosis. Symptoms include increased mucus production, skin lesions, and respiratory distress (Ahmad, 2024a; Bakke et al., 2007). *Gyrodactylus salaris* has been especially devastating in salmonid populations in Europe, causing near-total stock losses in some rivers (Moges & Dibaba, 2024). In tilapia systems, heavy infestations of *Gyrodactylus* spp. impair respiration and increase vulnerability to bacterial co-infections. Preventive measures include disinfection of equipment, reduction of fish densities, and use of resistant strains where available (FAO, 2021).

Parasitic infestations, such as those caused by *Gyrodactylus* spp. and *Ichthyophthirius*

Table 2.2: Common Parasitic Diseases in Aquaculture (Source: (Austin & Austin, 2012))

Disease Condition	Symptoms	Pathogens Involved
Ichthyophthiriasis (Ich)	Whitish cysts on skin, fins, and gills.	*Ichthyophthirius multifiliis*
Trichodiniasis	Whitish cysts on skin, fins, and gills.	*Trichodina* spp.
Dactylogyrosis (Gill Fluke)	Destruction of gill filaments, white masses on gills.	*Dactylogyrus* spp.
Gyrodactylosis (Skin Fluke)	Destruction of skin and gills with white masses.	*Gyrodactylus* spp.
Argulosis (Carp Lice)	Skin lesions, secondary bacterial infections, hemorrhagic spots.	*Argulus* spp.
Myxosporidiasis	Cysts on body, internal organs, and gill filaments.	*Myxosporidium* spp.

multifiliis, can result in severe health issues and economic losses in aquaculture systems (Ferreira et al., 2022; Sandeep et al., 2022). For example, Argulosis caused by *Argulus* spp. leads to dermal ulceration and physiological stress (Monir et al., 2015; Mukherjee, 2002).

Overall, parasitic infestations can lead to reduced growth rates, lower feed conversion ratios, increased susceptibility to secondary infections, and other indirect effects that contribute to economic losses in aquaculture (Farhaduzzaman, 2010; Gautam et al., 2025). Effective management and control strategies are crucial to mitigate these impacts and ensure the sustainability of aquaculture systems.

2.5.4 Fungal Diseases

Although less common, fungal infections can still pose significant challenges in aquaculture:

2.5.4.1 *Saprolegnia* spp.

Causes saprolegniosis, characterized by cotton-like fungal growths on the skin, gills, and eggs of fish. This disease often affects fish under stress or with compromised immune systems (Thompson et al., 2024; Rodger, 2016). Saprolegniosis is one of the most frequently encountered fungal infections in hatcheries, where fish eggs are particularly vulnerable. Egg mortality due to Saprolegnia outbreaks can exceed 50% in the absence of treatment (Bwoga, 2021). Historically, malachite green was widely used for control, but its ban due to carcinogenicity has created a gap in effective antifungal treatments. Alternative management strategies now include the use of hydrogen peroxide, formalin, and natural plant extracts, which are showing promise in reducing infection rates. In East Africa, sporadic cases of saprolegniosis have been reported in Nile tilapia hatcheries, underscoring the importance of water quality and egg-handling practices (Njiru et al., 2021).

2.5.4.2 *Branchiomyces* spp.

Responsible for branchiomycosis or gill rot, leading to gill necrosis and respiratory distress. This fungus thrives in poor water conditions and can lead to high mortality rates (Fijan, 1972; Pachauri & Maurya, 2022). Branchiomycosis is strongly associated with eutrophic ponds where high levels of organic matter and elevated temperatures favor fungal proliferation. Outbreaks can result in sudden and massive fish kills, particularly in carp culture systems (Abdelrhman et al., 2022). Infected gills become necrotic and lose their capacity for oxygen exchange, leading to rapid asphyxiation. Preventive measures include good pond management, regular removal of organic sludge, and maintaining

stocking densities at sustainable levels. Though not yet widely reported in Kenya, the increasing intensification of pond and cage culture suggests a potential future risk.

2.5.4.3 *Aphanomyces invadans*

Causes epizootic ulcerative syndrome (EUS), affecting both freshwater and brackish water fish with severe skin ulcers and high mortality. EUS outbreaks are often associated with environmental stressors and poor water quality (Boyd, 2019; Choudhury et al., 2014; Singh et al., 2024). EUS is considered one of the most destructive fungal-like infections in aquaculture globally, first reported in Southeast Asia but now spreading to Africa and other regions (Alsulami & El-Saadony, 2024). The disease is caused by the oomycete *Aphanomyces invadans*, which invades muscle tissue, creating deep ulcers that predispose fish to secondary bacterial infections. Mortality rates can exceed 70% in uncontrolled outbreaks. The World Organisation for Animal Health (OIE) has listed EUS as a notifiable disease, requiring countries to report cases (OIE, 2019). In East Africa, suspected cases have been reported in wild and cultured fish, raising concerns for regional aquaculture sustainability (Opiyo et al., 2018).

Pathogenic microorganisms, including bacteria, viruses, parasites, and fungi, present significant challenges to aquaculture systems. These pathogens can lead to severe health issues, economic losses, and negatively impact fish welfare. To mitigate these risks, effective management strategies are crucial. This includes maintaining optimal water quality, implementing robust biosecurity measures, and conducting regular health monitoring. By addressing these challenges proactively, aquaculture practitioners can enhance fish health and improve the sustainability and productivity of their operations.

2.5.5 Fish Disease Management in Kenya

Fish disease management has become increasingly important in Kenya, especially in Uasin Gishu County and the North Rift region, due to the rapid growth of aquaculture as a key economic activity. The intensification of aquaculture, characterized by the increased stocking density of fish, has led to higher risks of disease outbreaks, which can have devastating effects on fish populations, fish farmers' livelihoods, and regional economies. Factors such as environmental stress, poor water quality, and the introduction of fish from different regions without proper health screening have been identified as primary contributors to the spread of fish diseases (Mohapatra et al., 2013; Opiyo et al., 2018). This situation is compounded by global concerns, including climate change, which exacerbates environmental stressors affecting fish health (Reid, 2019).

2.5.5.1 Factors Influencing Disease Outbreaks in Aquaculture

Fish diseases arise due to the interaction between the host (fish), pathogen (disease-causing agents), and the environment (such as water quality, temperature, and stress). These factors are illustrated in the host-pathogen-environment model (Bondad-Reantaso et al., 2005) (Figure 2.1).

Fluctuations in water quality are significant contributors to stress in fish, making them more susceptible to infections (Assefa & Abunna, 2018). Key pathogens identified in this region include *Aeromonas hydrophila* and *Streptococcus iniae*, which are responsible for bacterial infections in Nile tilapia and African catfish (Magondu et al., 2011).

The movement of live fish for aquaculture purposes, particularly the transportation of broodstock and fingerlings, further amplifies the risk of spreading diseases across re-

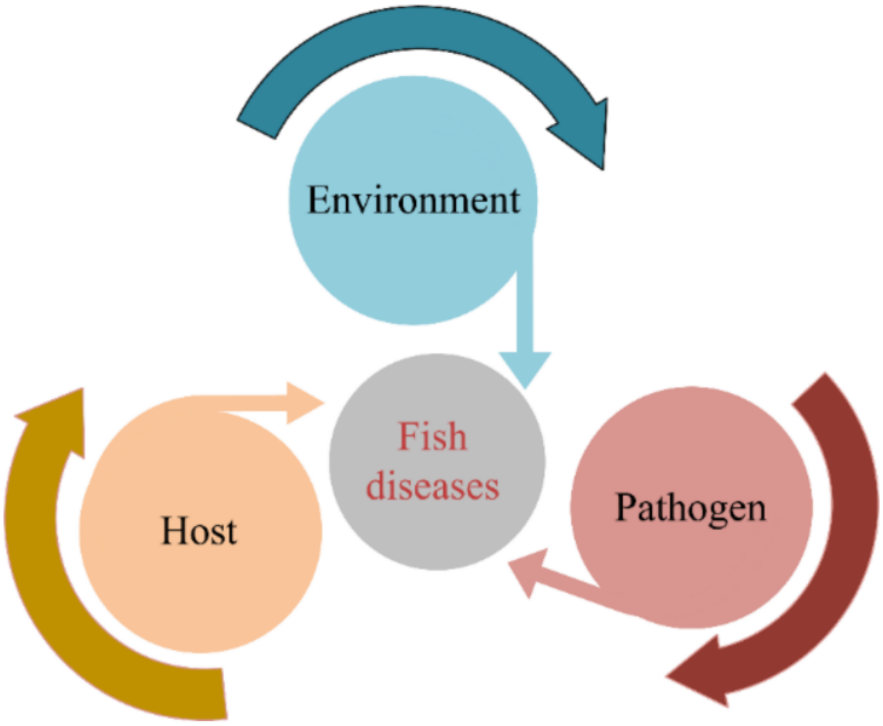


Figure 2.1: The interaction between host, pathogen, and environment in the development of fish diseases. Adapted from (Bondad-Reantaso et al., 2005)

gions and borders. This practice, while essential for the aquaculture industry, can inadvertently introduce new pathogens into local fish populations (Bondad-Reantaso et al., 2005). This translocation of fish without adequate quarantine measures has been recognized as a significant pathway for the introduction of both endemic and exotic diseases in Kenya (Opiyo et al., 2018).

Despite some advancements in aquaculture, fish disease management in Kenya still faces significant challenges, particularly in the North Rift region. One of the major issues is the limited capacity for disease diagnostics. Although policies exist that promote fish health management, the lack of diagnostic laboratories, quarantine facilities, and specialized expertise in fish diseases remains a significant bottleneck to effective disease management (Akoll & Mwanja, 2012). In Uasin Gishu County, for example, the absence of adequate disease surveillance infrastructure limits the timely detection of dis-

ease outbreaks, making it harder to manage and control infections effectively (Uasin Gishu Government, 2015).

2.5.5.2 Diagnostic and Management Challenges

Some farmers may resort to traditional knowledge and experience to manage diseases, often resorting to chemical treatments without accurate diagnoses of the underlying pathogens (Opiyo et al., 2023). This approach is unsustainable, as it may lead to the misuse of antibiotics and other chemicals, increasing the risk of antibiotic resistance in aquaculture systems (Nyonje et al., 2018; Subasinghe & Chief, 2016). As pointed out by (Thompson et al., 2024), the overuse of antibiotics like oxytetracycline - which is still common in some private hatcheries - poses serious risks, not only to fish populations but also to human health, as resistant bacteria can potentially be transmitted to humans through the consumption of contaminated fish.

2.5.5.3 Commonly Used Treatments and Concerns

In Uasin Gishu County, fish farmers rely on several prophylactic measures to reduce the likelihood of disease outbreaks. Common chemicals used include potassium permanganate and sodium chloride to eliminate bacterial and fungal infections (DeBruyn, 2022). However, the over-reliance on chemical treatments is concerning, as it not only increases the risk of developing resistant pathogens but also has detrimental effects on the aquatic environment (Henriksson et al., 2018).

To address this, there is a growing emphasis on alternative, non-antibiotic-based disease management strategies. Research conducted in Kenya and other parts of East Africa

has shown that plant-based compounds with antimicrobial properties can be used effectively as preventive measures against bacterial infections (Ndegwa et al., 2025). These natural treatments, which include the use of indigenous plant extracts, provide a more sustainable solution for managing fish diseases in the region (Opiyo et al., 2018).

The future of fish disease management in Uasin Gishu County and the North Rift region lies in a multi-pronged approach that emphasizes preventive measures, improved surveillance, and sustainable treatments. Enhanced disease surveillance is essential to monitor fish health and detect emerging pathogens in real time. Government agencies, such as the Kenya Marine and Fisheries Research Institute (KMFRI), are currently working on programs to improve disease surveillance in aquaculture systems across the country, with a focus on regions like Uasin Gishu (kenyaFisheriesService2025). Farmers and extension officers need training on best practices for disease management, including the proper use of chemicals and non-antibiotic treatments. Strict biosecurity protocols should be enforced to minimize the spread of diseases, especially during the transportation of live fish between regions. Quarantine facilities must be established to monitor and screen fish before they are introduced to new environments.

There is also a growing need to invest in the development of vaccines against key fish pathogens, which could drastically reduce the reliance on chemical treatments and antibiotics in aquaculture (Henriksson et al., 2018; Opiyo et al., 2018). As of 2023, workshops and educational initiatives led by the Food and Agriculture Organization (FAO) and local research institutes have been rolled out to raise awareness on biosecurity measures and best practices for disease prevention in aquaculture. In 2024, KMFRI is expected to launch a comprehensive fish disease surveillance program that will involve real-time monitoring of disease outbreaks in key aquaculture regions, including Uasin

Gishu County (Kenya Fisheries Service, 2025; Opiyo et al., 2023).

Research on the use of plant-based alternatives for fish disease management continues to gain traction, with local universities and research centers exploring various indigenous plants that exhibit antimicrobial properties (Ndegwa et al., 2025). These developments provide hope for a more sustainable future in aquaculture disease management.

2.5.5.4 Challenges in Fish Health Management in Kenya

Fish health management in Kenya is hindered by significant challenges, particularly due to the absence of quarantine facilities and insufficient biosecurity measures to monitor the introduction and spread of diseases. (Obwanga et al., 2020) emphasized that the lack of reported fish diseases, coupled with a shortage of specialized human resources in aquaculture health, discourages the establishment of necessary quarantine measures. This issue is exacerbated by the increasing importation of non-indigenous species, notably Nile tilapia broodstock, which elevates the risk of introducing diseases and parasites (Hamisi et al., 2024).

The inadequacy of biosecurity protocols to prevent the escape of cultured fish into wild habitats further jeopardizes local fish populations (Kubečka et al., 2016). Such escapes can lead to genetic dilution of native stocks and increased competition for resources (Ogello et al., 2013). The absence of robust biosecurity measures can facilitate the rapid spread of pathogens throughout the region, compromising both wild and cultured fish populations (Kubečka et al., 2016).

The detection of Tilapia Lake Virus (TiLV) in the Tanzanian and Ugandan parts of Lake Victoria highlights the vulnerability of farmed fish in cages to infectious diseases.

While there have been no clinical signs or mortality linked to TiLV in these regions, the virus has resulted in substantial losses in Nile tilapia stocks in countries such as Israel, Ecuador, and Egypt (Bacharach et al., 2016; Njiru et al., 2021). The risk is particularly pronounced given the intensification of cage culture in Lake Victoria, which creates open systems that facilitate pathogen exchange between cultured and wild fish (Munguti et al., 2021).

Kenya currently lacks specialized fish diagnostic laboratories recognized by the World Organization for Animal Health (OIE). Disease diagnostics are typically performed at local universities and public research institutions, including University of Eldoret, Moi, Kenyatta, Egerton, and Maseno Universities, as well as the Kenya Marine and Fisheries Research Institute (Syanya & Mathia, 2023). This fragmented diagnostic capacity can delay the response to disease outbreaks, making it difficult to manage fish health effectively (Munguti et al., 2021).

In light of the scarcity of fish disease specialists in Kenya, it is essential for aquaculture farmers to adopt preventative measures. These include maintaining optimal environmental conditions for fish, ensuring the stocking of healthy fish, utilizing high-quality feeds, and minimizing stress to mitigate disease risks in intensive farming systems (Petrikova et al., 2024; Syanya & Mathia, 2023). Moreover, there is a growing need for training programs aimed at enhancing the skills of local farmers and technicians in fish health management to improve overall aquaculture sustainability (Moges & Dibaba, 2024).

2.6 Antimicrobial Resistance in Fish Pathogens

Alongside the expansion of aquaculture, there is increased dependence on antimicrobials to control bacterial infections in farmed fish. Excessive and/or improper antibiotic use in

aquaculture has led to the selection and dissemination of antimicrobial-resistant bacteria, posing risks to aquatic animal health, environmental sustainability, and human wellbeing (Ljubojević Pelić et al., 2024). A wide range of fish pathogens have been shown to develop significant antimicrobial resistance (AMR), including *Aeromonas*, *Vibrio*, *Edwardsiella*, *Streptococcus*, and *Flavobacterium* species. For instance, multidrug-resistant (MDR) *A. hydrophila* has been isolated from farmed *C. gariepinus* in Africa, carrying -lactam, tetracycline, and sulfonamide resistance genes (Adah et al., 2024). In marine systems, *V. anguillarum* and *V. parahaemolyticus* exhibit resistance to ampicillin, tetracycline, and streptomycin, largely due to prolonged antibiotic exposure (Bhat & Altinok, 2023). *S. agalactiae* and *S. iniae*, important pathogens of tilapia, have also shown resistance to erythromycin and tetracyclines (Kelany et al., 2024).

Globally, AMR prevalence in aquaculture environments appears widespread. A meta-analysis covering 20 years of data from 749 point-prevalence surveys in Asia revealed that one-third of antimicrobial compounds tested displayed resistance rates above 50% (Zhao, 2024). Similar reviews from Africa indicate high rates of resistance to tetracyclines, ampicillin, gentamicin, and co-trimoxazole, suggesting that MDR bacteria are becoming common in fish farms (Adinortey et al., 2020). The development of resistance in fish pathogens follows well-characterized mechanisms. Resistance arises via target modification, enzymatic inactivation, or active efflux, and is often facilitated by mobile genetic elements, plasmids, integrons, and transposons, that promote horizontal gene transfer (HGT) between aquatic and terrestrial bacteria (Darshanbhai, 2018). These mobile elements frequently carry resistance determinants such as tet, sul, bla, and aadA genes, highlighting the role of aquaculture environments as gene reservoirs (Motlhalamme et al., 2024). The environmental dynamics of aquaculture contribute to

the persistence and dissemination of resistant bacteria. Residual antibiotics from feed or bath treatments enter sediments and surrounding waters, enabling the transfer of resistance genes to commensal and environmental bacteria (FAO, 2023). Inadequate farm-level biosecurity, along with the discharge of untreated effluents, exacerbates the spread of resistance through aquatic ecosystems. Although thorough cooking mitigates direct foodborne transmission, occupational exposure and the release of resistant bacteria into natural waters remain significant pathways of concern (Endale et al., 2023).

However, in the Kenyan context, the situation differs markedly. While antimicrobial use in terrestrial agriculture, particularly in livestock and poultry production, is well documented in regions such as Uasin Gishu County, antibiotic use for treating fish diseases in aquaculture is not a common practice. Farmers in this region generally rely on preventive measures such as maintaining good water quality, using high-quality feeds, and practicing proper pond hygiene rather than therapeutic antimicrobial treatments. This absence of antimicrobial use in fish farming reduces selective pressure for the emergence of resistant aquatic bacteria in the local aquaculture environment. Nevertheless, potential risks remain due to cross-contamination from surrounding agricultural runoff, where antibiotics used in crop and livestock production could enter fishponds via shared water sources or drainage systems (FAO, 2022). Consequently, monitoring of environmental antibiotic residues and resistance genes in Kenyan aquaculture systems remains important to ensure early detection and prevention of AMR introduction and spread. Surveillance systems for AMR in aquaculture remain fragmented globally and in Africa. Many countries lack harmonized programs for monitoring resistance in fish pathogens, and antimicrobial-susceptibility testing methods vary widely (Zhimin et al., 2024). The Food and Agriculture Organization (FAO, 2022) has developed regional guidelines em-

phasizing the need for standardized AMR surveillance within aquaculture and integration into national action plans. Kenya, being an emerging aquaculture producer, could benefit from adopting such frameworks to establish baseline data and inform policy interventions that prevent future AMR emergence in its fish production systems.

Multiple mitigation strategies are being explored to reduce antibiotic dependence in fish farming. Improved husbandry, optimized water quality, and strict biosecurity measures can lower disease incidence and antibiotic demand. Vaccination has proven effective for several bacterial diseases, including Vibrio and Aeromonas infections (Bhat & Altinok, 2023). Probiotics and immunostimulants also show potential for enhancing fish health and disease resistance, though large-scale field data remain limited (Ali et al., 2024). Novel approaches such as bacteriophage therapy and antimicrobial peptides are under investigation as additional non-antibiotic interventions (Endale et al., 2023). Despite these advances, several knowledge gaps persist. There is a need for harmonized global AMR surveillance protocols for aquatic pathogens, quantitative studies on gene transfer to human pathogens, and long-term environmental monitoring of antibiotic residues and resistance genes. In the Kenyan setting, future research should assess possible environmental transfer of AMR genes from livestock and crop sectors into aquaculture, even in the absence of direct antibiotic use in fish farming. Socioeconomic studies also indicate that fish farmers' awareness, training, and economic pressures influence antimicrobial practices, emphasizing that stewardship must integrate both technical and behavioral components (Ali et al., 2024).

CHAPTER THREE

MATERIALS AND METHODS

3.1 Study Area and Study Sites

3.1.1 Study Area

The study was conducted from May 2023 to April 2024 in selected fish farms across five sub-counties in Uasin Gishu County (UG). Uasin Gishu County is located in the northwest of the Great Rift Valley region, approximately 330 km northwest of Nairobi along the Kenya–Uganda highway (Basweti et al., 2009; Petrikova et al., 2024). It shares borders with Trans-Nzoia County to the north, Elgeyo-Marakwet and Baringo counties to the east, Kericho County to the south, Nandi County to the southwest, and Kakamega County to the west. Covering an area of 2,955 km^2, the county lies between longitude 34°50″E and 35°37″W and latitude 0°03″S and 0°55″N. The topography of UG is a highland plateau with several perennial rivers and swampy wetlands as seen in Figure 3.1).

The climate of Uasin Gishu County is characterized as cool and temperate, with annual temperatures ranging between 7 °C and 29 °C. The region experiences high and reliable rainfall, which is evenly distributed throughout the year, with an annual precipitation range of 624.9 mm to 1560.4 mm. The wettest months are April and May, while the driest months occur in January and February (Njonge, 2023). Uasin Gishu, along with the neighboring Trans-Nzoia, is considered Kenya's breadbasket due to extensive maize and wheat farming, which produces a significant proportion of the country's total harvest (Kimani, 2017). In addition, the county supports substantial milk and horticultural

production, as well as diversified livestock farming (Otieno, 2020).

Aquaculture has been expanding in Uasin Gishu County in the last decade, with 1,728 operational fish ponds covering a total area of 486,000 m^2, producing an estimated annual fish yield of 593,000 kg valued at Ksh. 285,900,000. Furthermore, various private and public dams support capture fisheries, yielding approximately 33,048 kg of fish annually, with an estimated market value of Ksh. 9,914,400 (Uasin Gishu Government, 2015). Most farmers practicing fish farming in the county use earthen ponds, liner ponds, and other water reservoirs owned either by individuals or registered groups. The predominant species reared in the 1,728 operational ponds is Nile tilapia (*Oreochromis niloticus*), although some farmers also culture African catfish (*Clarias gariepinus*) (Mwangi et al., 2024).

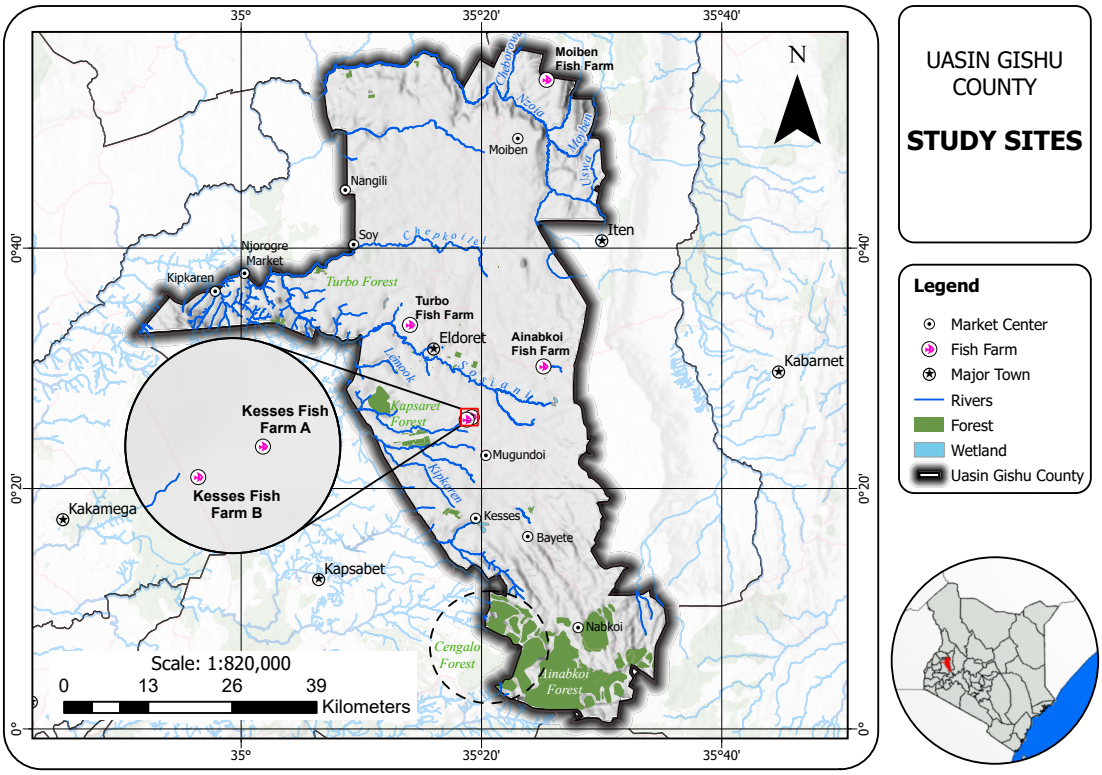


Figure 3.1: Map of Uasin Gishu showing its location in western Kenya with perennial rivers and swampy wetlands

3.1.2 Study Sites

The study was conducted in five operational aquaculture farms across four of the six sub-counties in Uasin Gishu County. The selection of the farms was based on their features such as; pond type, size, location, inputs (e.g., fertilisers, manure, or fish feeds), and duration of operation (minimum of one year) as shown in Table 3.1.

The study sites included Moiben farm in Moiben sub-county, which had a combination of raised liner and earthen ponds; Ainapkoi Farm Farm in Ainapkoi sub-county, which consisted of ground liner and earthen ponds; Kesses farm A Farm in Kesses sub-county, with raised liner ponds; Kesses farm B Farm in Kesses sub-county, with earthen ponds; and Turbo Farm Farm in Turbo Farm sub-county, which featured ground liner ponds. The details of the farms are summarized in Table 3.1.

Table 3.1: Location and Features of the Selected Fish farms in Uasin Gishu County where the study was carried out

Sub-County	Farm Name	Pond	Type of Pond
Moiben	Moiben Farm	1	Tank
		2	Earthen pond
		3	Earthen pond
		4	Earthen pond
Ainapkoi	Ainapkoi Farm	1	liner pond
		2	liner pond
		3	Earthen pond
Kesses	Kesses Farm A	1	Tank
		2	Tank pond
Kesses	Kesses Farm B	1	Earthen pond
		2	Earthen pond
Turbo	Turbo Farm	1	Ground liner pond
		2	liner pond

3.2 Study Design

3.2.1 Study Type

A longitudinal study design was used to evaluate the relationship between water quality parameters, parasite and microbial infestations, and pond management practices.

3.2.2 Sampling Method

A stratified random sampling approach was used to select fish farms, ensuring an equitable representation based on pond type, size, location, inputs used, and duration of operation

3.2.3 Sample Size

A total of 13 fish ponds in five fish farms across four sub-counties were sampled. Each farm was visited monthly for a duration of 12 months to enable seasonal data collection.

3.2.4 Study Population

The study population consisted of farmed fish from the selected fish farms in Uasin Gishu County, with a primary focus on Nile tilapia (*Oreochromis niloticus*).

3.3 Data Collection Methods

3.3.1 Physico-Chemical Parameters and Nutrient Sampling in Fish Pond Water

Physico-chemical parameters were measured in situ before the collection of water and fish samples to assess environmental conditions. The parameters evaluated included dissolved oxygen (mg/L), temperature (°C), pH, conductivity (µS/cm), and turbidity (NTU). Measurements were conducted using a Multi-probe HQ40D meter (HACH-LDO; PHC301 & CDC41), ensuring real-time data collection. Sampling occurred monthly

from May 2023 to April 2024, with readings taken between 6:00 AM and 6:00 PM to account for diurnal variations in water quality, which can influence pond dynamics and fish health (Njonge, 2023).

For nutrient analysis, water samples were collected in triplicates from each pond between 10am and 12pm, using 500 mL acid-washed plastic bottles to prevent contamination. These samples were immediately stored in cool boxes and transported to the laboratory for analysis. The parameters analyzed included ammonium nitrogen (NH_4-N), nitrate nitrogen (NH_3-N), nitrite nitrogen (NH_2-N), total nitrogen (TN), soluble reactive phosphorus (SRP), and total phosphorus (TP). Nutrient concentrations were determined calorimetrically by comparing sample absorbance values with known standards following guidelines from the American Public Health Association (APHA, 2023).

3.3.2 Determination of Nitrogen and Phosphorus

Total nitrogen and total phosphorus were measured using the wet combustion method described in the APHA (2023) guidelines, a widely used approach for determining nutrient concentrations in aquaculture environments (Mwangi et al., 2024).

Ammonium nitrogen (NH_4-N) was analyzed using the phenol-hypochlorite method (APHA, 2023), while nitrite nitrogen (NH_2-N) was determined through the sulphanilamide method. Nitrate nitrogen (NH_3-N) concentrations were measured using the sodium-salicylate method, with absorbance readings taken at 420 nm (Bhatnagar & Devi, 2013). Total nitrogen (TN) was determined using the persulphate oxidation method, which converts all nitrogen compounds in unfiltered water samples into nitrate for analysis at 220 and 275 nm.

Soluble reactive phosphorus (SRP) concentrations were measured using the ascorbic

acid method (APHA, 2023). Total phosphorus (TP) was determined by digesting unfiltered water samples with persulphate to convert all phosphorus into SRP, which was subsequently analyzed using the ascorbic acid method.

3.4 Fish Sampling

3.4.1 Sampling Method and Sample Size

The sample size for fish was determined following the Thrusfield formular (Thrusfield et al., 2017), with a 95% confidence interval and 5% absolute precision as shown in equation 1.

$$n = \frac{(1.96)^2 \cdot p(1-p)}{d^2} \tag{1}$$

where n is the required sample size, 1.96 is the standard deviation unit at confidence level of 95%, p is the expected prevalence, and d is the desired absolute precision.

Fish were sampled using seine nets with a mesh size of 1 mm, a length of 15m, and a width of 2 m, allowing for the collection of individuals across different size classes. Three (3) fish were selected randomly per pond from the sampled fish and transported in cool boxes to the laboratory for further analysis. The sampled fish from the 13 ponds from all the fish farms in a month was 39 and a total of 468 for the entire sampling period of 12 months.

3.4.2 Determination of the Fish Condition Factor

The Fulton's condition factor (K) was calculated to assess the health of the fish, using Froese formular (2006) as shown in equation 2.

$$K = \frac{100W}{L^3} \tag{2}$$

where W is the weight of the fish in grams and L is the total length in centimeters (Froese, 2006). The resulting values were compared with the reference scale provided by Barnham and Baxter.

3.4.3 Fish Tissue preparation

A total of 468 fish samples were randomly sampled from the ponds in the selected fish farms. Gross physical examination of the external features of the samples was done to check for abnormalities (if any); and the fish transported in cool box containers to the laboratory. The total length (cm) was measured using a measuring board; and weighed (g) using a digital balance (Model and Company/Manufacturer).

3.4.4 Bacterial Isolation and Identification

3.4.4.1 Sample processing and enrichment of bacteria

Aseptic measures were maintained during the sampling procedure for bacteria to prevent contamination of the samples. Three types of specimens were collected from different organs and locations of infected fish such as intestine, skin and gill, and examined using microbiological test. These specimens were placed on sterile chopping board and then properly minced and ground together. Ten (10) gm of samples were homogenized with 90 milliliters (ml) of freshly prepared 0.1% peptone water and 0.1 ml of the homogenized sample were inoculated according to standard methods on to selective media such as: Rimler Shotts Medium Base agar (*Aeromonas* spp.), Pseudomonas Base agar (for *Pseudomonas* spp), Thiosulfate citrate bile salt sucrose (TCBS) agar (*Vibrio* spp.), Tryptic Soy Agar (TSA) for enrichment of bacterial isolates, Brain Heart Infusion (BHI) Agar (for fastidious organisms) and incubated at 37°C for 24 hours. Pure isolates were characterized using morphological and biochemical tests, including Gram staining, ox-

idase, catalase, motility, indole, urease and citrate tests. The identification followed Bergey's manual of bacteriology (Bergey, 1994).

3.4.4.2 Identification of bacterial pathogens

Suspected bacterial colonies obtained from different culture plates were isolated and then streaked on TSA slants, MIU medium, Simon citrate agar slant and incubated overnight at 37°C. The pure isolates were identified by bacterial cell morphology, alkaline and acidic reaction, H2S (hydrogen sulfide production) and gas production, motility test, indole production, urease test, oxidase test, catalase test, Methyl Red (MR) test, and Voges Praskaure (VP) test. The Gram staining techniques were performed to identify Gram positive and Gram negative bacteria, while biochemical tests were carried out to identify the pathogens. The growth and identification of bacterial pathogens was done following Bergey's manual of Bacteriological classification (John, 1998) and bacterial isolates were subsequently stored for antibiotic susceptibility testing.

3.4.5 Fish Parasite Examination and Identification

The outer layer of the skin was scraped from the right and left sides of the back and posterior of the fish body, transferred on to a microscope slide, diluted with a drop of sterilized water, cover-slipped and examined under a microscope (Olympus CX40). Large parasites were expressed by their absolute numbers, while the microscopic parasites were expressed by decanting serially and determining their minimum, maximum and average numbers in each field of view of microscope at a definite magnification.

The intestines of fish samples were removed and separated into stomach and intestine sections. Parasite cysts located on their surfaces were located and examined micro-

scopically and recorded by their location. The parasites were then transferred using a dissection needle to a slide containing sterilized water after getting rid of their slime and examined at high magnification (400X). Smears were made from samples collected from the skin, gills, stomach and intestines. These specimens were maintained in petri dishes with few drops of 9% saline solution to keep the parasites alive. Smears were prepared on sterilized slides and viewed microscopically under low and high power (400X) magnification.

The body cavity, pericardial cavity and muscle tissues of the fish were also examined for endoparasites. The collected parasites were counted and preserved in either 4% formalin or 96% Ethanol for further identification and analysis later. The parasites were identified morphologically using standard identification keys and pictorial guides as previously described (Kuchta et al., n.d.; Scholz et al., 2007; Paperna, 1996).

The parameters of infection such as prevalence, mean intensity of infection and abundance of parasites were calculated according to Bush et al methods (Bush et al., 1997).

3.4.6 Determination of the diversity of parasitic and bacterial organisms in fish Collected from the fish farms

Shannon-Wiener diversity index for the species community was calculated using biodiversity calculator (Nolan & Callan, 2006). The diversity of the parasitic and bacterial organisms infecting fish was determined using Shannon-Wiener diversity index as shown in equation 3.

$$H = \sum_{i=1}^{R} P_i \ln P_i \tag{3}$$

Where H'= Shannon's diversity index, R = Total number of species, i= the ith species, In = natural logarithm and Pi = the proportion of individuals belonging to the ith species

and n = Total number of individuals of all species of parasites or bacterial colonies.

3.4.7 Antimicrobial Suscebtibility Testing

The susceptibility of isolates was assessed using the standard disc diffusion method on Mueller-Hinton agar, following CLSI (Clinical and Laboratory Standards Institute) guidelines. Six antibiotics were selected for resistance profiling based on common usage in aquaculture and veterinary settings: Amoxicillin (AMX), Erythromycin (ERY), Cotrimoxazole (CT), Doxycycline (DO), Streptomycin (STR), and Ciprofloxacin (CIP). All discs were purchased from Oxoid Ltd.

3.5 Data Management and Statistical Analyses

All the collected data were tested for normality using the Shapiro-Wilk test, and homogeneity of variance was assessed using Levene's test. The results of these tests indicated that the data were not normally distributed; therefore, non-parametric tests were used for statistical analysis.

For Objective 1, Standard statistical computations (prevalence, mean intensity, and mean abundance) were used to analyze bacterial and parasite diversity across fish organs, farms, ponds, pond types, and measurement dates (Bush et al., 1997). The Kruskal-Wallis test assessed significant differences in bacterial prevalence across these factors. When significant differences were found, Dunn's post hoc test identified the specific groups responsible for the variation. Logistic regression model examined the relationship between predictor variables (measurement date, pond name, organ, and bacteria type) and the binary outcome variable indicating bacterial presence (1 = present, 0 = absent). Predictor variables were used to estimate the probability of bacterial presence, with each coefficient representing the log odds of presence relative to a reference cate-

gory.

For Objective 2, the Kruskal-Wallis test was used to compare differences in water quality parameters across the selected fish farms. Where significant differences were observed, Dunn's post-hoc test with Bonferroni correction was applied to determine specific farm-to-farm variations at a significance level of $p \leq 0.05$.

For Objective 3, Spearman's rank correlation was used to assess relationships between water quality and fish microbial and parasitic infection, diversity and abundance. Hierarchical Cluster Analysis (HCA) classified fish farms based on water quality and infection rates. PCA identified key environmental drivers of microbial and parasitic infections.

For Objective 4, Fisher's exact test was employed to determine whether significant differences existed in resistance patterns among bacterial species for each antibiotic. A significance threshold of $p < 0.05$ was used.

To complement the statistical analysis, Principal Component Analysis (PCA) was used to identify key environmental drivers influencing microbial and parasitic infections. All statistical analyses were conducted using R software 4.4.2 (Pile of Leaves) with $p \leq 0.05$ considered statistically significant.

3.6 Ethical Considerations

This study was conducted in line with the principles of responsible research practice and received the necessary approvals prior to commencement of field activities. Ethical clearance was granted by the University of Eastern Africa, Baraton, under reference Ser. No. B0202032023, dated 2nd March 2023 (Appendix 1). In addition, a research license was obtained from the National Commission for Science, Technology, and Innovation (NACOSTI) under reference License. No. NACOSTI/P/23/24537, dated 11th April

2023 (Appendix I1), authorizing the study in Uasin Gishu County.

Participation by fish farmers was voluntary. Before data collection, the objectives, scope, and procedures of the study were clearly explained and informed consent were obtained. To safeguard confidentiality, personal identifiers were excluded from all datasets, reports, and publications.

Fish handling during sampling was undertaken with care to minimize stress. Length and weight measurements were conducted non-invasively, while dissections for microbiological and parasitological analyses were performed in accordance with standard aquaculture diagnostic procedures (Paperna, 1996; Scholz et al., 2007). Fish selected for dissection were humanely euthanized prior to processing, and no experimental manipulations beyond routine diagnostic and laboratory analysis were carried out.

All data and specimens collected were stored securely, with electronic records maintained in password-protected files and physical samples kept in lockable storage accessible only to the researcher and academic supervisors. The principles of integrity, respect, and responsibility guided all research activities, ensuring appropriate treatment of both human participants and aquatic animals involved in the study.

CHAPTER FOUR

RESULTS

4.1 Bacterial organisms isolated from selected fish farms in Uasin Gishu County, Kenya

4.1.1 Isolation and identification of bacterial species

A total of 468 fish samples collected from selected fish farms in Uasin Gishu County were Investigated for bacterial characterization over a one-year period, resulting in 154 bacterial colony isolates. The 154 bacterial colony isolates were identified which displayed a variety of distinct cultural and biochemical characteristics that enabled for their identification. These isolates were distributed across 12 bacterial species, including both Gram-positive and Gram-negative organisms, each exhibiting unique colony morphology and biochemical properties (Table 4.1).

Table 4.1: Classification of Isolated Bacteria from Fish Samples

Gram Positive Bacteria		**Gram Negative Bacteria**	
Genera	**Species**	**Genera**	**Species**
Bacillus	*Bacillus spp.*	Eschirichia	*Eschirichia coli*
Streptociccus	*Streptociccus spp.*	Pseudomonas	*Pseudomonas aeruginosa*
Micrococcus	*Micrococcus spp.*	Aeromonas	*Aeromonas hydrophila*
			Aeromonas caviae
			Aeromonas sobria
		Vibrio	*Vibrio harveyi*
			Vibrio alginolyticus
		Flavobacterium	*Flavobacterium columnare*
		Plesiomonas	*Plesiomonas shigelloides*

Bacillus spp. produced large, dry, and irregular colonies with a distinctive amoebic-like shape on blood agar, often showing haemolytic activity. These isolates were confirmed as Gram-positive, Catalase positive, spore-forming rods. These organisms were able to

degrade starch and were positive for motility test (Figure 4.1 A – C).

Streptococcus spp. generated pinpoint, purple non-haemolytic colonies on blood agar. These colonies were small and exhibited a characteristic coloration, with the bacteria arranged in chains, making them easily distinguishable from other species by their size and color. They exhibited positive reactions in tests for fermentation of sugars (glucose and lactose) (Figure 4.1 D – F).

Micrococcus spp., on the other hand, formed small, yellow-pigmented colonies on nutrient agar and were identified as Gram-postive cocci, arranged in tetrads or clusters and were catalase-positive (Figure 4.1 G – I). They were catalase-positive and oxidase positive.

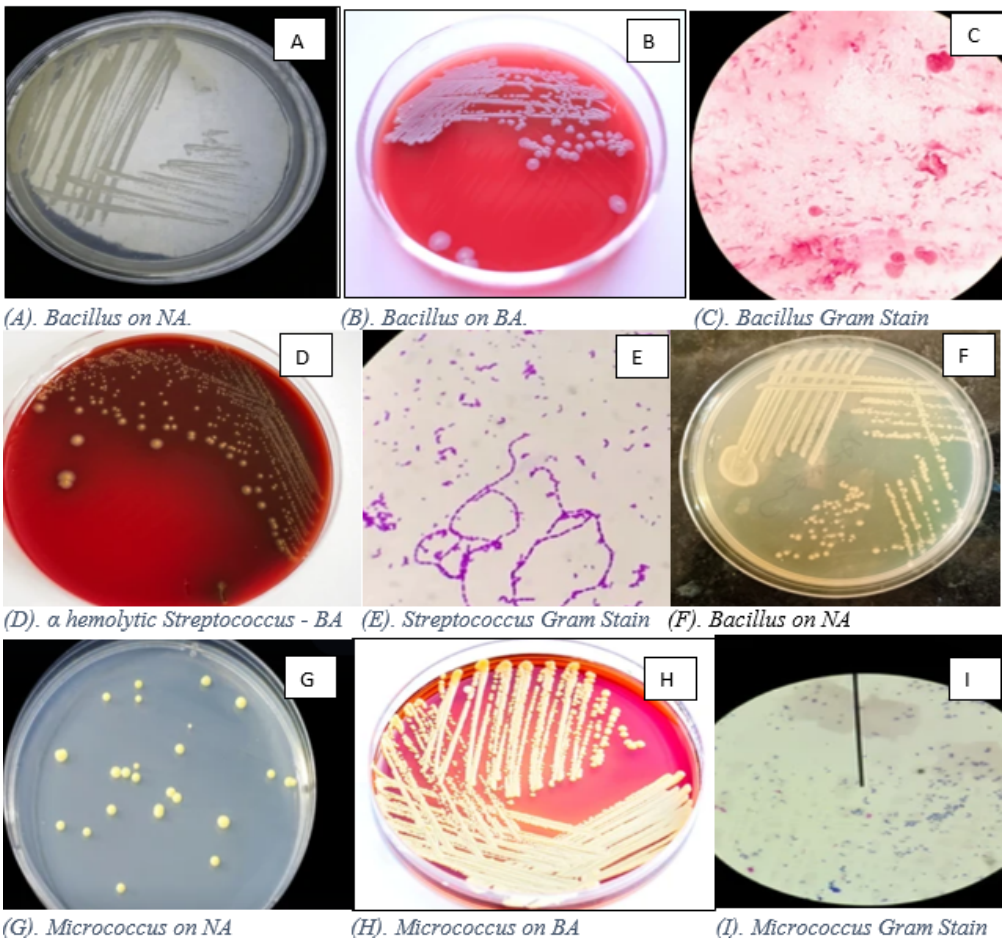


Figure 4.1: Bacterial Colony Morphology and Microscopical Characteristics

Among the Gram-negative bacterial isolates, *Escherichia coli* colonies appeared pink on MacConkey agar, reflecting their ability to ferment lactose and indicating a strong lactose-positive reaction. These colonies were confirmed as Gram-negative rods (Figure 4.2 A – E). *Pseudomonas aeruginosa* produced β-hemolytic colonies on blood agar and exhibited the characteristic green pigmentation resulting from pyocyanin production. This species was also identified as a Gram-negative rod (Figure 4.2 F – I).

Aeromonas hydrophila colonies appeared off-white and circular, exhibiting β-hemolysis on blood agar. Biochemical tests confirmed its identification as a Gram-negative rod, underscoring its virulence potential in aquatic environments (Figure 4.2 J – L). *Aeromonas caviae*, although morphologically similar to *A. hydrophila*, was differentiated by biochemical tests such as oxidase activity and glucose fermentation patterns, which established its distinct identity as a Gram-negative rod (Figure 4.2 L). *Aeromonas sobria* displayed colony morphology and hemolytic activity similar to other *Aeromonas* spp. but was likewise confirmed as a Gram-negative rod based on its biochemical characteristics.

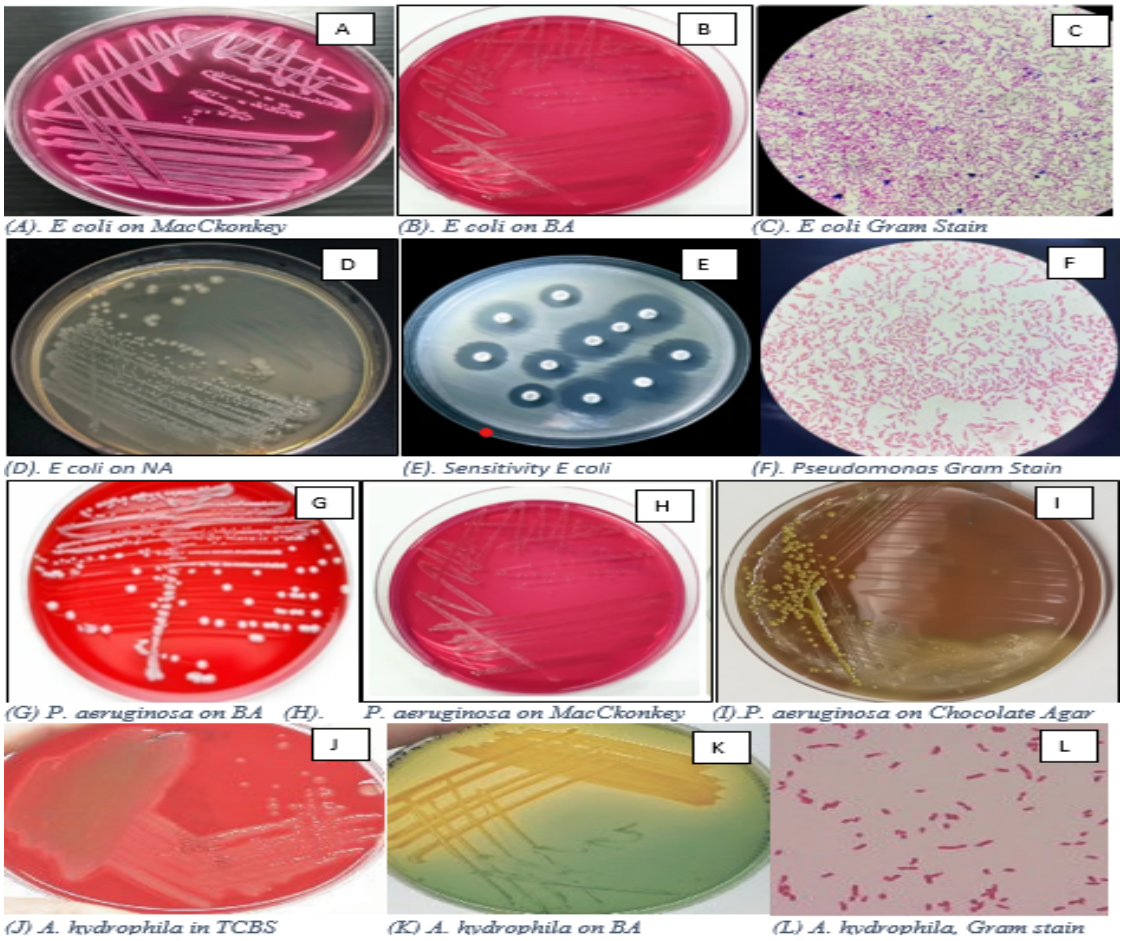


Figure 4.2: Colony Morpholgy and Microscopic characteristics of *E. coli*, *Pseudomonas* spp. and *Aeromonas* spp.

The *Plesiomonas spp*. exhibited non-hemolytic, small colonies that were identified as Gram-negative rods based on biochemical testing, further distinguishing them from other genera in the same family (Figure 4.3 A – C). Vibrio species were identified using their growth on thiosulfate-citrate-bile salts-sucrose (TCBS) agar. *Vibrio alginolyticus* colonies appeared yellow on TCBS agar and also demonstrated sucrose fermentation. This organism, like *V. harveyi*, was identified as a halophilic Gram-negative rod with distinctive biochemical properties (Figure 4.3 D – F). Similarly, *V. harveyi* formed distinct yellow colonies on TCBS, indicative of sucrose fermentation, a characteristic feature of this species, and was identified as a halophilic Gram-negative rod (Figure 4.3 J – L). Finally, *Flavobacterium columnare* formed non-hemolytic, yellow-pigmented

colonies on blood agar, typical of its characteristic morphology and non-hemolytic behavior. This organism was identified as a Gram-negative rod through its biochemical profiling, including its ability to degrade starch.

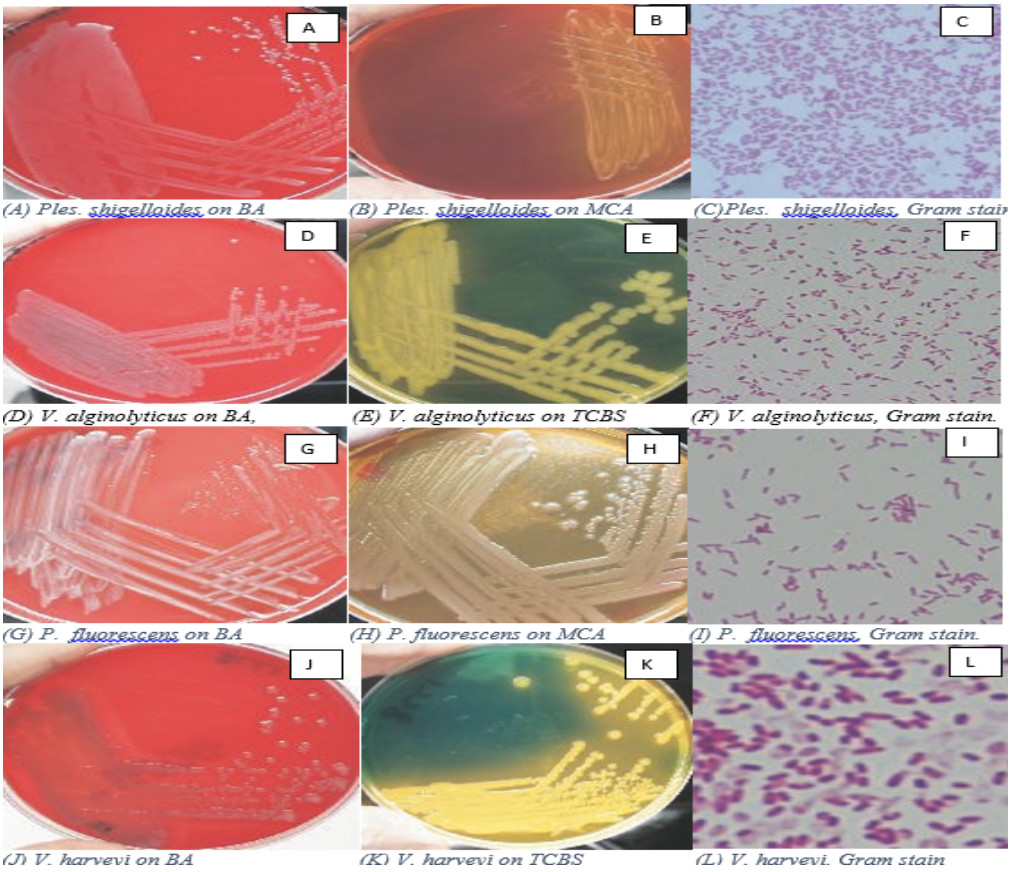
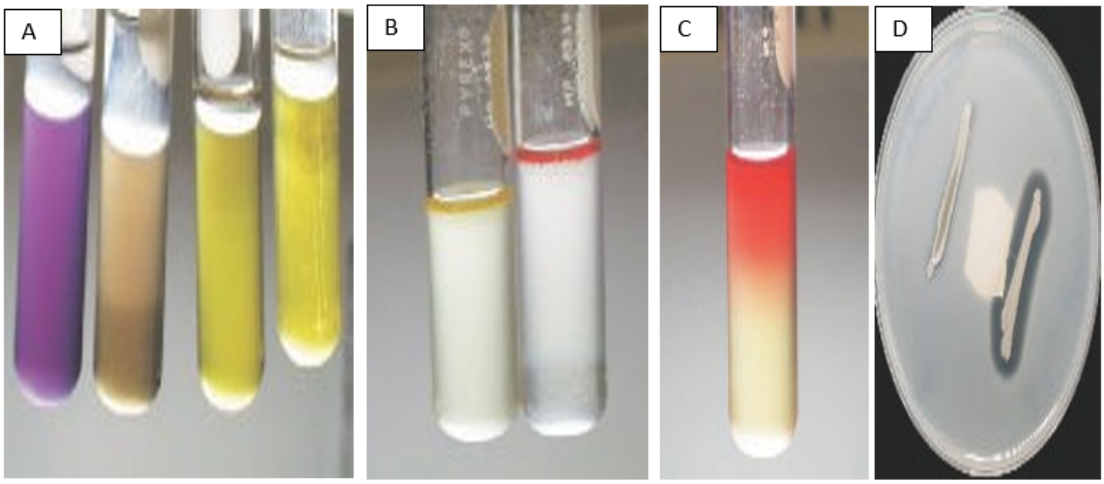


Figure 4.3: Colony Morpholgy and Microscopic characteristics of Plesiomonas spp and Vibrio spp

The biochemical characteristics of these isolates further differentiated them. *E. coli* was catalase-negative, oxidase-negative, and fermented glucose with acid and gas production. *P. aeruginosa*, on the other hand, was oxidase-positive, catalase-positive, and produced a distinctive blue-green pigment in the presence of sodium chloride. The *Aeromonas* spp., including *A. hydrophila*, were oxidase-positive and exhibited fermentative behaviour, with some species showing positive reactions for arginine dihydrolase and gelatin liquefaction, both of which are indicative of their pathogenic potential in

aquatic environments. *Vibrio spp.* demonstrated a strong oxidative reaction, with *V. harveyi* showing the ability to reduce nitrate, while *V. alginolyticus* fermented sucrose and was able to produce hydrogen sulfide. *Flav. columnare* was oxidase-negative but exhibited the ability to degrade starch, which is a key characteristic of this genus, (Figure 4.4 A – D).



(A) Decarboxylase reactions. Left to right: arginine dihydrolase (positive); lysine decarboxylase (positive); ornithine decarboxylase (negative); and control tube (negative).

(B) Figure 4.3(b) Indole reaction. Negative on the left and posi- tive on the right. Vibrio parahaemolyticus with 0.85% NaCl, and 2% NaCl,

(C). Methyl Red reaction. Positive

(D) DNase reaction. Negative reaction on left and positive reaction on right

Figure 4.4: Biochemical Characteristics of Bacterial isolates

4.1.2 Tissue-Specific Distribution and Diversity of bacterial Species across Farms, Facility Types, and Seasons

4.1.2.1 Organ-Specific Distribution of Bacteria

Table 4.2 shows the distribution of bacterial isolates across different organs (gills, intestines, skin, and kidney), highlighting both shared and organ-specific bacterial occurrence. *E coli* and *P. aeruginosa* were detected in all four tissues. *P. fluorescens* was uniquely found in the skin while *Flav. columnare* was limited to the skin and intestines. Among all tissues, the intestines exhibited the highest bacterial diversity.

Table 4.2: Summary of isolated species by organ

Gills	Intestines	Skin	Kidney
E. coli	*E. coli*	*E. coli*	*E. coli*
P. aeruginosa	*P. aeruginosa*	*P. aeruginosa*	*P. aeruginosa*
V. harveyi	*V. harveyi*	*P. fluorescens*	
V. alginolyticus	*A. hydrophila*	*A. hydrophila*	
	Flav. columnare	*Flav. columnare*	
	V. alginolyticus		

4.1.2.2 Farm Level and Pond Level Variability

Shannon diversity by farm and pond/tank, revealed that bacterial diversity varied notably across farms, with some consistently exhibiting greater microbiological complexity than others, as summarized in Table 4.3. Turbo Farm recorded the highest bacterial diversity with a Shannon index of 1.94, indicating a rich and relatively even bacterial community. This was followed closely by Kesses Farm B (1.75) and Moiben (1.75). In contrast, Kesses Farm A showed the lowest bacterial diversity at 1.67. At the pond/tank level, diversity differences were also apparent within farms. For instance, Pond 1 in Kesses Farm B had a higher Shannon index (1.76) than Pond 2 (1.75), while in Ainapkoi Farm, bacterial diversity ranged from 1.69 to 1.72 across ponds.

Table 4.3: Shannon Diversity Index of Bacterial Communities by Farm and Pond/Tank

Farm	Pond/Tank	Bact Shannon Index	Bacterial Richness (S)	Rank
Moiben Farm		1.753949	6.25	7
	1	1.723553	6.00	16
	2	1.712425	6.17	12
	3	1.723553	6.14	15
	4	1.712425	5.58	18
Ainapkoi Farm		1.709018	6.25	7
	1	1.723553	5.92	17
	2	1.689764	6.50	4
	3	1.713737	6.42	6
Kesses Farm A		1.672010	6.46	5
	1	1.619156	6.25	7
	2	1.724865	6.17	12
Kesses Farm B		1.753949	6.25	7
	1	1.760372	6.17	12
	2	1.747526	6.21	11
Turbo Farm		1.935360	8.00	1
	1	1.941783	7.92	3
	2	1.928937	7.96	2

4.1.2.3 Facility Type distribution and diversity

Facility type comparison revealed that bacterial diversity varied across different aquaculture systems, as shown in Table 4.4. Liner ponds exhibited the highest bacterial

diversity with a Shannon index of 1.82, suggesting a richer and more even microbial community. This was followed by earthen ponds, which recorded a slightly lower but still substantial diversity index of 1.73. Tank systems demonstrated the lowest bacterial diversity at 1.69, indicating a more limited bacterial population structure.

Table 4.4: Shannon Diversity Index of Bacterial Communities by Facility Type

Farm	Shannon Index (H)	Rank	Estimated Species Richness (S)
Earthen Pond	1.728	1	6
Liner Pond	1.821	2	6
Tank	1.689	3	5

The ANOVA results, presented in Table 4.5, revealed that both season and farm exerted a statistically significant influence on bacterial presence ($p < 0.001$). While pond and facility type also demonstrated statistically significant effects ($p < 0.001$), their influence was comparatively smaller.

Table 4.5: Analysis of Variance (ANOVA) of Bacterial Presence by Farm, Pond, Facility Type, and Season

Source	sum_sq	df	F	PR(>F)
Across Farm	47.59864	4	11.15822	0.0000
Across Ponds/Tanks	93.74603	3	29.30164	0.0000
Across Facility Type	18.30575	2	8.582582	0.0002
Across Seasons (date)	103.739	11	8.843206	0.0000

Significant differences in bacterial infestation were observed across the sampled fish farms, with patterns varying by organ and bacterial species as shown in Table 4.6. In the kidney, *P. aeruginosa* was found to be significantly more prevalent in fish from Turbo farm than in all other farms ($p < 0.001$). Similarly, in the gills, *V. alginolyticus* exhibited significantly higher infestation levels in Turbo Farm compared to Ainapkoi, Kesses A, Kesses B, and Moiben Farms($p < 0.001$). In the intestines, multiple bacterial species displayed significant variation between farms. *P. aeruginosa* levels were notably higher in fish from Turbo compared to Ainapkoi and Moiben. For *Flav. columnare*, significant differences were found between Kesses B and Moiben farms, as well as between Moiben and Turbo Farms. Additionally, *V. alginolyticus* was significantly more prevalent in intestines of fish from Turbo and Kesses B farms than in those from Ainapkoi and Moiben Farms. The skin showed the greatest diversity in bacterial infestation patterns. All five bacteria analyzed (*P. fluorescens*, *A. hydrophila*, *P. aeruginosa*, *V. alginolyticus*, and *Flav. columnare*) exhibited significant differences across farms. Notably, *P. fluorescens* and *A. hydrophila* infestations were significantly lower in Ainapkoi, while

Table 4.6: Significant Pairwise Differences in Bacterial Species Infestation across Fish Organs and Farms (Significance Column Removed)

Organ	Bacterial Spp.	Farm Group 1	Farm Group 2	Difference	p-value
Kidney	*P. aeruginosa*	Ainapkoi	Turbo	0.25	<0.001
		Kesses A	Turbo	0.25	<0.001
		Kesses B	Turbo	0.25	<0.001
		Moiben	Turbo	0.25	<0.001
Gills	*V. alginolyticus*	Ainapkoi	Turbo	0.5	<0.001
		Kesses A	Turbo	0.5	<0.001
		Kesses B	Turbo	0.5	<0.001
		Moiben	Turbo	0.5	<0.001
Intestines	*P. aeruginosa*	Ainapkoi	Turbo	0.417	0.008
		Kesses B	Moiben	-0.333	0.038
		Moiben	Turbo	0.417	0.004
	Flav. columnare	Kesses B	Moiben	0.25	0.038
		Moiben	Turbo	-0.25	0.038
	V. alginolyticus	Ainapkoi	Kesses B	0.333	<0.001
		Ainapkoi	Turbo	0.333	<0.001
		Kesses B	Moiben	-0.333	<0.001
		Moiben	Turbo	0.333	<0.001
Skin	*P. fluorescens*	Ainapkoi	Kesses A	-0.444	<0.001
		Ainapkoi	Kesses B	-0.444	<0.001
		Ainapkoi	Turbo	-0.444	<0.001
		Kesses A	Moiben	0.5	<0.001
		Kesses B	Moiben	0.5	<0.001
		Moiben	Turbo	-0.5	<0.001
	A. hydrophila	Ainapkoi	Kesses A	-0.25	0.031
		Ainapkoi	Kesses B	-0.25	0.031
		Ainapkoi	Turbo	-0.25	0.031
		Kesses A	Moiben	0.25	0.019
		Kesses B	Moiben	0.25	0.019
		Moiben	Turbo	-0.25	0.019
	P. aeruginosa	Ainapkoi	Kesses A	0.333	<0.001
		Ainapkoi	Kesses B	0.583	<0.001
		Ainapkoi	Turbo	0.833	<0.001
		Kesses A	Kesses B	0.25	0.046
		Kesses A	Moiben	-0.333	<0.001
		Kesses A	Turbo	0.5	<0.001
		Kesses B	Moiben	-0.583	<0.001
		Kesses B	Turbo	0.25	0.046
		Moiben	Turbo	0.833	<0.001
	V. alginolyticus	Ainapkoi	Kesses A	0.333	0.001
		Ainapkoi	Kesses B	0.333	0.001
		Ainapkoi	Turbo	0.75	<0.001
		Kesses A	Moiben	-0.333	<0.001
		Kesses A	Turbo	0.417	<0.001
		Kesses B	Moiben	-0.333	<0.001
		Kesses B	Turbo	0.417	<0.001
		Moiben	Turbo	0.75	<0.001

Moiben and Turbo Farms displayed elevated infection levels. *P. aeruginosa* and *V. alginolyticus* followed similar patterns, with Turbo Farm showing consistently higher infestations, especially when compared with Ainapkoi and Kesses A Farms.

4.1.2.4 Seasonal and Temporal Variation

The mean bacterial presence by facility type and season reveals important trends in microbial dynamics within aquaculture systems as illustrated in Figure 4.5. Across all facility types, Earthen, Liner, and Tank, the highest bacterial loads were observed

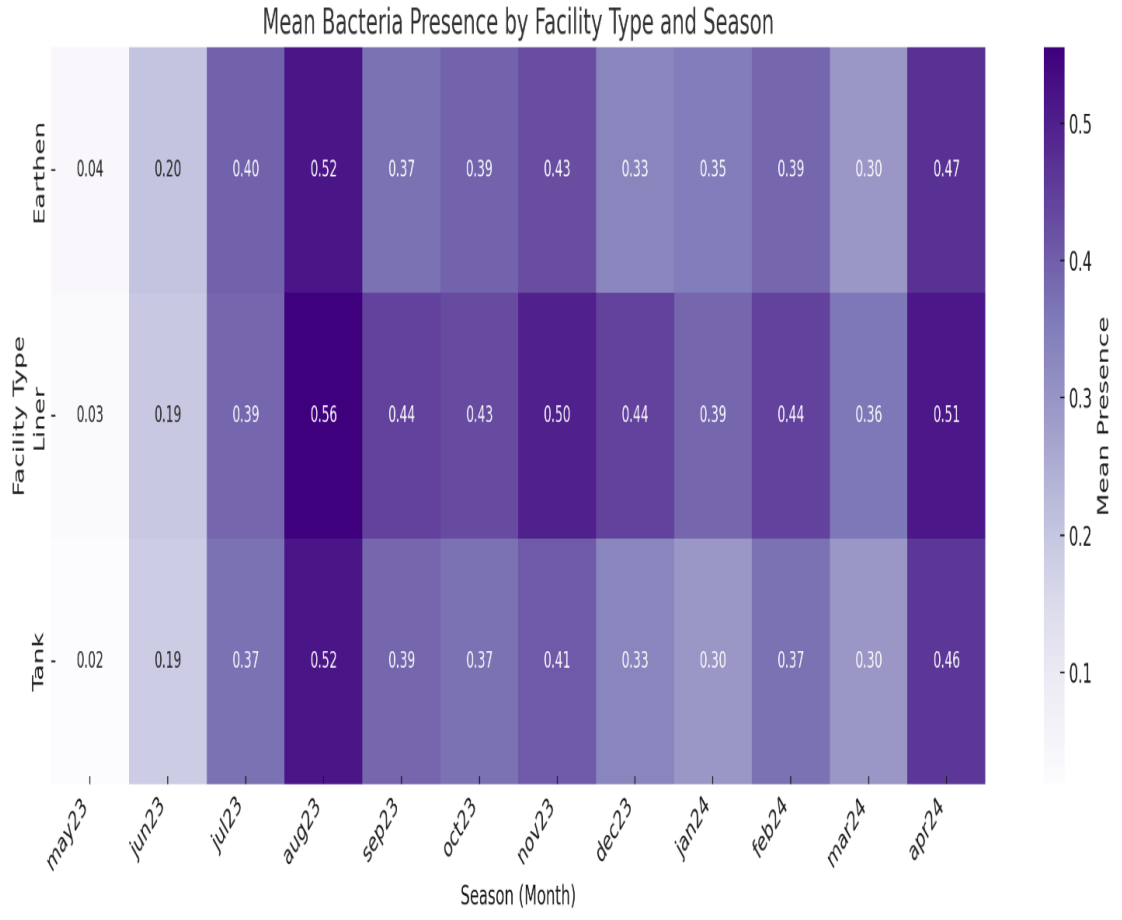


Figure 4.5: Mean Bacterial Presence by Farm, Tissue Type, and Season

during the months of August (Earthen: 0.52, Liner: 0.56, Tank: 0.52) and April (Earthen: 0.47, Liner: 0.51, Tank: 0.46), with additional peaks in September (Earthen: 0.40, Liner:

0.44, Tank: 0.39) and November (Earthen: 0.43, Liner: 0.50, Tank: 0.41). Among the facility types, liner systems consistently recorded the highest bacterial presence, followed closely by earthen ponds. Tank systems exhibited relatively lower bacterial levels. Notably, bacterial presence remained elevated in liner and earthen systems even during cooler months, indicating that open systems may retain residual microbial load longer than closed ones.

The spatial and temporal distribution of bacterial occurrence across farms, fish organs, and seasons, as illustrated in Figure 4.6, revealed consistent trends of higher bacterial loads in gills, followed by intestines and skin. Among the farms, Turbo Farm stood out with the highest mean bacterial occurrence, particularly in gill samples, which maintained a mean value of 1.00 from August 2023 through April 2024. Other farms,

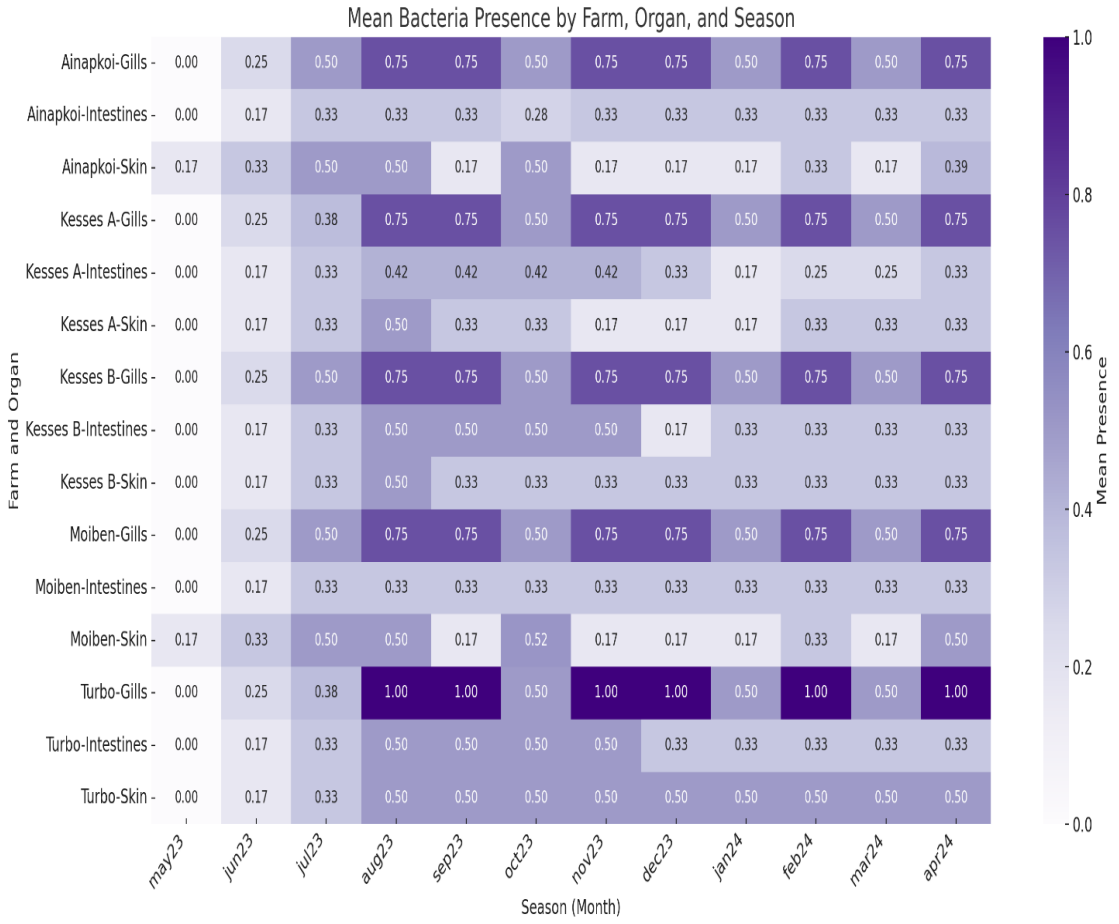


Figure 4.6: Mean Bacterial Presence by Farm, Tissue Type, and Season

including Moiben, Kesses B, and Ainapkoi Farms, also showed moderately elevated bacterial levels in the gills, with peak values ranging from 0.75 to 0.83 during the same period. Seasonal variation was also apparent with bacterial occurrence generally increasing from July through February, aligning with periods of higher temperature and potential organic matter buildup. In contrast, values were lowest in May and June, when environmental conditions may be less favorable for bacterial growth.

4.1.3 Bacterial species Co-occurrence

Table 4.7 shows the co-occurrence of bacterial species isolated from different fish organs. *E. coli* consistently isolated across all organs either alone or as a co infection with most bacterial combinations. Co-infections were especially common in the intestines and skin, where complex associations co-occurred while the kidney did not exhibit any co-occurrence, with *E. coli* and *P. aeruginosa* being isolated independently.

Table 4.7: Distribution of Bacterial Species Co-occurrence across Fish Organs

Bacterial Co-occurrence	Gills	Intestines	Skin	Kidney
E. coli	✓	✓	✓	✓
E. coli/*P. aeruginosa*	✓	✓	✓	
E. coli/*P. aeruginosa* /*V. harveyi*	✓			
E. coli/*P. aeruginosa*/*V. alginolyticus*	✓	✓	✓	
E. coli/*A. hydrophila*		✓	✓	
E. coli/*Flav. columnare*		✓		
E. coli/*V. harveyi*		✓		
E. coli/*V. alginolyticus*		✓	✓	
P. aeruginosa				✓
E. coli/*P. fluorescens*			✓	
E. coli/*P. fluorescens*/*A. hydrophila*			✓	
E. coli/*P. fluorescens*/*Flav. columnare*			✓	

The results for bacterial species co-occurrence per farm revealed distinct farm-specific trends as shown in Table 4.8. Moiben Farm consistently showed the highest overall bacterial diversity and frequency of co-infections. Turbo Farm stood out for its dominance in complex co-occurrence patterns. It recorded the highest presence of *P. aeruginosa* in kidney samples (27.3%), a bacterium that was absent from kidneys in all other farms. The skin samples from Turbo also revealed a high rate (72.7%) of complex co-infections involving *E. coli*, *P. aeruginosa*, and *V. alginolyticus*. Ainapkoi Farm showed simpler co-occurrence patterns while Kesses Farms A and B displayed moderate co-occurrence levels.

Table 4.8: Percentage Distribution of Bacterial Species Co-occurrence across Farms

Organ / Species	Farm				
	Moiben	**Ainapkoi**	**Kess. A**	**Kess. B**	**Turbo**
Kidney					
E. coli	37.5	38.9	37.5	37.5	45.5
P. aeruginosa	0	0	0	0	27.3
Gills					
E. coli	8.3	8.3	8.3	8.3	9.1
E. coli, *P. aeruginosa*	33.3	33.3	33.3	33.3	36.4
E. coli, *P. aeruginosa*, *V. harveyi*	50	50	50	50	0
E. coli, *P. aeruginosa*, *V. alginolyticus*	0	0	0	0	45.5
Intestines					
E. coli	8.3	8.3	16.7	16.7	9.1
E. coli, *A. hydrophila*	8.3	8.3	0	0	0
E. coli, *Flav. columnare*	25	25	12.5	0	0
E. coli, *P. aeruginosa*	25	25	33.3	41.7	45.5
E. coli, *V. harveyi*	25	25	8.3	0	0
E. coli, *P. aeruginosa*, *V. alginolyticus*	0	0	8.3	16.7	18.2
E. coli, *V. alginolyticus*	0	0	8.3	16.7	18.2
Skin					
E. coli	50	50	33.3	8.3	9.1
E. coli, *A. hydrophila*	8.3	8.3	0	0	0
E. coli, *P. fluorescens*	16.7	16.7	0	0	0
E. coli, *P. fluorescens*, *A. hydrophila*	16.7	16.7	0	0	0
E. coli, *P. fluorescens*, *Flav. columnare*	8.3	8.3	0	0	0
E. coli, *P. aeruginosa*	0	0	25	50	9.1
E. coli, *P. aeruginosa*, *V. alginolyticus*	0	0	8.3	8.3	72.7
E. coli, *V. alginolyticus*	0	0	25	25	0

4.2 Parasite Species Occurrence in the Fish farms

4.2.1 Identification of the parasite species

Examination of the fish samples revealed the occurrence of parasitic species affecting various tissues, including the gills, muscles, and internal organs as shown in Table 4.9. The parasites include monogeneans, digenean trematodes, and ciliate protozoans, with organ-specific distributions. Monogeneans were predominantly found on the gills and skin, digenean trematodes in the intestines, and ciliate protozoans in both gills and skin.

Table 4.9: Classification of Parasite Species Identified in Fish Organs

Organ	Parasite Group	Parasite Genera	Parasite Species
Gills	Ciliate Protozoan	Trichodina	*Trichodina nigra*
	Monogenean	Cichlidogyrus	*Cichlidogyrus tilapiae*
	Monogenean	Dactylogyrus	*Dactylogyrus vastator*
Intestines	Digenean Trematode	Clinostomum	*Clinostomum complanatum*
	Digenean Trematode	Haplorchis	*Haplorchis spp.*
Skin	Monogenean	Gyrodactylus	*Gyrodactylus elegans*
	Ciliate Protozoan	Ichthyophthirius	*Ichthyophthirius multifiliis*

Nematode larvae, primarily belonging to the *Contracaecum* spp., were frequently observed in the visceral cavity, intestines, and gills (Figure 4.7 A). The parasites were particularly concentrated in the peritoneal cavity, causing visible inflammation and tissue damage (Figure 4.7 B). *Harpochilus* spp., also found within the gastrointestinal tract of fish (Figure 4.7 C).

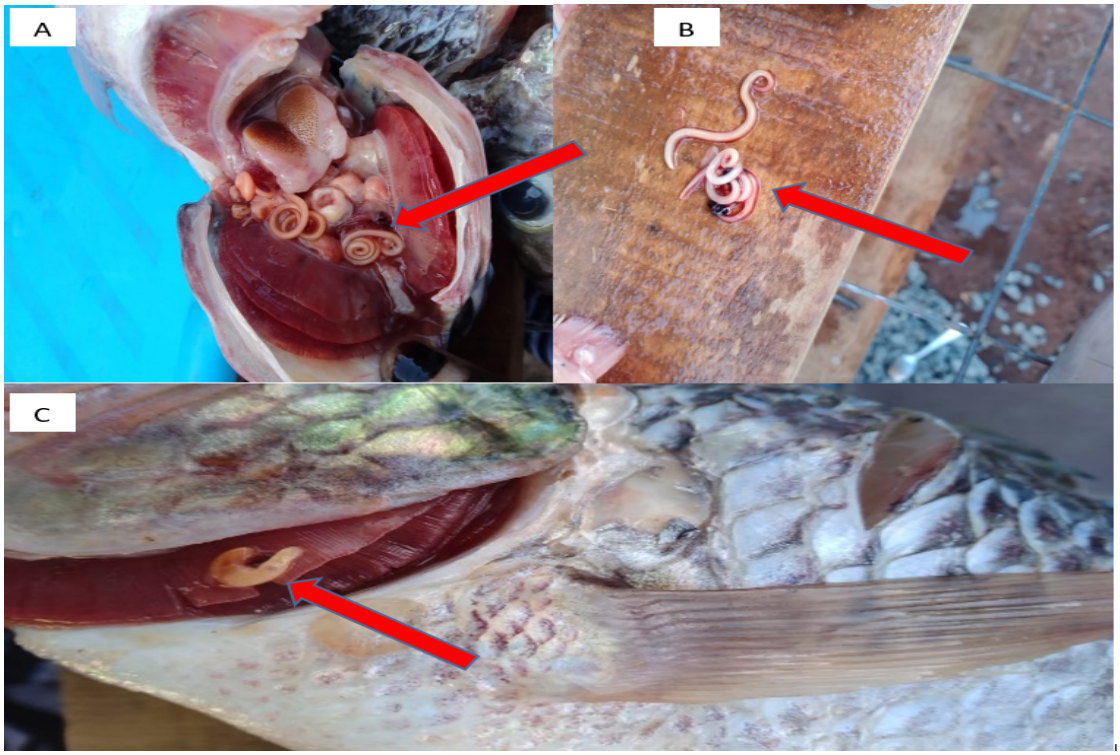


Figure 4.7: (A) Larval and adult stage *Contracaecum* spp. In the Gills, (B) *Contracaecum* spp. Extracted from the fish's intestines and (C) larval-stage (L3 or L4) *Contracaecum* spp. embedded in the gills of fish

Encysted trematode metacercariae, identified as belonging to *C. complanatum*, were observed within the gills and muscle tissues (Figure 4.8 A and B).

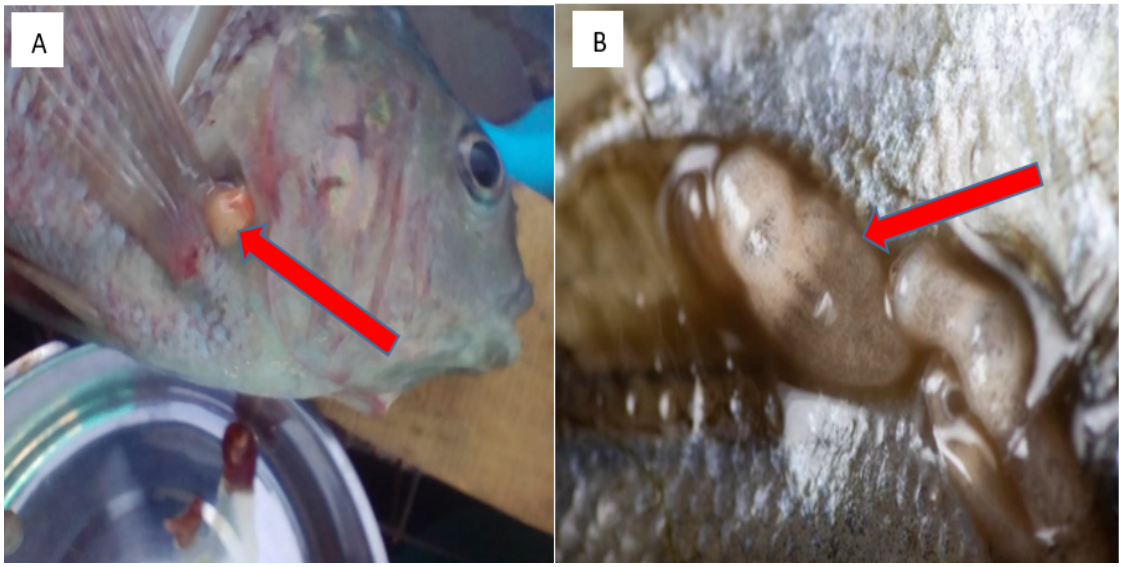


Figure 4.8: (A) Parasitic cyst on the skin Caused by *Clinostomum* spp. and (B) *Clinostomum* spp. metacercariae within fish tissue

Monogenean parasites, identified as *D. vastator*, were found predominantly in the gill filaments (Figure 4.9 A and B). Affected fish exhibited increased mucus secretion and hyperplasia of gill tissues.

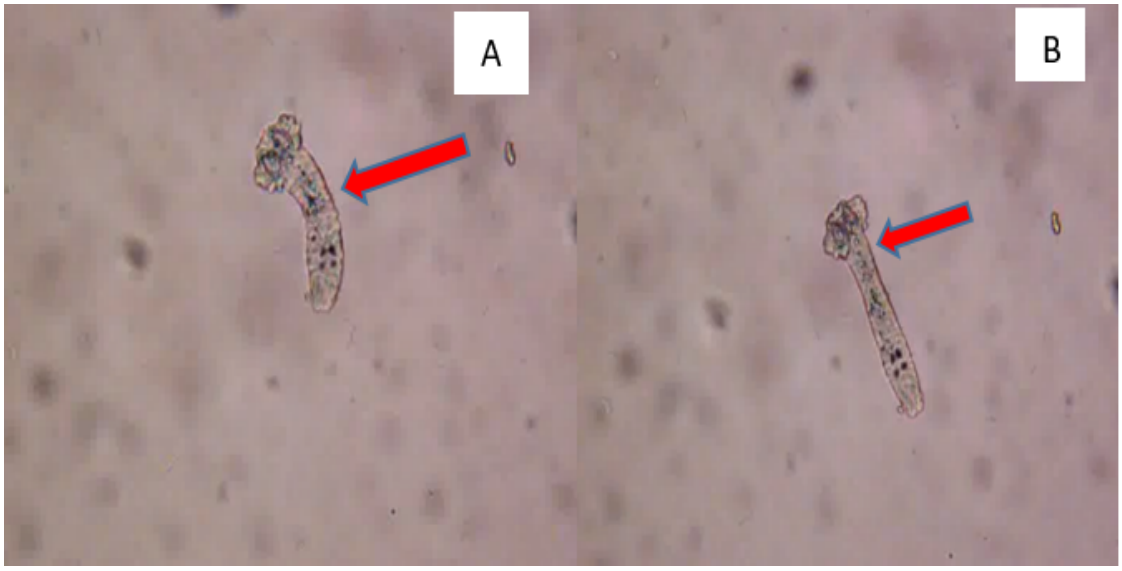


Figure 4.9: (A) Microscopic view of *Dactylogyrus* spp. with (A) Elongated body and attachment showing the internal structures and (B) Haptor, a specialized organ with hooks used for attachment to fish gills

Protozoan parasites, including *I. multifiliis* ("Ich") and *T. nigra*, were identified on the skin and gills of fish (Figure 4.10 A and B). The affected fish showed signs of irritation, erratic swimming, and excessive mucus production. *T. nigra* was found adhering to the gill filaments and skin surface of infected fish (Figure 4.10 C and D). Their presence was associated with epithelial erosion and increased mucus secretion.

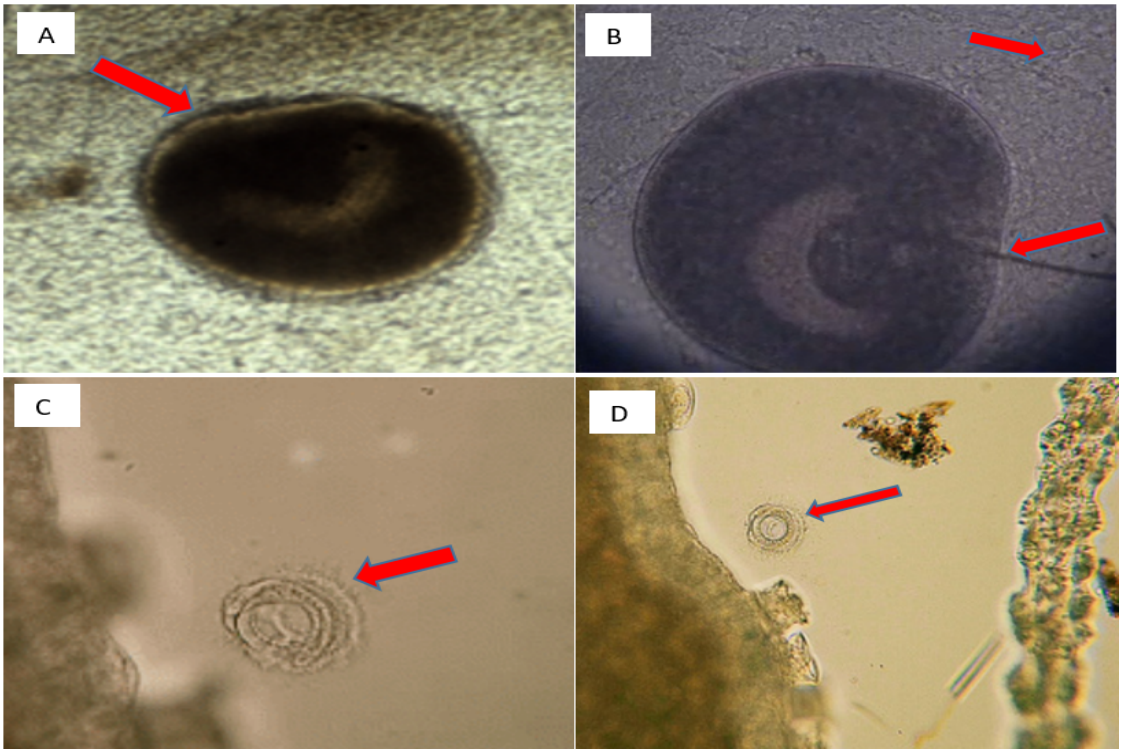


Figure 4.10: (A) Trophonts of *I. multifiliis* in the skin epidermis, (B) *Ichtyoptirius* spp. (Top Left) With *T. nigra*, (C) Microscopic image of *T. nigra*. circular body with radial cilia and attachment disc visible and (D). *T. nigra* with surrounding organic debris and fish epithelial tissue

4.2.2 Tissue-Specific Distribution and occurrence of parasite Species across Farms, Facility Types and Seasons

Shannon diversity results revealed that parasite diversity varied considerably across farms and Ponds/Tanks, with certain locations consistently exhibiting higher levels of parasitic complexity than others, as shown in Table 4.10. Turbo Farm recorded the highest overall parasite diversity, with a Shannon index of 0.88, followed by Moiben and Ainapkoi Farm, each with an index around 0.60, reflecting moderate richness and evenness of parasite species. In contrast, Kesses Farm A demonstrated the lowest diversity (0.06), suggesting limited parasite species richness or dominance by one or two species. At the pond level, noticeable differences in parasite diversity were observed even within the same farm. For instance, in Moiben Farm, Pond 2 had a Shannon index of 1.38,

significantly higher than Pond 1 (0.50) and Pond 4 (0). Similarly, Kesses B Farm Pond 2 showed elevated diversity (1.19), while Pond 1 had none recorded.

Table 4.10: Shannon Diversity Index of Parasites by Farm and Pond

Farm	Pond/Tank	Parasite Shannon	Parasite Richness (S)	Rank
Moiben Farm		0.596	1.00	1
	1	0.496	3.42	2
	2	1.379	1.75	3
	3	0.548	0.50	1
	4	0.000	0.50	2
Ainapkoi Farm		0.595	0.83	1
	1	0.126	4.25	2
	2	1.101	1.42	1
	3	0.558	5.17	2
Kesses Farm A		0.055	1.83	3
	1	0.058	0.50	4
	2	0.053	2.67	1
Kesses Farm B		0.596	3.75	2
	1	0.000	1.00	1
	2	1.191	3.42	2
Turbo Farm		0.877	1.75	3
	1	0.777	0.50	1
	2	0.977	0.50	2

Facility type comparison revealed that parasite diversity varied notably across aquaculture systems as shown Table 4.11. Liner ponds exhibited the highest parasite diversity, with a Shannon index of 0.75, indicating a more diverse and evenly distributed parasite population. This was followed by earthen ponds, which showed moderate diversity at 0.61. In contrast, tank systems recorded the lowest parasite diversity, with a Shannon index of just 0.20, suggesting a more limited parasite community or dominance by a few

species.

Table 4.11: Shannon Diversity Index of Parasites by Facility Type

Facility Type	Parasite Shannon Index (H)	Parasite Richness (S)	Rank
Earthen Ponds	0.613	2.15	2
Liner Ponds	0.745	2.88	1
Tanks	0.202	0.50	3

The ANOVA results indicate that for parasites, both season and farm had a statistically significant influence on their presence ($p < 0.05$) as shown in Table 4.12. In contrast, pond and facility type did not show significant effects when considered alongside parasite occurrence, suggesting that their influence may be more context-specific or limited under seasonal factors.

Table 4.12: ANOVA Results for Parasite Occurrence by Farm, Pond, Facility Type, and Season

Source	Sum of Squares	df	F	PR(>F)
Across Farm	2.336051	4	2.726663	0.0278
Across Pond/Tank	0.011256	3	0.017517	0.9968
Across Facility Type	0.005956	2	0.013904	0.9862
Across Seasons (Measurement date)	45.339650	11	19.24397	0.0000

4.2.2.1 Farm level variability

Significant variations in parasite infestation were observed across the five fish farms, with distinct patterns evident in different organs and among parasite species as shown in

Table 4.13. In the gills, *T. nigra*. showed markedly higher infestation levels in fish from Turbo farm compared to Ainapkoi, Kesses A, Kesses B, and Moiben Farm. The difference between Ainapkoi and Turbo was especially large (difference = 2.528, $p < 0.001$), while Kesses A also showed significantly higher infestation than Kesses B, Moiben, and Turbo Farm. On the skin, *G. elegans* infestation was significantly higher in Turbo farm compared to Ainapkoi Farm ($p < 0.001$) and showed notable differences in other farm pairs, including between Kesses Farm A and both Kesses B and Turbo Farms.

Table 4.13: Significant Pairwise Differences in Parasite Species Infestation across Fish Organs and Farms

Organ	Parasite Spp.	Farm		Difference	p-value	Significance
		Group 1	Group 2			
Gills	*T. nigra*	Ainapkoi	Turbo	2.528	<0.001	Yes
		Kesses A	Kesses B	2	0.002	Yes
		Kesses A	Moiben	1.479	0.013	Yes
		Kesses A	Turbo	3.75	<0.001	Yes
		Kesses B	Turbo	1.75	0.01	Yes
		Moiben	Turbo	2.271	<0.001	Yes
	D. vastator	Ainapkoi	Moiben	0.771	<0.001	Yes
		Kesses A	Moiben	1.104	<0.001	Yes
		Kesses B	Moiben	0.812	<0.001	Yes
		Moiben	Turbo	-0.771	<0.001	Yes
Skin	*G. elegans*	Ainapkoi	Turbo	0.875	<0.001	Yes
		Kesses A	Kesses B	0.583	0.048	Yes
		Kesses A	Turbo	1.167	<0.001	Yes
		Kesses B	Turbo	0.583	0.048	Yes
		Moiben	Turbo	0.958	<0.001	Yes
	I. multifilis	Kesses A	Kesses B	0.417	0.009	Yes
Intestines	*C. complanatum*	Kesses A	Turbo	0.5	0.008	Yes

Moiben Farm also had higher infestation levels compared to Turbo farm. Another skin

parasite, *I. multifilis*, showed a significant difference only between Kesses Farm A and Kesses Farm B ($p = 0.009$). In the intestines, *C. complanatum* was significantly more prevalent in fish from Turbo Farm compared to Kesses Farm A ($p = 0.008$). Overall, Turbo Farm emerged as the farm with the highest infestation levels across multiple parasite species and organs, especially in the gills and skin. In contrast, Ainapkoi Farm often showed lower parasite occurrence.

4.2.2.2 Facility type Variability

The analysis of mean parasite presence across different facility types and seasons revealed clear and consistent trends as shown in Figure 4.11. Liner and earthen systems exhibited markedly higher levels of parasite presence compared to tank systems, which maintained relatively low parasite loads throughout the year. Seasonal dynamics were also prominent. Parasite levels increased steadily from July onward, with significant peaks observed in October, December, February, and April. The highest mean parasite presence was recorded in April 2024, particularly in liner systems (1.57) and earthen ponds (1.24), highlighting a clear seasonal buildup that may be tied to temperature, rainfall, and fish stress conditions.

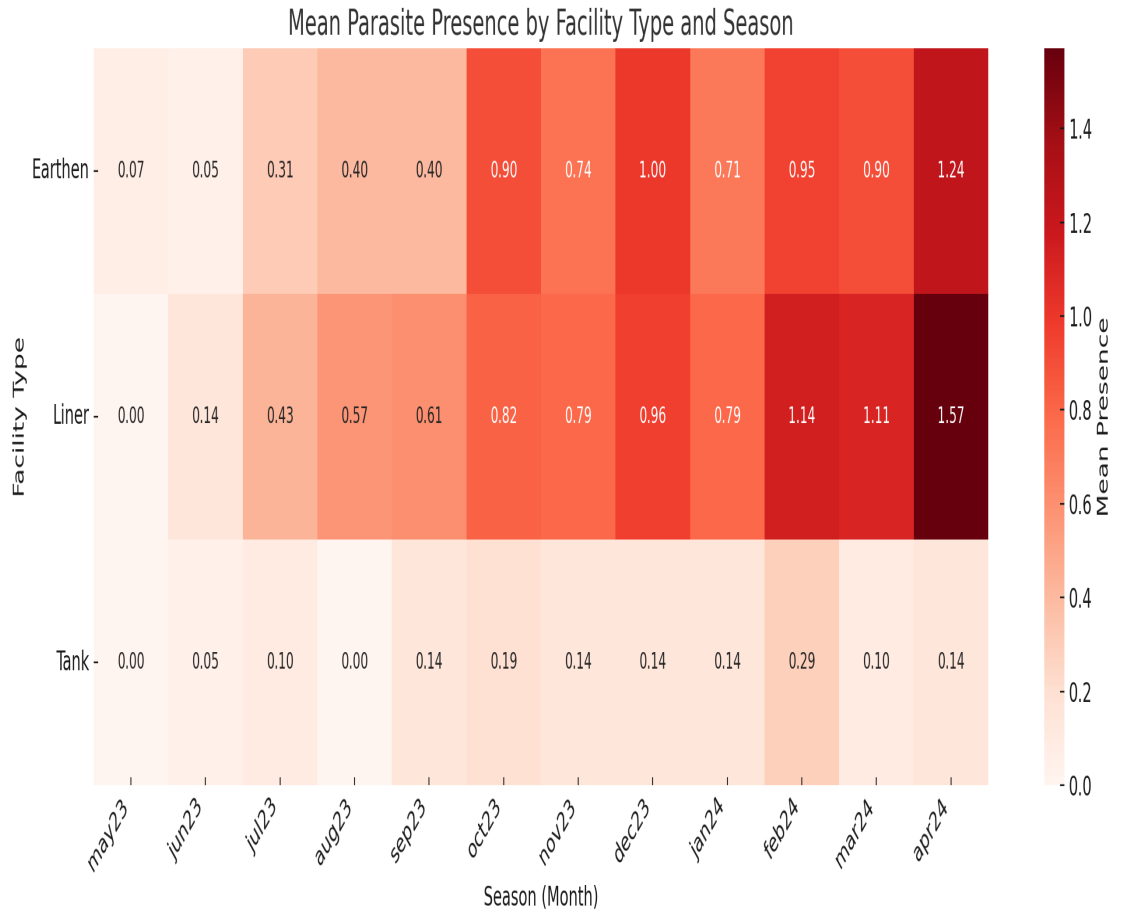


Figure 4.11: Heatmap of Bacterial Species Occurrence by facility type and season

4.2.2.3 Seasonal Variability

The analysis of mean parasite presence across farms, fish organs, and seasons, as shown in Figure 4.12, revealed substantial spatial and temporal variation. The gill tissues consistently experienced the highest parasite loads, particularly in Turbo Farm, where presence peaked at 3.17 in April 2024, and the highest observed value across all combinations. Moiben and Kesses B Farms also exhibited elevated Gill infections across multiple months. In contrast, intestinal infections remained relatively low and stable across farms and time. These trends highlight distinct seasonal and anatomical patterns of parasitic infestation, with Turbo and Moiben Farms emerging as hotspots, especially during late

rainy and early dry seasons.

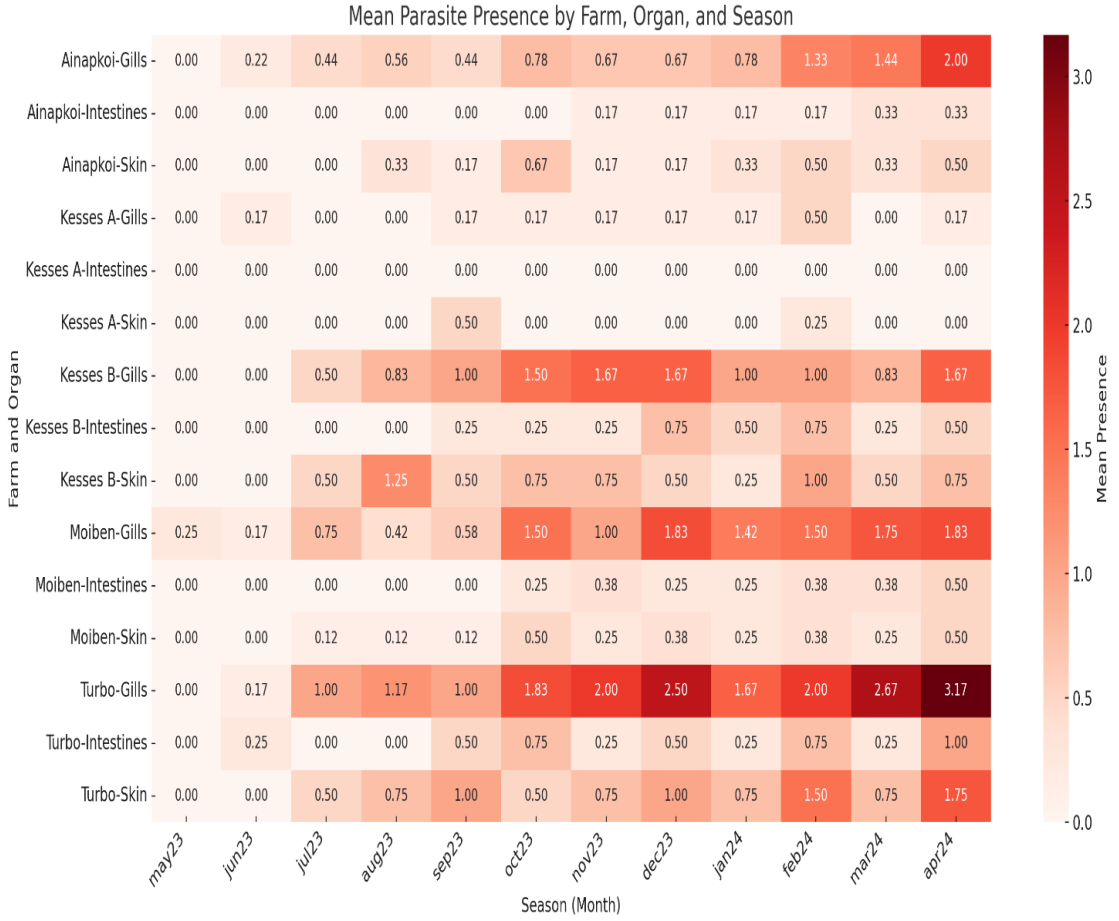


Figure 4.12: Mean parasite presence across fish farms, organs, and sampling seasons (May 2023 – April 2024)

4.3 Water Quality status in the study fish farms

4.3.1 Physico-chemical Parameters

The Kruskal-Wallis test results revealed statistically significant differences in water quality parameters across the farms as illustrated in Table 4.14. All the six parameters (Temperature, DO, pH, COD, BOD, and Coliforms counts) exhibited highly significant variation between farms, with p-values below 0.001. The most pronounced difference was observed in pH values ($p = 7.3 \times 10^{-9}$), followed closely by differences in DO ($p = 9.8 \times 10^{-8}$ and BOD ($p = 6.9 \times 10^{-8}$). COD, Temperature and Coliform counts

differences were also statistically significant but to a slightly lesser degree.

Table 4.14: Summary Statistics and Significance Levels of Water Quality Parameters across Farms

Water Quality Parameter across Farms (Sites)	Statistic	p-value
Temperature	32.98889	0.0000
Dissolved Oxygen (DO)	38.28488	0.0000
PH	43.72483	0.0000
Chemical oxygen demand (COD)	37.61697	0.0000
Biological Oxygen Demand (BOD)	39.02404	0.0000
Coliform Counts	33.28807	0.0000

The Kruskal-Wallis analysis revealed that certain water quality parameters varied significantly across different facility types (Earthen ponds, Liner ponds, and Tanks) as shown in Table 4.15. Specifically, temperature and BOD demonstrated statistically significant differences (p = 0.0001 and p = 0.0007, respectively). In contrast, dissolved oxygen (DO), pH, and COD did not show significant variation across facility types ($p > 0.1$).

Table 4.15: Summary Statistics and Significance Levels of Water Quality Parameters across Facility Types

Water Quality Parameter across Facility Type	Statistic	p-value
Temperature	17.8137	0.0014
Dissolved Oxygen (DO)	4.3663	0.1127
pH	2.8507	0.2404
Chemical Oxygen Demand (COD)	0.5365	0.7647
Biological Oxygen Demand (BOD)	14.4044	0.0074
Coliform Counts	11.7026	0.0288

The analysis of seasonal variation in water quality parameters revealed that most variables remained relatively stable throughout the study period, with only a few exhibiting significant changes across months as presented in Table 4.16. Coliforms counts had the most pronounced seasonal fluctuation ($p < 0.001$). Similarly, BOD varied significantly across months (p = 0.0018). On the other hand, temperature, dissolved oxygen (DO), pH, and chemical oxygen demand (COD) did not exhibit statistically significant variation across months.

Table 4.16: Summary Statistics and Significance Levels of Water Quality Parameters across Seasons (Months)

Water Quality Parameter Across Seasons	Statistic	p-value
Temperature	12.6725	0.3153
Dissolved Oxygen (DO_2)	7.4462	0.7619
pH	7.7742	0.7334
Chemical Oxygen Demand (COD)	8.4672	0.6709
Biological Oxygen Demand (BOD)	29.6994	0.0018
Coliform Counts	68.2189	0.0000

The results for water quality among the ponds are shown in Table 4.17. Temperature values across all farms remained below the optimal growth range for *O. niloticus* (25–30°C), with recorded means ranging from 21.0 °C to 22.8 °C. Dissolved oxygen (DO) levels varied slightly between farms but generally remained above the minimum requirement for tilapia (3 mg/L), except at Kesses Farm B, which recorded a mean DO of 1.8 ± 0.66 mg/L, falling below the limiting threshold. The salinity among ponds was low with all the values being less than 1%. A level of 0.07% was recorded in Moiben Farm which was tenfold than the values recorded in all other ponds during the study period. During the study period, the mean pH values across farms ranged from 8.02 to 9.04, which falls within the optimal range for tilapia culture (6.5 – 9.0). COD, a measure of oxidizable organic matter, varied from 32.1 to 95.2 mg/L, with the highest levels observed at Kesses Farm A. The mean BOD, a measure of microbial, ranging from 33.8 to 103 mg/L, again highest at Kesses Farm A.

Table 4.17: Means and ranges of values for physicochemical parameters across the farms

Farm	Temp (°C)	DO (mg/L)	Salinity (%)	pH	COD (mg/L)	BOD (mg/L)
Moiben	21.0 ± 1.31	3.9 ± 1.64	0.072 ± 0.132	8.77 ± 0.696	70.3 ± 56.6	49.6 ± 39.9
	[18.1–23.2]	[1.48–7.23]	[0.400–0.987]	[6.62–10.1]	[2.77–234]	[1.54–172]
Ainapkoi	22.7 ± 2.00	4.2 ± 1.45	0.0048 ± 0.020	9.04 ± 0.482	53.7 ± 31.1	58.4 ± 33.5
	[20.0–30.6]	[1.25–7.60]	[0.020–0.128]	[8.01–10.2]	[10.0–115]	[3.00–150]
Kesses A	22.8 ± 1.22	3.5 ± 0.979	0.035 ± 0.012	8.49 ± 0.833	95.2 ± 35.0	103.0 ± 55.2
	[20.2–25.5]	[1.84–5.30]	[0.020–0.080]	[6.94–10.1]	[34.0–212]	[34.0–212]
Kesses B	21.6 ± 2.50	1.8 ± 0.660	0.0398 ± 0.012	8.02 ± 0.720	32.1 ± 26.4	33.8 ± 27.8
	[18.6–25.1]	[0.83–3.24]	[0.020–0.060]	[6.60–9.14]	[3.00–112]	[1.00–103]
Turbo	22.4 ± 1.29	4.5 ± 1.63	0.0386 ± 0.014	8.08 ± 0.640	89.7 ± 39.0	78.9 ± 31.1
	[20.2–24.6]	[1.43–6.83]	[0.020–0.060]	[6.77–9.34]	[30.0–168]	[16.0–123]

The diurnal temperature and dissolved oxygen (DO) profiles observed in the study farms for selected periods highlight key environmental dynamics across the day. Moiben Farm ponds for the month of September 2023, showed a consistent diurnal trend, with water temperatures increasing steadily from early morning to late afternoon as illustrated in Figure 4.13. In the morning hours, temperatures were relatively uniform across depths, generally ranging between 19 and 20°C. This uniformity suggests that the water columns were well-mixed before solar heating intensified. As the day progressed, surface waters in all ponds warmed significantly, creating temperature gradients, particularly in the upper layers. Pond 2 exhibited the most pronounced temperature shift, with surface

temperatures rising sharply from about 13°C in the morning to nearly 28°C by mid-afternoon. This steep gradient indicates strong surface heating with limited vertical mixing. Ponds 1 and 4 also experienced considerable warming, reaching around 24 to 25°C at the surface, though the stratification was less severe. Pond 3 stood out for the relatively even temperature distribution across depths, suggesting more effective vertical circulation or mixing throughout the day.

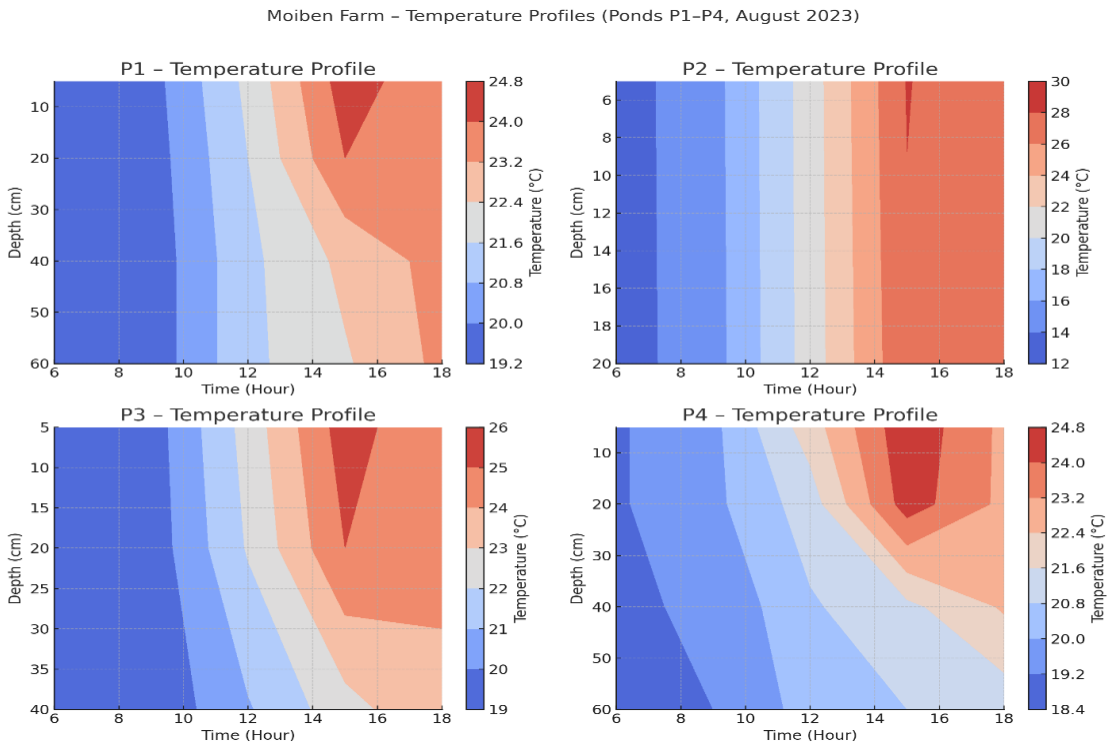


Figure 4.13: Temperature Profiles in Ponds 1 - 4 at Moiben Farm (August 2023)

The dissolved oxygen (DO) levels in all four ponds at Moiben Farm exhibited a clear diurnal trend, increasing steadily from morning to afternoon as illustrated in Figure 4.14. In the early hours, DO concentrations were low across all ponds, reflecting oxygen depletion overnight due to respiration and absence of photosynthesis. As daylight intensified, oxygen levels rose consistently, driven by increased photosynthetic activity. Pond 1 experienced the highest afternoon DO peak, exceeding 8 mg/L. Pond 2 followed a similar pattern, with levels rising sharply from about 3 mg/L in the morning to nearly 8

mg/L later in the day. Pond 3 also showed an upward trend, although it began at lower levels around 2.5 mg/L. Pond 4 similarly started with the lowest morning values, just under 2 mg/L, but still climbed above 6 mg/L by late afternoon.

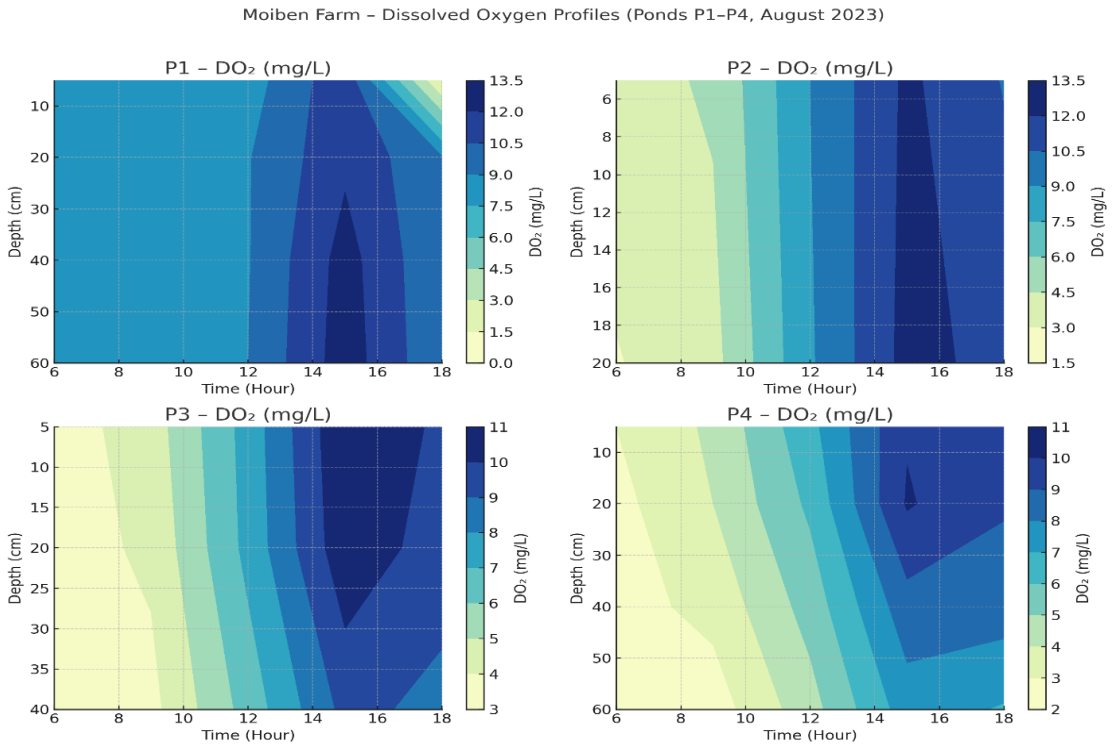


Figure 4.14: Dissolved Oxygen (DO) Profiles in Ponds 1 - 4 at Moiben Farm (August 2023)

The contour plots for Kesses Farm A and Kesses farm B Ponds, recorded in June 2023, provide a clear picture of the thermal and oxygen dynamics across the day. In terms of temperature, all four ponds exhibited a typical diurnal warming pattern as shown in Figure 4.15. Early in the morning, water temperatures were relatively cool and uniform across depths, generally ranging between 18°C and 20°C. As the day progressed, surface waters warmed significantly, with temperatures peaking in the afternoon. Notably, Pond 2 (Kesses Farm A) experienced the highest temperatures, reaching close to 30°C, indicating either shallower depth or higher sun exposure. Pond 1 also showed warming, but with more evident stratification, surface layers warmed while bottom layers remained

cooler. In contrast, Ponds 1 and 2 (Kesses Farm B) displayed a more even distribution of temperature across depths, suggesting good vertical mixing or relatively shallow depth profiles.

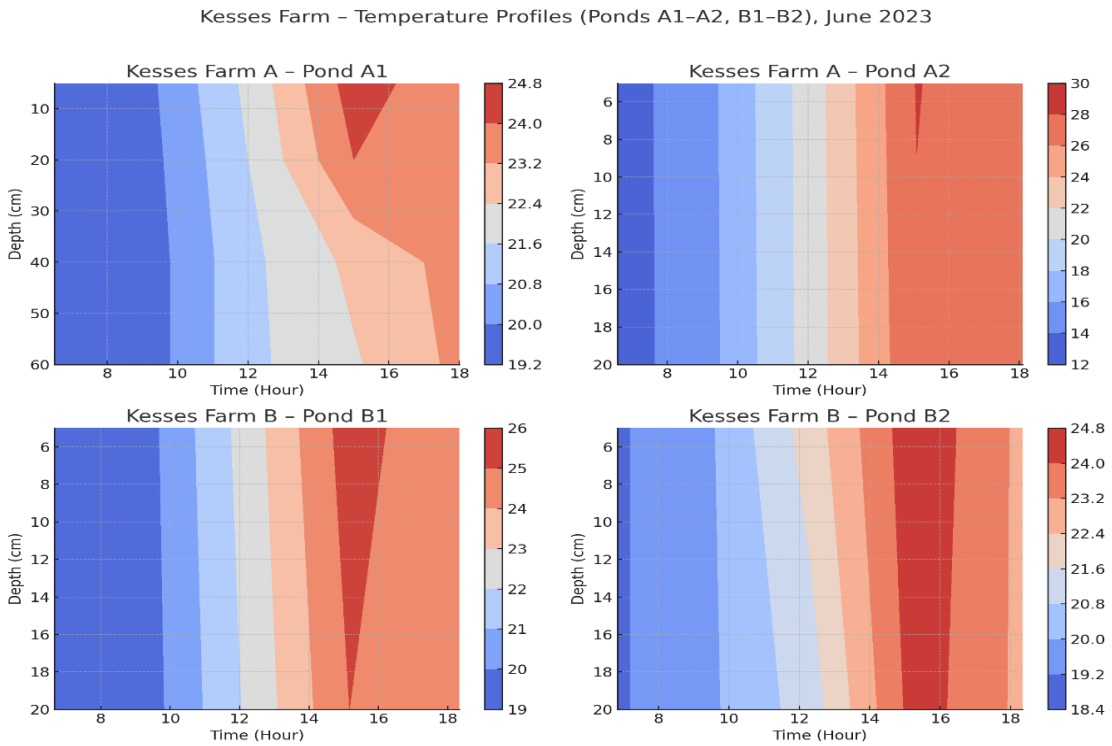


Figure 4.15: Temperature profiles of Kesses Farm A ponds (A1 - A2) and Kesses B ponds (B1–B2) in June 2023

Dissolved oxygen (DO) followed a similar diurnal rhythm to that of Temperature, increasing from morning to afternoon as photosynthesis intensified as illustrated in Figure 4.16. Morning DO levels were generally low in all ponds, with values around 1.2 to 2.5 mg/L in deeper waters, reflecting limited oxygen production overnight. As sunlight increased, DO concentrations rose, especially in surface and mid-depth layers. Kesses Farm A Pond 1 showed the most pronounced oxygen gain, reaching levels of up to 8.8 mg/L in the afternoon, indicating strong photosynthetic activity. Pond 2 also showed good oxygen production, while Kesses Farm A Ponds 1 and 2 had slightly lower afternoon peaks, of around 6.6 to 7.2 mg/L.

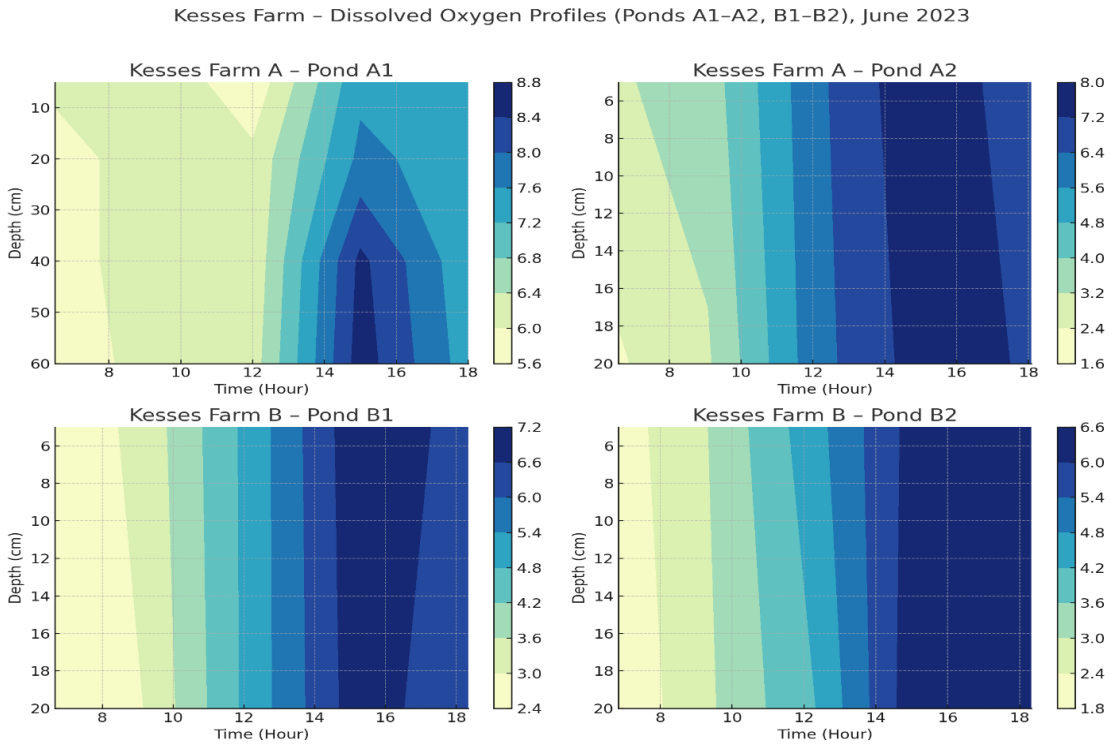


Figure 4.16: Temperature profiles of Kesses Farm A ponds (1 - 2) and Kesses Farm B ponds (1–2) in June 2023

4.3.2 Bacterial counts for Coliforms and Total bacterial counts (TBC)

Figure 4.17 a illustrates observed growth of heterotrophic bacteria in the water sample from ponds, providing an estimate of the Total Bacterial Count (TBC) while Figure 4.17 b shows a membrane filter on m-Endo agar with coliforms bacterial growth. Figure 4.17 c shows a completed MPN test, showing positive results in multiple wells. The yellow coloration indicates acid production, confirming coliform presence.

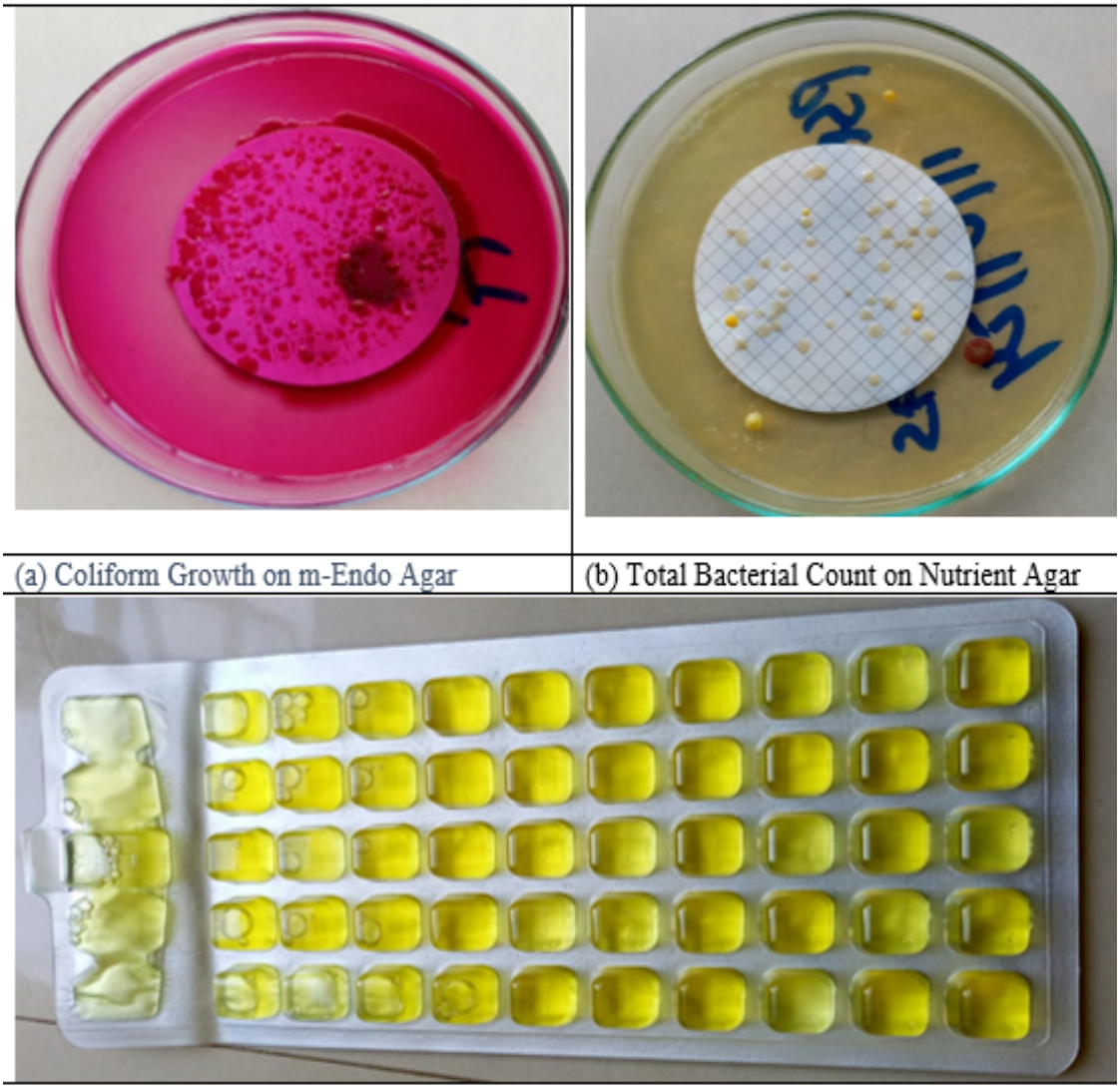


Figure 4.17: Microbiological assays for bacterial detection in water samples (a) Coliform colonies on m-Endo Agar, (b) Enumeration of total bacterial count on Nutrient Agar by membrane filtration, and (c) Most Probable Number (MPN) test setup for quantitative estimation of coliforms

Table 4.18 shows the means and ranges of bacterial count values (CFU) for coliforms and total bacterial counts (TBC) across the fish farms. The highest bacterial counts were recorded in Turbo Farm, particularly in Pond 1, which had coliform levels of 129 ± 47.6 CFU with a range of 12.0 to 180, and a TBC of 1290 ± 476 CFU ranging from 118 to 1800. These values suggest potential microbial contamination risks in that Farm. In contrast, Moiben Farm Pond 1 recorded the lowest coliform levels, with a mean of 11.5 ±

13.7 CFU and a range of 2.0 to 45.0, indicating relatively better water quality conditions. Ainapkoi, Kesses A, and Kesses B Farms exhibited moderate bacterial levels across their respective ponds, with some variation between individual pond measurements.

Table 4.18: Means and ranges for bacterial count values (CFU) in the fish farms

Farm	Pond	Coliforms (CFU)	TBC (CFU)
Moiben Farm	1	11.5 ± 13.7 [2.0–45.0]	143 ± 195 [31.7–650]
	2	84.3 ± 69.5 [4.0–214]	830 ± 688 [45.0–2120]
	3	41.9 ± 31.9 [2.0–112]	399 ± 319 [0–1100]
	4	46.3 ± 37.6 [4.0–123]	443 ± 376 [20.0–1210]
Ainapkoi Farm	1	23.7 ± 23.4 [3.0–82.0]	280 ± 281 [32.0–980]
	2	32.3 ± 29.3 [3.0–96.0]	383 ± 352 [32.0–1150]
	3	44.8 ± 44.8 [2.0–126]	533 ± 537 [20.0–1510]
Kesses Farm A	1	37.6 ± 30.1 [5.0–89.0]	410 ± 331 [52.0–976]
	2	39.3 ± 25.9 [4.0–85.0]	468 ± 310 [44.0–1020]
Kesses Farm B	1	41.7 ± 33.1 [2.0–95.0]	453 ± 364 [17.0–1040]
	2	45.5 ± 16.6 [13.0–70.0]	413 ± 150 [120–635]
Turbo Farm	1	129 ± 47.6 [12.0–180]	1290 ± 476 [118–1800]
	2	94.4 ± 59.4 [12.0–180]	844 ± 535 [103–1620]

Table 4.19 summarizes the bacterial counts in different aquaculture Facility Types used

in the Farms. Liner ponds exhibited the highest bacterial levels, with coliforms averaging 68.1 ± 59.9 CFU (range: 3.00–180) and TBC at 684 ± 572 CFU (range: 32.0–1800), suggesting greater microbial accumulation in these systems. Earthen ponds showed moderate bacterial levels, with coliforms and TBC counts. Conversely, Tank-based systems recorded the lowest bacterial counts, with coliforms at 29.5 ± 26.8 CFU and TBC at 340 ± 312 CFU, indicating better microbial water quality control.

Table 4.19: Means and ranges of bacterial counts (CFU) by facility type

Facility Type	Coliforms (CFU)	Total Bacteria Counts (CFU)
Earthen Pond	50.7 ± 43.4	512 ± 449
	[2.0–214]	[0–2120]
Liner Pond	68.1 ± 59.9	684 ± 572
	[3.0–180]	[32.0–1800]
Tanks	29.5 ± 26.8	340 ± 312
	[2.0–89.0]	[31.7–1020]

Correlation analysis among the physico-chemical and microbial parameters revealed several significant interrelationships as shown in Table 4.20. Temperature demonstrated a near-perfect positive correlation with pH (r = 0.99). Similarly, dissolved oxygen (DO) was positively correlated with both temperature (r = 0.91) and pH (r = 0.93). Moderate positive correlations were observed between Chemical Oxygen Demand (COD) and Biological Oxygen Demand (BOD) (r = 0.56), confirming their shared representation of organic loading (total vs. biodegradable). Furthermore, BOD and COD were positively

associated with microbial indicators, including Total Bacterial Count (TBC) and Faecal Coliforms, reinforcing the link between organic matter and microbial proliferation.

Table 4.20: Correlation analysis of water quality parameters

Factor	Temp	DO	pH	COD (mg/L)	BOD (mg/L)	Coliforms (CFU/ml)	TBC (CFU/ml)
Temp	1.000	0.915	0.994	0.030	-0.025	-0.082	-0.082
DO	0.915	1.000	0.925	0.084	0.025	-0.088	-0.086
pH	0.994	0.925	1.000	0.037	-0.039	-0.095	-0.094
COD (mg/L)	0.030	0.084	0.037	1.000	0.556	0.350	0.364
BOD (mg/L)	-0.025	0.025	-0.039	0.556	1.000	0.379	0.421
Coliforms (CFU/ml)	-0.082	-0.088	-0.095	0.350	0.379	1.000	0.991
TBC (CFU/ml)	-0.081	-0.086	-0.094	0.364	0.421	0.991	1.000

4.3.3 Water Quality Index (WQI) by Farm and Facility Type

The WQI results revealed substantial variation in water quality across farms and facility types, as presented in Table 4.21. The highest overall WQI was recorded at Kesses Farm B (Earthen system) with a score of 86.9, indicating excellent water conditions. This was followed closely by Turbo Farm (Liner system) at 84.7 and Moiben Farm (Earthen) at 82.3, both reflecting generally favorable aquaculture environments. In contrast, Kesses Farm A (Tank system) showed the lowest WQI score of 62.6, suggesting moderate to poor water quality. This lower score was primarily influenced by elevated levels of BOD and COD, along with less favorable pH values. Similarly, Ainapkoi's Farm liner system also ranked slightly lower, with a WQI of 74.0, attributed to increased organic loads and microbial counts, although still within acceptable operational limits.

Table 4.21: Water Quality Index (WQI) by Farm and Facility Type

Farm	Facility Type	Overall WQI	Temp	DO	pH	COD	BOD	Coliforms	TBC
Ainapkoi	Earthen	81.81	77.39	100	75.49	67.68	70.32	97.76	84.01
Ainapkoi	Liner	82.30	79.47	100	78.55	75.90	53.52	98.60	90.06
Kesses A	Tank	62.63	61.78	100	11.47	52.39	27.84	98.08	86.82
Kesses B	Earthen	86.94	72.42	100	91.07	83.96	76.32	97.82	87.01
Moiben	Earthen	77.25	68.96	100	79.98	55.30	56.13	97.13	83.29
Moiben	Tank	91.02	73.59	100	82.22	93.50	92.68	99.43	95.71
Turbo	Liner	75.94	76.26	100	94.36	55.71	43.41	94.32	67.48

4.4 Effect of Bacteria and parasites on fish growth and the influence of water Quality on occurrence of bacteria and parasites

4.4.1 Effect of Bacteria and parasites on fish growth

The results for the influence of bacterial species isolated in fish organs on fish growth are summarized in Table 4.22. Among the bacterial species detected in the gills, *V. alginolyticus* had a significant negative effect on fish growth (Beta coefficient = -0.428, $p < 0.0001$). The other species did not significantly affect fish performance. Among the bacteria that infected the kidney, *P. aeruginosa* significantly affected fish performance (Beta coefficient = -0.282, p = 0.0005) while rest of the bacteria did not have any significant influence on the fish performance. None of the bacterial species isolated from the intestines showed significant effect on the fish growth. Among the bacteria that affected the skin, *P. aeruginosa* had a significant negative effect on fish growth (Beta coefficient = -0.222, p = 0.0168) while ther species, including *E. coli*, *P. fluorescens*, *A. hydrophila*, *Flav. columnare*, and *V. alginolyticus*, did not significantly affect fish growth.

Table 4.22: Effect of bacterial species on productivity of *O. niloticus*

Parameter	Beta Coefficient	Standard Error	T Statistic	P-Value
Bacterial species in Gills				
E. coli	-0.001806	0.097104	-0.01860	0.98520
P. aeruginosa	0.003260	0.104748	0.03112	0.97520
V. harveyi	0.122564	0.086917	1.41012	0.16060
V. alginolyticus	-0.427968	0.077534	-5.51972	0.0000
Bacterial Species in Kidney				
E. coli	-0.062227	0.078632	-0.79137	0.4300
P. aeruginosa	-0.281635	0.078632	-3.58168	0.0005
Bacterial Species in Intestines				
V. harveyi	-0.062656	0.125937	-0.49752	0.6196
A. hydrophi	-0.063651	0.092241	-0.69005	0.4912
P. aeruginosa	-0.110619	0.134795	-0.82064	0.4132
Flav. columnare	-0.025538	0.114468	-0.22311	0.8238
V. alginolyticus	-0.042316	0.086879	-0.48707	0.6269
E. coli	0.014003	0.103631	0.13512	0.8927
Bacterial Species in Skin				
E. coli	0.033839	0.080848	0.41855	0.6761
P. fluorescens	-0.172665	0.118352	-1.45892	0.1467
A. hydrophila	-0.030111	0.106093	-0.28382	0.7769
Flav. columnare	-0.010467	0.092413	-0.11327	0.9100
P. aeruginosa	-0.222369	0.091950	-2.41836	0.0168
V. alginolyticus	-0.121395	0.089949	-1.34960	0.1792

The results for the influence of parasite species found in fish organs on fish growth are summarized in Table 4.23. Among the gill-associated parasites, *T. nigra* exhibited a statistically significant negative association with growth rate (Estimate = –0.482, $p < 0.0001$). In contrast, *C. tilapiae* (p = 0.5539) and *D. vastator* (p = 0.7125) showed no significant effect on growth rate. In the intestine, *C. complanatum* was significantly negatively associated with growth (Estimate = -0.252, p = 0.0034), while *Haplorchis* spp. showed no effect on growth rate (Estimate = -0.157, p = 0.0648). Among skin parasites, *G. elegans* showed a significant negative relationship with growth rate (Estimate

= –0.355, $p < 0.0001$), while *I. multifilis*, was not significantly associated with growth rate (p = 0.2296).

Table 4.23: Means and Ranges of Values for Physicochemical Parameters Across the Farms

Parameter	Estimate	Standard Error	T Statistic	P-Value
Parasite Species in Gills				
Trichodina nigra	-0.482351	0.080212	-6.01349	0.0000
Cichlidogyrus tilapiae	-0.049159	0.082870	-0.59321	0.5539
Dactylogyrus vastator	0.030886	0.083673	0.36913	0.7125
Parasite Species in Intestines				
Clinostomum complanatum	-0.251887	0.084597	-2.97749	0.0034
Haplorchis spp.	-0.157369	0.084597	-1.86022	0.0648
Parasite Species in Skin				
Gyrodactylus elegans	-0.355187	0.083295	-4.26423	0.0000
Ichthyophthirius multifiliis	-0.100461	0.083295	-1.20609	0.2296

4.4.2 Impact of Water Quality on Bacterial Infestation by Organ, and Farm

4.4.2.1 Influence of Water Quality on Bacterial infestation of Fish Organs across Farms

The analysis revealed significant associations between water quality parameters and bacterial species infestations in different fish organs, with distinct patterns observed across farms as shown in Table 4.24. In the kidney, *P. aeruginosa* infestation showed a strong positive association with BOD across all farms. The relationship was statistically significant in Turbo Farm (coefficient = 0.88, p = 0.001), Kesses A (p = 0.023), and Moiben (p = 0.045). Similarly, *A. hydrophila* in the kidney was positively associated with TBC, with the strongest associations observed in Turbo Farm (p = 0.005) and Moiben Farm (p = 0.032), and weaker significance in Kesses Farm A, Kesses Farm B, and Ainapkoi Farm (p = 0.055 – 0.071). For the skin, *A. hydrophila* was negatively associated with pH, most notably in Ainapkoi Farm (p = 0.023), Kesses Farm B (p = 0.034), and Turbo Farm (p = 0.044), with marginal significance in Kesses Farm A and Moiben Farm. Additionally,

P. aeruginosa showed a strong positive correlation with TBC, particularly in Turbo (p = 0.002) and Ainapkoi Farm (p = 0.031). In the gills, *V. alginolyticus* was negatively associated with both Dissolved Oxygen (DO) and Coliform levels. The association with DO was significant in Turbo Farm (p = 0.010) and Moiben Farm (p = 0.019), with decreasing significance across Kesses Farm A (p = 0.063), Kesses Farm B (p = 0.072), and Ainapkoi Farm (p = 0.088). A similar trend was observed for Coliforms, with strongest significance in Turbo Farm (p = 0.033) and Moiben Farm (p = 0.048), again reducing in the other sites.

Table 4.24: Impact of Water Quality Factors on Bacterial Species Infestation across Fish Organs and Farms

Organ	Bacterial Spp.	Parameter	Farm	Coefficient	p-value
Kidney	*P. aeruginosa*	BOD	Turbo	0.88	0.001
			Kesses A	0.88	0.023
			Kesses B	0.88	0.057
			Ainapkoi	0.88	0.118
			Moiben	0.88	0.045
	A. hydrophila	TBC	Turbo	0.67	0.005
			Moiben	0.67	0.032
			Kesses A	0.67	0.055
			Kesses B	0.67	0.066
			Ainapkoi	0.67	0.071
Skin	*A. hydrophila*	pH	Ainapkoi	-0.53	0.023
			Kesses A	-0.53	0.081
			Kesses B	-0.53	0.034
			Moiben	-0.53	0.092
			Turbo	-0.53	0.044
	P. aeruginosa	TBC	Turbo	0.72	0.002
			Moiben	0.72	0.045
			Kesses A	0.72	0.083
			Kesses B	0.72	0.092
			Ainapkoi	0.72	0.031
Gills	*V. alginolyticus*	Dissolved Oxygen	Turbo	-0.41	0.010*
			Moiben	-0.41	0.019
			Kesses A	-0.41	0.063
			Kesses B	-0.41	0.072
			Ainapkoi	-0.41	0.088
	V. alginolyticus	Coliforms	Turbo	-0.39	0.033
			Moiben	-0.39	0.048
			Kesses A	-0.39	0.061
			Kesses B	-0.39	0.075
			Ainapkoi	-0.39	0.082

4.4.2.2 Influence of Water Quality on Bacterial infestation of Fish Organs across Facility Type

The regression analysis revealed strong and consistent associations between water quality parameters and bacterial species infestation across fish organs, with variations noted by facility type (Earthen, Tank, and Liner) as shown in Table 4.25. In the kidney, *P. aeruginosa* infestation was positively associated with BOD across all facility types, with a highly significant relationship in Earthen ponds (p = 0.001), followed by Tanks (p = 0.023), and Liners (p = 0.057). Similarly, *A. hydrophila* infestation in the kidney was strongly linked to Total Bacterial Count (TBC), with significance highest in Earthen systems (p = 0.005), and declining in Tanks (p = 0.032) and Liners (p = 0.055). In the skin, *A. hydrophila* infestation showed a negative correlation with pH, indicating increasing infestation at lower pH values. This relationship was statistically significant in Earthen systems (p = 0.023) and Liners (p = 0.034) only. On the other hand, *P. aeruginosa* skin infestation was positively associated with TBC, with strong significance in Earthen facilities (p = 0.002) and moderate in Tanks (p = 0.045), and not significant in Liners (p = 0.083).

In the gills, *V. alginolyticus* infestation was negatively associated with Dissolved Oxygen (DO), showing statistically significant relationships in Earthen (p = 0.010) and Tank facilities (p = 0.019). Additionally, coliform levels were negatively correlated with *V. alginolyticus* presence in the gills, with descending significance across Earthen (p = 0.033), Tank (p = 0.048), and Liner systems (p = 0.061).

Table 4.25: Impact of Water Quality Factors on Bacterial Species Infestation by Organ and Facility Type

Organ	Bacterial Spp.	Water Quality Factor	Facility Type	Coefficient	p-value
Kidney	*P. aeruginosa*	BOD	Earthen	0.88	0.001
			Tank	0.88	0.023
			Liner	0.88	0.057
Kidney	*A. hydrophila*	TBC	Earthen	0.67	0.005
			Tank	0.67	0.032
			Liner	0.67	0.055
Skin	*A. hydrophila*	pH	Earthen	-0.53	0.023
			Tank	-0.53	0.081
			Liner	-0.53	0.034
	P. aeruginosa	TBC	Earthen	0.72	0.002
			Tank	0.72	0.045
			Liner	0.72	0.083
Gills	*V. alginolyticus*	Dissolved Oxygen	Earthen	-0.41	0.010
			Tank	-0.41	0.019
			Liner	-0.41	0.063
		Coliforms	Earthen	-0.39	0.033
			Tank	-0.39	0.048
			Liner	-0.39	0.061

4.4.2.3 Influence of Water Quality on Bacterial infestation of Fish Organs across seasons

The influence of water quality parameters on bacterial infestations was found to vary significantly across fish organs and seasons as shown in Table 4.26. In the kidney, *P. aeruginosa* infestation during the Short Rains showed a strong negative correlation with pH ($p = 0.017$), and was positively associated with both BOD ($p = 0.044$) and temperature ($p = 0.032$). A second, independent significant relationship was observed during the Low Rains, where COD positively predicted *P. aeruginosa* infestation ($p = 0.017$).

The gills exhibited multifactorial susceptibility across seasons. *E. coli* infestation was significantly influenced by BOD during both the Long Rains ($p = 0.017$) and the Low Rains ($p < 0.001$), while during the Short Rains, temperature, DO, and pH were highly significant ($p \leq 0.001$). A similar seasonal profile was observed for *P. aeruginosa*, which responded strongly to BOD, temperature, and DO during the Short Rains. *V.*

alginolyticus demonstrated season-specific sensitivity to pH, with highly significant negative associations during both the Short ($p = 0.003$) and Low Rains ($p = 0.001$), while temperature in the Low Rains also showed a positive correlation with infestation levels ($p = 0.003$).

In the intestines, *E. coli* infestation was significantly predicted by BOD during the Long Rains ($p = 0.019$), and by temperature, DO, and pH during the Short Rains ($p \leq 0.018$). *V. harveyi* showed a negative association with temperature during the Low Rains ($p = 0.027$), while *A. hydrophila* exhibited increased occurrence in response to pH during the Short Rains ($p = 0.043$). Notably, *P. aeruginosa* responded positively to BOD during both the Long Rains ($p = 0.007$) and the Low Rains ($p = 0.005$), while temperature ($p = 0.008$) and pH ($p = 0.032$) were also significant during the Low Rains. Additionally, *Flav. columnare* infestation was negatively associated with temperature in the Low Rains ($p = 0.040$).

On the skin, *E. coli* infestation was strongly associated with temperature, DO, and pH during the Short Rains (all $p \leq 0.018$), and with BOD and COD during the Low Rains (both $p < 0.001$). *P. fluorescens* showed a significant relationship with pH across seasons, being positively correlated in both the Short ($p = 0.036$) and Low Rains ($p = 0.014$), while temperature exhibited a negative correlation during the Low Rains ($p = 0.003$). *A. hydrophila* also displayed a significant positive response to pH in the Short Rains ($p = 0.036$). For *P. aeruginosa*, pH sensitivity was evident in both the Short ($p = 0.016$) and Low Rains ($p = 0.012$), with temperature additionally showing a positive association in the Low Rains ($p = 0.004$). *V. alginolyticus* infestation was influenced by DO, pH, and BOD during the Short Rains ($p = 0.045$, $p < 0.001$, and $p = 0.002$, respectively), and by temperature ($p = 0.005$) and pH ($p = 0.020$) during the Low Rains.

Table 4.26: Statistically Significant Water Quality Factors on Bacterial Species Infestation across Seasons and Fish Organs

Organ	Bacteria	Season	Water Quality Factor	Coefficient	p-value
Kidney	*P. aeruginosa*	Short Rains	pH	-0.198	0.017
			BOD	0.004	0.044
			Temperature	0.015	0.032
			pH	-0.043	0.016
		Low Rains	COD	0.001	0.017
Gills	*E. coli*	Long Rains	BOD	0.004	0.017
		Short Rains	Temperature	0.0001	0.001
			Dissolved Oxygen	0.0001	0.018
			pH	0.0001	0.000
		Low Rains	BOD	0.0001	0.000
			COD	0.0001	0.000
	P. aeruginosa	Long Rains	BOD	0.004	0.017
		Short Rains	Temp	0.0001	0.001
			Dissolved Oxygen	0.0001	0.018
			pH	0.0001	0.000
	V. alginolyticus	Short Rains	pH	-0.249	0.003
		Low Rains	Temperature	0.036	0.003
		Low Rains	pH	-0.096	0.001
Intestines	*E. coli*	Long Rains	BOD	0.004	0.019
		Short Rains	Temperature	0.0001	0.001
			Dissolved Oxygen	0.0001	0.018
			pH	0.0001	0.000
	V. harveyi	Low Rains	Temperature	-0.045	0.027
	A. hydrophila	Short Rains	pH	0.208	0.043
	P. aeruginosa	Long Rains	BOD	0.005	0.007
		Low Rains	Temperature	0.056	0.008
			pH	-0.112	0.032
			BOD	0.004	0.005
	Flav. columnare	Low Rains	Temperature	-0.027	0.040
Skin	*E. coli*	Short Rains	Temperature	0.0001	0.001
			Dissolved Oxygen	0.0001	0.018
			pH	0.0001	0.000
		Low Rains	BOD	0.0001	0.000
			COD	0.0001	0.000
	P. fluorescens	Short Rains	pH	0.229	0.036
		Low Rains	Temperature	-0.063	0.003
			pH	0.131	0.014
	A. hydrophila	Short Rains	pH	0.229	0.036
	P. aeruginosa	Short Rains	pH	-0.326	0.016
		Low Rains	Temperature	0.057	0.004
			pH	-0.122	0.012
	V. alginolyticus	Short Rains	Dissolved Oxygen	0.004	0.045
			pH	-0.378	0.000
			BOD	0.006	0.002
		Low Rains	Temperature	0.054	0.005
			pH	-0.111	0.020

4.4.3 Impact of Water Quality on arasite Infestation by Organ, and Farm

4.4.3.1 Influence of Water Quality on Bacterial infestation of Fish Organs across Farms

The relationship between water quality parameters and parasite species infestation was examined across different fish organs, revealing consistent patterns influenced by specific environmental factors and varying levels of statistical significance across farms as shown in Table 4.27. In the gills, *T. nigra* infestation was positively associated with water temperature across all farms. This association was highly significant in Turbo (p = 0.003) and Kesses Farm A (p = 0.041), with weaker significance in Kesses Farm B (p = 0.079) and Moiben farm (p = 0.112), and non-significant in Ainapkoi Farm (p = 0.188). *G. elegans* in the gills showed a significant negative association with coliform levels in Moiben Farm (p = 0.016), while other farms did not show statistically strong relationships.

On the skin, *G. elegans* exhibited a negative association with dissolved oxygen (DO), with statistically significant effects in Turbo Farm (p = 0.015) and Moiben Farm (p = 0.022), and marginal effects in Ainapkoi Farm (p = 0.084) with no significant associations in Kesses Farm A and Kesses farm B. In contrast, *T. nigra* infestation on the skin was positively associated with total bacterial count (TBC) across all farms, with significant associations in Turbo Farm (p = 0.004), Moiben Farm (p = 0.011), and Kesses Farm A (p = 0.036). The relationship remained near-significant in Kesses B (p = 0.054) and Ainapkoi Farm (p = 0.072), indicating a broad but variable influence of TBC. Within the intestines, *C. complanatum* infestation showed a consistent positive association with BOD and coliforms. For BOD, significant effects were found in Kesses Farm A (p =

Table 4.27: Impact of Water Quality Factors on Parasite Species Infestation across Fish Organs and Farms

Organ	Parasite Spp.	Water Quality Factor	Farm	Coefficient	p-value
Gills	*T. nigra*	Temperature	Turbo	0.62	0.003
			Kesses A	0.62	0.041
			Ainapkoi	0.62	0.188
			Kesses B	0.62	0.079
			Moiben	0.62	0.112
	G. elegans	Coliforms	Turbo	-0.45	0.061
			Moiben	-0.45	0.016
			Kesses A	-0.45	0.134
			Kesses B	-0.45	0.147
			Ainapkoi	-0.45	0.158
Skin	*G. elegans*	DO_2	Turbo	-0.48	0.015
			Moiben	-0.48	0.022
			Ainapkoi	-0.48	0.084
			Kesses A	-0.48	0.145
			Kesses B	-0.48	0.173
	T. nigra	TBC	Turbo	0.61	0.004
			Moiben	0.61	0.011
			Kesses A	0.61	0.036
			Kesses B	0.61	0.054
			Ainapkoi	0.61	0.072
Intestines	*C. complanatum*	BOD	Kesses A	0.55	0.021
			Turbo	0.55	0.027
			Ainapkoi	0.55	0.089
			Kesses B	0.55	0.132
			Moiben	0.55	0.105
	C. complanatum	Coliforms	Turbo	0.58	0.027
			Moiben	0.58	0.051
			Kesses A	0.58	0.028
			Kesses B	0.58	0.049
			Ainapkoi	0.58	0.061

0.021) and Turbo Farm (p = 0.027), while associations in Ainapkoi, Moiben, and Kesses B Farms were less statistically significant ($p > 0.05 but < 0.15$). Regarding coliforms, infestation levels were significantly associated in Turbo Farm (p = 0.027), Kesses Farm A (p = 0.028), and Kesses Farm B ($p = 0.049$).

4.4.3.2 Influence of Water Quality on Bacterial infestation of Fish Organs across Facility types

Regression analysis revealed notable relationships between specific water quality parameters and parasite infestations in fish, with varying levels of statistical significance across facility types (Earthen, Tank, and Liner) as shown in Table 4.28. In the gills, *T. nigra* infestation was positively associated with water temperature across all systems.

The association was statistically strongest in Earthen facilities (p = 0.003), followed by Tanks (p = 0.029), and approaching significance in Liners (p = 0.051). On the skin, *G. elegans* infestation showed a negative correlation with dissolved oxygen (DO), indicating higher parasite loads under lower oxygen conditions. The relationship was statistically significant in Earthen (p = 0.015) and Tank systems (p = 0.022), while Liners were not significant (p = 0.067), but still pointing to a meaningful trend. In the intestines, *C. complanatum* infestation was positively associated with Biological Oxygen Demand (BOD) with significant relationship in Tanks (p = 0.021), Earthen systems (p = 0.027), and marginal significance in Liners (p = 0.058).

Table 4.28: Impact of Water Quality Factors on Parasite Species Infestation by Organ and Facility Type

Organ	Parasite Spp.	Parameter	Facility Type	Coefficient	p-value
Gills	*T. nigra*	Temperature	Earthen	0.62	0.003
			Tank	0.62	0.029
			Liner	0.62	0.051
Skin	*G. elegans*	DO	Earthen	-0.48	0.015
			Tank	-0.48	0.022
			Liner	-0.48	0.067
Intestines	*C. complanatum*	BOD	Earthen	0.55	0.027
			Tank	0.55	0.021
			Liner	0.55	0.058

4.4.3.3 Influence of Water Quality on Bacterial infestation of Fish Organs across Seasons

The influence of water quality parameters on Parasite species infestations was found to vary significantly across fish organs and seasons as shown in Table 4.29. In the gills, *C. tilapiae* infestation exhibited a positive and statistically significant association with COD during both the Short Rains (p = 0.007) and Low Rains (p = 0.040). Similarly, *D.*

vastator also showed a positive correlation with COD during the Short Rains (p = 0.019) and Low Rains (p = 0.021). In addition to COD, *D. vastator* infestation was negatively associated with temperature in the Low Rains (p = 0.025). In the intestines, *Haplorchis* spp. was significantly influenced by COD during the Short Rains (p = 0.025), while during the Low Rains, infestation levels were positively associated only with the pH (p = 0.045).

Table 4.29: Statistically Significant Water Quality Factors on Parasite Species Infestation across Seasons and Fish Organs

Organ	Parasite	Season	Parameter	Coefficient	p-value
Gills	*Cichlidogyrus spp.*	Short Rains	COD	0.010	0.007
		Low Rains	COD	0.003	0.040
	D. vastator	Short Rains	COD	0.012	0.019
		Low Rains	Temperature	-0.073	0.025
		Low Rains	COD	0.005	0.021
Intestines	*Haplorchis spp.*	Short Rains	COD	0.006	0.025
		Low Rains	pH	0.072	0.045

4.5 Antibiotic sensitivity of bacterial isolates from farmed fish to commonly used antibiotics

The results for antibiotic resistance profiles of thirteen bacterial species assessed across six antibiotics: amoxicillin (AMX), ciprofloxacin (CIP), cotrimoxazole (CT), doxycycline (DO), erythromycin (ERY), and streptomycin (STR), isolated from fish farms in Uasin Gishu County are shown in Table 4.30. Amoxicillin and Erythromycin exhibited highly significant interspecies variability in resistance. Both antibiotics yielded p-values of 0.0005, well below the conventional significance threshold of 0.05. This indicates that susceptibility to these two drugs was not uniform across the bacterial isolates, suggesting species-specific resistance dynamics.

In contrast, the remaining four antibiotics; Cotrimoxazole, Doxycycline, Streptomycin,

and Ciprofloxacin, did not show statistically significant variation in resistance patterns among the bacterial species. Cotrimoxazole yielded a p-value of 0.3183, Doxycycline 0.3618, Streptomycin 0.7561, and Ciprofloxacin 0.8541. These results suggest that resistance to these antibiotics was relatively consistent across the bacterial isolates examined.

Table 4.30: P-values for interspecies variation in antibiotic resistance among bacterial isolates ($p < 0.05$)

Antibiotic	p_value	Significance	Significance
Amoxicillin (AMX)	0.0005	***	***
Erythromycin (ERY)	0.0005	***	***
Cotrimoxazole (CT)	0.3183	ns	ns
Doxycycline (DO)	0.3618	ns	ns
Streptomycin (STR)	0.7561	ns	ns
Ciprofloxacin (CIP)	0.8541	ns	ns

*** - Highly significant differences in resistance patterns
ns - No significant differences in resistance patterns

The results for antibiotic resistance patterns assessed across six antibiotics are presented in Figure 4.18. Overally, ciprofloxacin, doxycycline, and streptomycin exhibited the highest efficacy, with susceptibility rates exceeding 80% in most bacterial groups. In contrast, amoxicillin and erythromycin demonstrated reduced effectiveness, with resistance observed in up to 60% of isolates for certain taxa.

Within the Aeromonas genus, *A. caviae* and *A. sobria* showed particularly high resistance to amoxicillin, with approximately 45–55% of isolates classified as resistant, while *A. hydrophila* remained largely susceptible ($\geq$ 85%) across the antibiotic panel. Moderate resistance to erythromycin was also observed in *A. caviae* (about 30%) and *A. sobria* (nearly 35%). In contrast, Bacillus spp. and Micrococcus spp. demonstrated strong susceptibility profiles, with $\geq$ 90% of isolates responding to all antibiotics tested, and

minimal intermediate responses (typically under 10%).

E. coli exhibited moderate resistance to amoxicillin and erythromycin, with approximately 30–35% of isolates resistant, though susceptibility to ciprofloxacin, doxycycline, and streptomycin remained high ($\geq$ 70%). *Flav. columnare* showed near-complete sensitivity to all six antibiotics, with resistance levels below 5%. Similarly, *P. aeruginosa* demonstrated consistent susceptibility across the board, with $\geq$ 85% of isolates classified as sensitive for each antibiotic.

Notable resistance patterns were seen in *Plesiomonas spp*. and *Streptococcus spp.*, particularly to amoxicillin and erythromycin, where resistance rates reached 40–50%. However, these genera maintained high susceptibility ($\geq$ 80%) to ciprofloxacin and doxycycline. The *Vibrio spp.* (*V. alginolyticus* and *V. harveyi*) showed greater heterogeneity in resistance patterns. *V. harveyi*, for instance, exhibited resistance in 30% of isolates to both erythromycin and cotrimoxazole, while *V. alginolyticus* showed slightly lower resistance at around 20 – 25% for these antibiotics.

In summary, ciprofloxacin, doxycycline, and streptomycin were the most consistently effective antibiotics, with over 80% susceptibility across most bacterial species. In contrast, amoxicillin and erythromycin were the least effective, with resistance rates ranging from 30% to over 50% in several taxa, particularly among *Aeromonas* spp., *Streptococcus* spp., and *Vibrio* spp. These findings highlight the critical need for targeted antibiotic selection based on species-level resistance patterns to optimize therapeutic outcomes and mitigate resistance development.

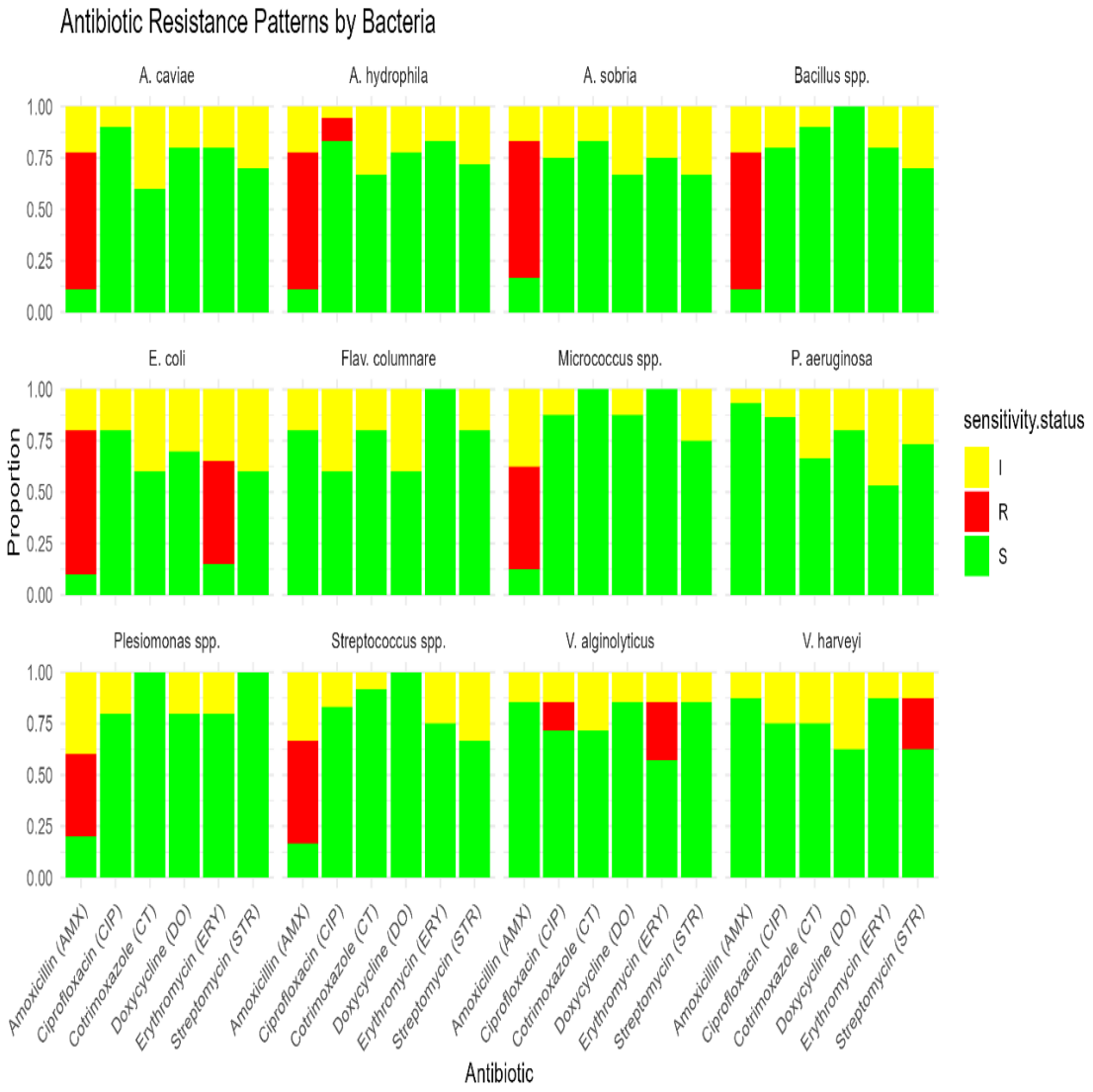


Figure 4.18: Antibiotic Resistance Patterns of Bacterial Isolates from Fish farms in Uasin Gishu County

Figure 4.19 illustrates the antibiotic resistance profiles of bacterial isolates using a heatmap with hierarchical clustering. The clustering reveals clear patterns of elevated resistance to Amoxicillin and Erythromycin among several isolates, particularly *E. coli*, *A. hydrophila*, and *Streptococcus* spp., which show strong red signals indicating resistance levels above 60%. In contrast, antibiotics such as Ciprofloxacin, Cotrimoxazole, and Doxycycline showed minimal resistance across all isolates, reflected by the predominance of white or pale pink shading. The dendrogram also groups species with

similar resistance behaviors, highlighting the coherence of certain taxa in their antibiotic responses. These visual patterns align with statistical findings from Fisher's exact test, which confirmed significant inter-species variation only for Amoxicillin and Erythromycin.

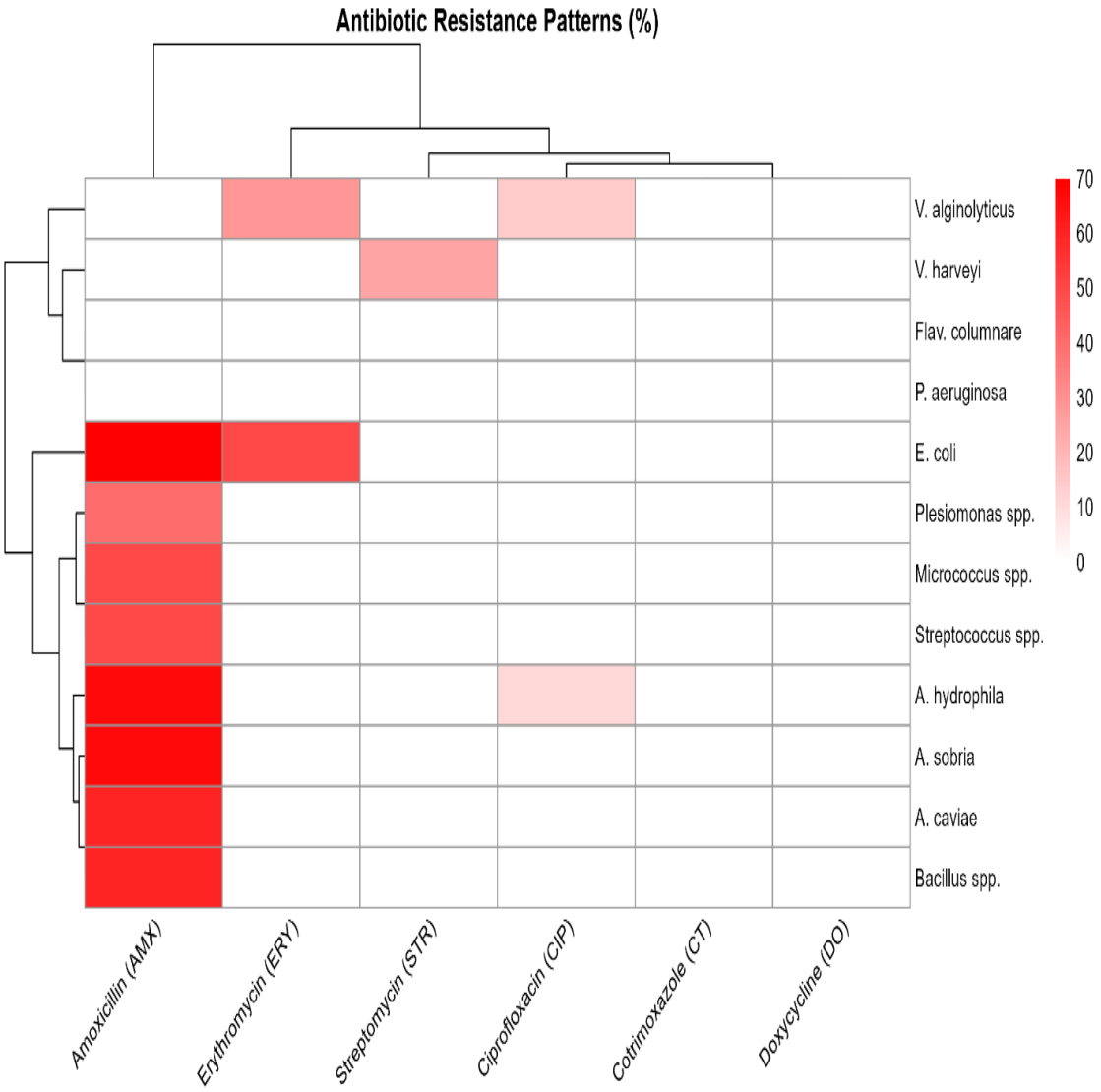


Figure 4.19: Heatmap showing percentage resistance of bacterial isolates to six antibiotics across the fish farms. (The intensity of red color represents the level of resistance, with darker shades indicating higher percentages)

The PCA biplot (Figure 4.20 summarizes the multidimensional antibiotic resistance data by reducing it into two principal components: Dim1 (37.1% variance) and Dim2 (31.6% variance). Amoxicillin (AMX) and Erythromycin (ERY) project strongly along the posi-

tive Y-axis and negative Y-axis respectively, suggesting they are key drivers of resistance variability among the isolates. *E. coli* and *A. hydrophila* appear more distant from the origin in relation to these two antibiotics, indicating species-specific resistance trends. In contrast, antibiotics like Ciprofloxacin (CIP), Cotrimoxazole (CT), and Doxycycline (DO), which are less variable according to Fisher's test, contribute minimally to dimensional separation and cluster near the origin.

The species clustering further reinforce the heatmap and statistical analysis findings, where isolates with similar resistance responses are grouped together. For instance, *V. harveyi* and *V. alginolyticus* lies away from others, indicating distinct resistance behaviours. This PCA visualization supports the interpretation that Amoxicillin and Erythromycin are the most discriminative agents in explaining resistance diversity across the bacterial spectrum.

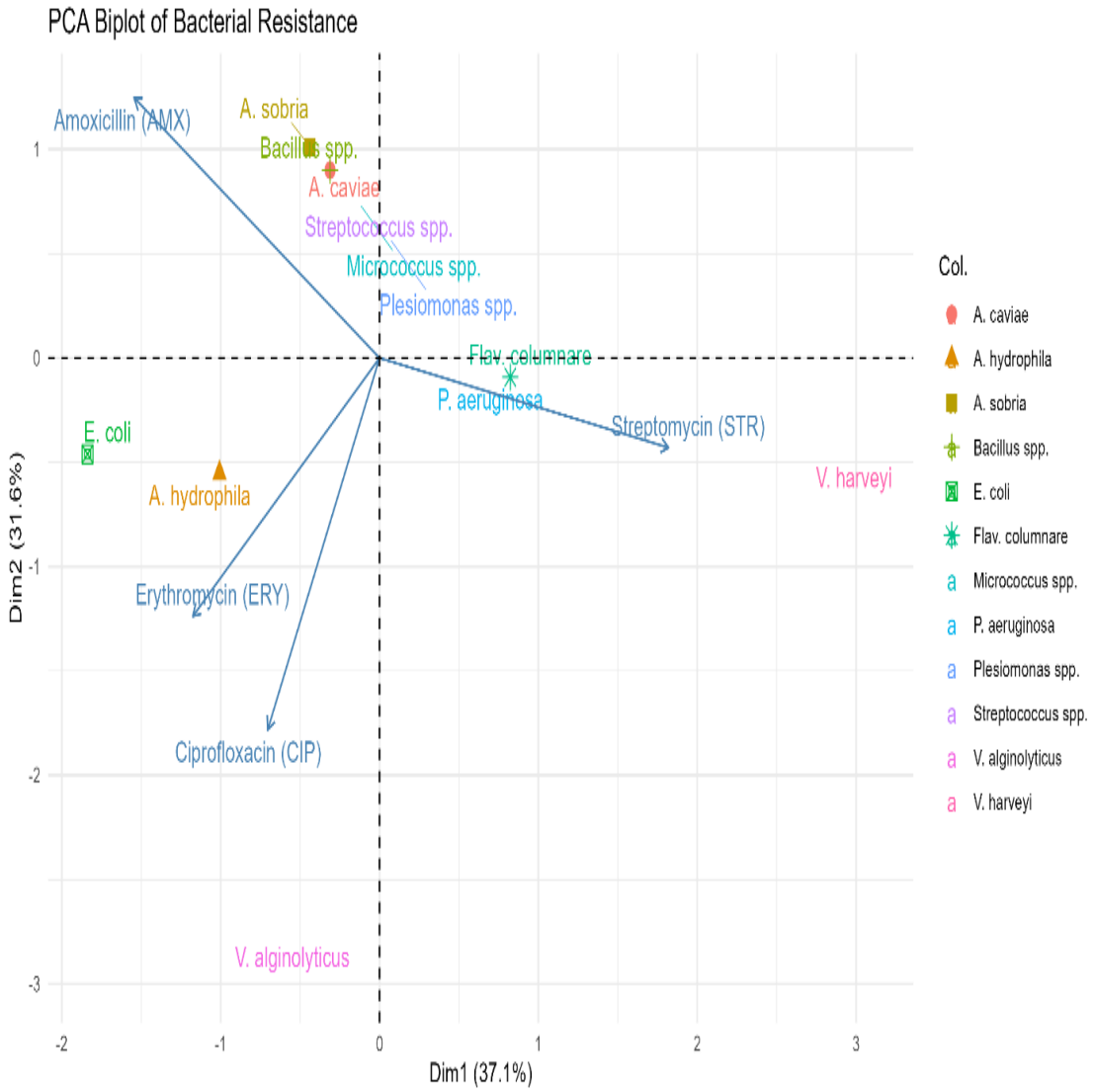


Figure 4.20: Principal Component Analysis (PCA) biplot illustrating variation in bacterial

CHAPTER FIVE

DISCUSSION

5.1 Isolation and Identification of Bacterial Species

5.1.1 Bacterial Organisms Isolated from Selected Fish Farms

The identification of 154 bacterial isolates from 468 fish samples across aquaculture farms in Uasin Gishu County revealed a broad spectrum of bacterial taxa, spanning both Gram-positive and Gram-negative groups. This microbial diversity aligns with the established understanding that fish and aquaculture systems harbor a dynamic microbiota influenced by water quality, stocking density, feeding practices, and environmental hygiene (Ferreira et al., 2022; Onyango et al., 2024).

Among the Gram-positive bacteria, *Bacillus* spp. and *Streptococcus* spp. were the most prevalent. Bacillus species are known for their dual role in aquaculture: while generally regarded as beneficial due to their probiotic properties and ability to degrade organic waste (Mzula et al., 2021a), certain strains have been implicated in opportunistic infections under stressed conditions (Wanja et al., 2020). *Streptococcus* spp. have been reported in streptococcal outbreaks in East African aquaculture systems, particularly affecting tilapia species (Akoll & Mwanja, 2012). The identification of *Micrococcus* spp. and *Staphylococcus* spp., although less commonly associated with pathogenicity, suggests environmental contamination, given their ubiquity in air and water surfaces.

Gram-negative isolates dominated the microbial profile, with *Escherichia coli*, *Pseudomonas aeruginosa*, and *Aeromonas* spp. being the most frequently encountered. The presence of *E. coli*, a well-established fecal contamination indicator, raises public health

concerns and reflects potential runoff from agricultural or domestic sources (Liao et al., 2021). *P. aeruginosa* was distinguishable by its β-hemolytic activity and green pigmentation due to pyocyanin production. This species is a known opportunistic pathogen capable of causing ulcerative lesions in fish and has been increasingly reported in Kenyan aquaculture systems (Igbinosa et al., 2017; Ferreira et al., 2022). Its detection in all organs underlines its adaptive versatility and persistence in aquatic environments.

Several Aeromonas species were also isolated, including *A. hydrophila*, *A. caviae*, and *A. sobria*. These bacteria are frequently implicated in hemorrhagic septicemia, especially in warm, nutrient-rich waters (Magouz et al., 2024). Their identification through hemolysis, oxidase positivity, and fermentative behavior confirms their pathogenic potential in both fish and humans.

Other Gram-negative bacteria included *Vibrio alginolyticus*, *Vibrio harveyi*, *Flavobacterium columnare*, and *Plesiomonas shigelloides*. The Vibrio species, identifiable via yellow colonies on TCBS agar, are halophilic organisms commonly associated with vibriosis and skin ulceration in marine and estuarine fish but have increasingly been isolated from freshwater farms (Shafiee et al., 2024). Their presence in Uasin Gishu freshwater systems may reflect introduction from contaminated water sources or their known ability to adapt and persist in low-salinity environments under favorable nutrient and temperature conditions

Flav. columnare, the causative agent of columnaris disease and a major concern in tilapia production, was among the pathogens detected in this study, highlighting its continued presence in regional aquaculture systems. Its considerable genomic variability and environmental resilience, as documented in earlier research (Duchaud et al., 2018; Conrad et al., 2022), likely contribute to its persistence under the diverse water quality

and management conditions observed in Uasin Gishu County.

The identification of *P. shigelloides*, a less frequently reported aquatic bacterium, is noteworthy. Though typically associated with gastrointestinal infections in humans, its occurrence in aquaculture systems has been linked to high organic loads and poor hygiene (Kariuki et al., 2021).

5.1.2 Tissue-Specific Distribution and Diversity of Bacterial Species across Farms, Facility Types, and Seasons

5.1.2.1 Organ-Specific Distribution of Bacteria

The study demonstrated distinct patterns of bacterial distribution across fish tissues (Table 4.2). *E. coli* and *P. aeruginosa* were consistently isolated from gills, intestines, skin, and kidneys, confirming their status as dominant opportunistic pathogens in aquaculture systems. This widespread colonization has been attributed to their ability to form biofilms, exhibit high motility, and tolerate environmental stressors, which collectively enable persistence across multiple tissue types (Zhang et al., 2022). The detection of these species in all examined organs aligns with their frequent association with fecal contamination and environmental exposure (Gundi et al., 2025).

Similarly, *Flav. columnare* was restricted to the intestines and skin, reinforcing its tropism for mucosal tissues where it exploits epithelial and digestive tract surfaces (Conrad et al., 2022). Notably, the intestines exhibited the greatest bacterial richness, reflecting their role as a primary microbial reservoir shaped by host diet, water intake, and metabolic processes. These findings emphasize the significance of organ-specific niches in structuring microbial communities and highlight the importance of targeted monitoring and intervention strategies.

5.1.2.2 Farm Level and Pond Level Variability

Clear inter-farm differences in bacterial diversity were observed (Table 4.3). Turbo Farm recorded the highest Shannon diversity index (1.94), indicative of a rich and evenly distributed bacterial community, while Kesses Farm A exhibited the lowest diversity (1.67). These patterns likely reflect divergent management practices, such as differences in feed composition, stocking densities, and water exchange regimes, which are known to influence microbial complexity (Marmen et al., 2021; Debnath et al., 2023). Elevated diversity at Turbo Farm may be attributable to increased organic loads or less effective disinfection practices, both of which favor microbial proliferation.

Within farms, intra-pond differences were also detected. For example, in Kesses Farm B, Pond 1 exhibited slightly higher bacterial diversity (1.76) than Pond 2 (1.75), while in Ainapkoi Farm, diversity ranged from 1.69 to 1.72 across ponds. Such fine-scale variability is consistent with the findings of (Horn et al., 2023), who reported that even subtle environmental differences, including shading, aeration efficiency, and sedimentation dynamics, can alter microbial community structure within aquaculture ponds.

Pairwise comparisons (Table 4.6) revealed significant differences in bacterial infestation patterns across farms and organs. For instance, *P. aeruginosa* was significantly more prevalent in kidneys at Turbo Farm compared to all other farms ($p < 0.001$). Similarly, *V. alginolyticus* exhibited higher gill infestation levels at Turbo Farm relative to Ainapkoi, Kesses A, Kesses B, and Moiben Farms ($p < 0.001$). In the intestines, multiple species showed significant variation, including elevated *P. aeruginosa* levels at Turbo Farm and distinct differences in the distributions of *Flav. columnare* and *V. alginolyticus* among farms. Skin tissues displayed the greatest variability, with all five analyzed

species demonstrating significant inter-farm differences. Collectively, these findings indicate that specific farm environments strongly influence bacterial colonization pressures, likely mediated by the combined effects of water quality, management practices, and local ecological conditions.

5.1.2.3 Facility Type distribution and diversity

Facility type also influenced bacterial diversity (Table 4.4). Liner ponds recorded the highest Shannon index (1.82), followed by earthen ponds (1.73), with tanks showing the lowest diversity (1.69). The richer bacterial assemblages in liner and earthen systems may reflect greater exposure to environmental inputs such as soil, runoff, and rainwater, as well as more dynamic ecological interactions (Kariuki et al., 2021; Wolińska et al., 2022). By contrast, tanks, with their more controlled environments and limited organic inputs, supported comparatively simplified microbial populations. These findings align with previous research demonstrating that recirculating aquaculture systems often harbor lower alpha diversity compared to semi-open or open systems (Nsabimana et al., 2021; Obiero et al., 2019).

5.1.2.4 Seasonal and Temporal Variation

Seasonal variation exerted a significant effect on bacterial dynamics (Table 4.5; Figure 4.6). Bacterial loads peaked during August and April, with additional increases observed in September and November across all facility types. These peaks correspond to warmer months, when elevated water temperatures accelerate microbial metabolism, enzymatic activity, and organic matter decomposition (Jiang et al., 2021). Conversely, bacterial presence was lowest during May and June, suggesting that cooler conditions

suppress microbial growth.

Notably, gill tissues consistently exhibited the highest bacterial loads during warmer periods (Figure 4.7). This trend was most pronounced in Turbo Farm, where gill colonization remained elevated from August through April. These findings support the work of (Consuegra et al., 2023), who highlighted the gills' large surface area and continuous water contact as key factors predisposing them to bacterial adherence and colonization.

5.1.3 Bacterial Species Co-Occurrence in Organs across Farms, Facility Types, and Seasonal Patterns

5.1.3.1 Organ-Level Co-Occurrence

Bacterial species co-occurrence displayed strong organ-specific patterns. The gills supported the most complex associations, frequently involving *E. coli*, *P. aeruginosa*, and *Vibrio* spp. This complexity reflects the gills' continuous interaction with the external environment, making them highly susceptible to multi-species colonization. Comparable interactions among these bacteria have been identified in aquaculture systems with limited water management and poor biosecurity (Lian et al., 2023).

The intestines exhibited the highest overall diversity, with recurring co-infections involving *E. coli*, *P. aeruginosa*, *V. alginolyticus*, and *Flav. columnare*. This highlights the gut as a major microbial reservoir where nutrient availability and organic matter accumulation facilitate species interactions. Previous studies similarly identified intestinal microbial complexity as a marker of suboptimal water quality and nutrient loading (Clols-Fuentes et al., 2024; Horn et al., 2023; Jiang et al., 2021).

The kidneys exhibited the least complex bacterial associations, being dominated by *E.*

coli across most farms, with *P. aeruginosa* largely confined to Turbo Farm. The site-specific presence of *P. aeruginosa* in kidneys likely reflects environmental and management conditions, such as reduced water exchange and organic matter accumulation, which can create favorable niches for this opportunistic pathogen (Emam et al., 2024; Nsabimana et al., 2021).

5.1.3.2 Farm-Level, Facility-Type and Seasonal Variation effects on Bacterial Co-occurrence

Marked differences were observed between farms. Some farms exhibited relatively simple microbial associations, whereas others displayed complex multi-species co-infections, particularly in skin and intestinal tissues. Sites characterized by greater organic loading or weaker biosecurity, such as those with limited water treatment, were associated with more complex co-occurrence networks. These patterns support evidence that farm-level practices strongly influence microbial diversity and the likelihood of pathogen interaction (Opiyo et al., 2018).

The type of facility significantly influenced co-occurrence dynamics. Earthen ponds supported complex microbial interactions, particularly in gill and intestinal tissues, reflecting the contribution of soil contact and organic matter accumulation (Kariuki et al., 2021; Kasozi et al., 2024). Liner ponds displayed higher frequencies of multi-species associations, especially combinations involving E. coli and *Pseudomonas* spp., likely due to reduced water circulation and debris retention. In contrast, tank systems exhibited relatively simple bacterial profiles, usually dominated by E. coli, consistent with findings that closed, controlled systems suppress diversity but allow persistence of hardy pathogens (Mia et al., 2022).

Seasonal changes introduced an additional layer of variation in bacterial interactions. Opportunistic pathogens such as *P. aeruginosa* and *V. harveyi* increased in prevalence during warmer months, when higher temperatures and nutrient enrichment favor microbial proliferation. In contrast, *E. coli* maintained consistent presence throughout the year, reflecting its broad tolerance across environmental gradients. Seasonal dynamics of this kind have been linked to fluctuations in temperature, rainfall, and dissolved oxygen in aquaculture ecosystems (Mahmoud et al., 2019; Horn et al., 2023; Kariuki et al., 2021).

5.1.4 Distribution and Occurrence of Parasite Species in Cultured Fish

5.1.4.1 Parasite Diversity and Tissue-Specific Occurrence

Gills were the most heavily colonized, harboring protozoans and monogeneans that caused epithelial erosion, mucus hypersecretion, and reduced respiratory efficiency. Such pathology is consistent with earlier findings that highlight the gills as the primary target for parasites due to their vascularity, constant water exposure, and relatively lower immune protection (Rahat et al., 2022). Skin infestations were dominated by *Gyrodactylus* spp. and *Ichthyophthirius* spp., while intestinal infections were primarily associated with digenean trematodes. The visceral cavity carried *Contracaecum* spp. larvae, whose presence indicates complex transmission cycles involving avian hosts.

Importantly, encysted metacercariae of *C. complanatum* and *Haplorchis* spp. were detected in gills and muscle tissues, raising zoonotic risks when fish are consumed undercooked (Menconi et al., 2023). These findings underscore not only aquaculture health challenges but also food safety concerns with direct public health implications.

5.1.4.2 Variation in Parasite Diversity across Farms and Ponds/Tanks

Marked variability in parasite diversity was observed among farms, with Turbo Farm exhibiting the highest Shannon index values, followed by Moiben and Ainapkoi Farms, while Kesses Farm A showed very low diversity. Such farm-level differences likely reflect disparities in water management, stocking densities, and proximity to intermediate or reservoir hosts, factors that have been consistently linked to parasite transmission in tropical aquaculture (Yadav et al., 2023). Marked variability in parasite diversity was observed among farms, with Turbo Farm exhibiting the highest Shannon index values, followed by Moiben and Ainapkoi Farms, while Kesses Farm A showed very low diversity. Such farm-level differences likely reflect disparities in water management, stocking densities, and proximity to intermediate or reservoir hosts, factors that have been consistently linked to parasite transmission in tropical aquaculture (Yadav et al., 2023).

Turbo Farm consistently recorded elevated infestations of *T. nigra*, *D. vastator*, and *G. elegans*, suggesting higher environmental parasite pressure, possibly due to organic matter accumulation or reduced water turnover. In contrast, Ainapkoi and Kesses A farms often recorded lower parasite burdens, which may reflect stronger biosecurity practices or environmental constraints limiting parasite propagation. Intestinal infestations were relatively low overall, though *C. complanatum* was significantly more prevalent in Turbo Farm compared to Kesses Farm A, a finding that underscores the role of local snail populations and bird vectors in sustaining digenean transmission cycles (Menconi et al., 2023).

Intra-farm variability was also evident. For instance, Moiben Farm Pond 2 had significantly higher parasite diversity than other ponds, suggesting that pond-specific ecolog-

ical features, such as shade, snail abundance, organic load, or water exchange, play a critical role in shaping parasite communities. This aligns with observations that micro-habitat heterogeneity within farms can influence both parasite survival and host exposure (Mzula et al., 2021b; Abbas et al., 2023).

5.1.4.3 Influence of Facility Type on Parasite Occurrence

Facility design strongly influenced parasite occurrence. Liner ponds harbored the most diverse parasite communities, followed by earthen ponds, while tanks showed minimal infestations. The elevated diversity in liner and earthen systems likely reflects their semi-open nature, exposure to runoff and soil, and higher likelihood of harboring intermediate hosts such as mollusks and crustaceans (Onyango et al., 2024). Conversely, tank systems, with their greater biosecurity and controlled water quality, presented less favorable environments for sustaining parasite lifecycles. This facility-type gradient highlights an important management trade-off: while semi-open systems enhance productivity through natural food inputs, they also increase vulnerability to parasitic infections compared to closed, controlled tank systems.

5.1.4.4 Seasonal and Spatial Trends in Parasite Occurrence

Seasonal dynamics were pronounced, with parasite presence peaking during warmer and wetter months (October, December, February, and April). These trends are consistent with the influence of temperature and rainfall on parasite reproduction, intermediate host proliferation, and fish stress responses (Hasan et al., 2023). Cooler months (May - June) corresponded with suppressed parasite loads, supporting evidence that thermal conditions are major regulators of parasite transmission in aquaculture systems. Gill

tissues consistently carried the heaviest parasite burdens across farms, with Turbo Farm showing particularly high infestation peaks. This pattern reflects both the ecological vulnerability of gills and farm-specific factors, such as stocking density and water management that enhance pathogen proliferation (Consuegra et al., 2023).

5.2 Water Quality Status across Farms, Facility Types, and Seasonal Patterns

5.2.1 Farm-Level and Intra-Farm Variation

The study revealed pronounced differences in water quality among farms, particularly in pH, dissolved oxygen (DO), and biological oxygen demand (BOD). Although temperature remained consistently below the optimal range for *O. niloticus*, it followed a typical diurnal pattern across farms, with warmer afternoon surface layers and cooler morning or deeper layers. DO concentrations were generally adequate to support tilapia growth, but critically low levels at Kesses B Farm (mean 1.8 mg/L) indicated hypoxic stress. Such oxygen depletion is commonly linked to high organic loading and restricted reaeration, conditions known to impair fish growth and increase susceptibility to pathogens (Boyd, 2019; Elsayad et al., 2024). pH values ranged from slightly alkaline to highly alkaline, largely within the species' tolerance limits. However, elevated values above 9.0 in some systems raised concern due to the risk of ammonia toxicity. Elevated COD and BOD, particularly at Kesses Farm A, reflected high organic matter inputs and microbial oxygen demand, consistent with eutrophic conditions. These results suggest that waste accumulation and decomposition are primary drivers of water quality stress across sites.

Within farms, notable pond/tank-level differences were recorded. For example, in Turbo Farm, Pond 1 consistently exhibited higher bacterial loads than Pond 2, while Moiben Farm Pond 1 maintained the lowest contamination levels across the study. Such intra-

farm variability highlights the influence of localized management practices, including water exchange, aeration, and feeding intensity. Similar to previous observations in aquaculture systems, ponds with higher stocking densities and organic build-up tended to record poorer water quality, whereas those managed with effective filtration sustained more favorable conditions (Sardar et al., 2025).

5.2.2 Facility-Type Influence

Marked differences also emerged across production systems. Liner ponds exhibited the highest microbial loads, tanks maintained the lowest, and earthen ponds showed intermediate levels. Elevated coliform and total bacterial counts in liners are likely due to limited water exchange and accumulation of suspended organic matter on impermeable surfaces, which favor microbial proliferation. Conversely, tanks provided better microbial control due to smaller water volumes, higher exchange rates, and reduced sediment build-up.

Temperature and BOD also varied significantly by facility type. Tanks generally offered more stable conditions compared to earthen or lined ponds, underscoring the importance of facility design in regulating water quality. Such infrastructure-mediated differences not only shape microbial ecology but also directly influence fish health outcomes.

5.2.3 Seasonal Dynamics

Seasonal variation was less pronounced overall, with most physico-chemical parameters remaining relatively stable across months. However, BOD and coliform counts showed significant seasonal fluctuations. Peaks in microbial indicators during certain months likely reflected rainfall-driven runoff, feed residues, and thermal shifts that enhanced microbial metabolism (Das & Ghosh, 2023). In contrast, the relative stability of temper-

ature and pH aligned with tropical climatic conditions, which buffer extreme seasonal variability.

5.2.4 Water Quality Index (WQI) Patterns

The integrated Water Quality Index (WQI) provided a comparative assessment of farm suitability. Kesses B and Moiben scored the highest, reflecting generally favorable water quality, while Kesses A ranked lowest due to excessive organic loading and oxygen depletion. Liner-based systems such as Turbo scored moderately, balancing high COD with acceptable DO and pH levels. These results illustrate how farm management practices and facility design interact to determine culture system suitability, emphasizing the need for integrated monitoring to sustain aquaculture productivity.

5.3 Effect of Bacteria and Parasites on Fish Growth and the Impact of Water Quality on their Occurrence

5.3.1 Effect of Bacteria and Parasites on Fish Growth

5.3.1.1 Effect of Bacteria on Fish Growth

Bacterial impacts on tilapia growth were organ- and species-specific, with only a few taxa exerting significant effects. In the gills, *V. alginolyticus* was strongly associated with reduced growth. This aligns with previous reports showing that *Vibrio* spp. compromise gill function, impairing gas exchange and osmoregulation, thereby increasing energy expenditure and diverting resources from growth (Austin & Austin, 2016; Zhou et al., 2020).

In the kidneys, *P. aeruginosa* was the most detrimental bacterium, consistent with its recognition as an opportunistic pathogen that proliferates in aquaculture systems with

environmental stressors such as poor water quality and reduced water exchange (Nsabimana et al., 2021; Emam et al., 2024). Kidney colonization is particularly damaging because of the organ's central role in excretion and osmoregulation, meaning systemic physiology is compromised, ultimately slowing growth.

On the skin, *P. aeruginosa* again showed a clear suppressive effect. Previous studies demonstrate that this bacterium disrupts epithelial barriers and predisposes fish to secondary infections, both of which raise maintenance costs and reduce growth efficiency. In contrast, other bacteria isolated from the skin, such as *E. coli* and *Flav. columnare*, did not measurably affect performance, despite their frequent occurrence.

Interestingly, intestinal bacteria showed no significant association with growth, despite the intestine being the most microbially diverse organ. This suggests that many intestinal species act as commensals or conditional pathogens under stable conditions. However, other work has shown that shifts in gut microbial composition under stress can reduce feed conversion efficiency and nutrient absorption in tilapia (Clols-Fuentes et al., 2024). This indicates that the impact of gut bacteria may be context-dependent, intensifying under stressful or nutrient-limited conditions.

5.3.1.2 Effect of Parasites on Fish Growth

Parasites exerted a broader and more consistent influence on tilapia growth than bacteria. In the gills, *T. nigra* showed the most severe negative effect. This is consistent with the established pathogenicity of trichodinids, which damage gill epithelia, stimulate excess mucus production, and reduce respiratory efficiency (Abbas et al., 2023). Such impairments force fish to allocate more energy to maintenance, reducing resources

available for growth. By contrast, *C. tilapiae* and *D. vastator* appeared to have little impact, reflecting their lower pathogenic potential or reduced intensity of infection.

In the intestines, *C. complanatum* significantly constrained growth. Encysted metacercariae are known to damage the intestinal lining and interfere with nutrient absorption, thereby diminishing growth efficiency. In contrast, *Haplorchis* spp. had a weaker effect, suggesting that host tolerance or infection intensity may mediate its pathogenicity.

On the skin, *G elegans* emerged as a major constraint on growth, which is consistent with earlier reports of gyrodactylids reducing growth in tilapia and salmonids by direct tissue feeding, epithelial damage, and increasing susceptibility to secondary infections (García-Prieto et al., 2022). Conversely, *I. multifiliis* showed little measurable impact here, although it has been associated with severe disease outbreaks under other aquaculture conditions (Dickerson, 2006; Abbas et al., 2023).

5.3.2 Impact of Water Quality on Bacterial and Parasite Occurrence

5.3.2.1 Impact of Water Quality on Bacterial Occurrence

Clear farm-level variations revealed strong links between bacterial infestations and water quality parameters. For example, in Turbo, *P. aeruginosa* in the kidney was strongly associated with high Biological Oxygen Demand (BOD), reflecting how organic pollution and reduced oxygen favor opportunistic bacterial colonization. This trend aligns with Turbo's high coliform and bacterial counts, suggesting poor water conditions intensified systemic infections. Similar findings have been reported in Egypt and Nigeria, where *Pseudomonas* spp. thrived under eutrophic conditions in tilapia systems (Emam et al., 2024). Conversely, Moiben, with low microbial loads and favorable Water Quality Index (WQI) scores, exhibited weaker associations, highlighting the role of good water

management in reducing bacterial risks. Renal and dermal infections showed further water quality associations. *A. hydrophila* in the kidney and skin correlated positively with Total Bacterial Count (TBC) and BOD in farms such as Turbo and Kesses A Farm, both of which had elevated COD and BOD. These results confirm that nutrient-rich environments heighten risks of *Aeromonas* spp. outbreaks, consistent with East African reports linking Aeromonas infections to high organic waste in earthen ponds (Mzula et al., 2021b).

On the skin, *P. aeruginosa* responded positively to TBC in Turbo and Ainapkoi Farms, whereas *A. hydrophila* showed negative associations with pH, particularly in earthen and liner ponds. Elevated pH above 9.0, as observed in some farms, is known to exacerbate ammonia toxicity, impairing epithelial barriers and predisposing fish to opportunistic infections (Opiyo et al., 2020). Gill infections demonstrated different dynamics. *V. alginolyticus* was suppressed under higher dissolved oxygen (DO) and lower coliform loads in farms such as Turbo Farm and Moiben Farm. This agrees with findings from Vietnamese tilapia ponds, where hypoxic conditions promoted Vibrio outbreaks (Nguyen et al., 2021). At Kesses Farm B, where DO averaged only 1.8 mg/L, hypoxia likely facilitated Vibrio proliferation, underlining the central role of oxygen in moderating gill health.

Facility comparisons highlighted the vulnerability of earthen ponds, where associations between bacterial loads and organ infections were strongest. Earthen systems accumulated more organic matter, driving up BOD and TBC, which fueled *P. aeruginosa* and *A. hydrophila* infestations. By contrast, tanks maintained more stable physico-chemical conditions, buffering bacterial risks. Comparable results were documented in Ghana and Uganda, where earthen ponds supported higher bacterial burdens than lined or tank

systems (Nsabimana et al., 2021).

Seasonal shifts further influenced bacterial infestations. During the Short Rains, *P. aeruginosa* in the kidney was strongly linked to BOD and temperature, reflecting runoff-driven organic enrichment. Gill infections by *E. coli* and *Pseudomonas* spp. were also heightened under seasonal DO, pH, and thermal fluctuations, consistent with microbial peaks during rainy periods (Das & Ghosh, 2023; Njiru et al., 2021). During the Low Rains, infections were more closely tied to COD, showing that residual organic matter sustains bacterial proliferation when flushing is limited. Seasonal susceptibility of *V. alginolyticus* to pH and temperature reinforces its opportunistic character, as also observed in tropical aquaculture systems (Rodrigues et al., 2020).

5.3.2.2 Impact of Water Quality on Parasite Occurrence

Parasite infestations were similarly shaped by environmental dynamics across farms. In the gills, *T. nigra* increased with temperature, especially in Turbo Farm and Kesses Farm A, where diurnal warming cycles were more pronounced. This aligns with Egyptian findings that trichodinid outbreaks intensify with rising temperatures (El-Mowafy et al., 2017). In contrast, *G. elegans* was suppressed by higher coliform loads in Moiben, suggesting that microbial contaminants may competitively inhibit parasitic success, a phenomenon also noted in Ugandan tilapia ponds (Nsabimana et al., 2021). On the skin, *G. elegans* correlated negatively with DO in Turbo farm and Moiben farm, while *T. nigra* responded positively to TBC across farms, demonstrating that microbial enrichment facilitates secondary parasite colonization. In intestinal tissues, *C. complanatum* infestations were positively associated with BOD and coliforms, particularly in farms such as Turbo Farm and Kesses A, which had higher microbial contamination. This relationship

reflects the parasite's tolerance of polluted environments and transmission via contaminated water. Similar parasite–pollution interactions have been reported in Tanzanian tilapia aquaculture (Mzula et al., 2021b).

Facility design also shaped parasitic dynamics for example *T. nigra* infestations in gills were most strongly linked to temperature in earthen ponds, with weaker associations in tanks and liners, underscoring the buffering role of controlled systems. *G. elegans* infestations on the skin were negatively correlated with DO in earthen and tank systems, while intestinal *C. complanatum* consistently associated with BOD, strongest again in earthen ponds. These findings echo regional evidence showing earthen ponds sustain heavier parasitic loads due to organic accumulation (Kyule-Muendo et al., 2022).

Seasonal variation revealed that monogeneans (*C. tilapiae* and *D. vastator*) were positively linked to COD during both Short and Low Rains, while *D. vastator* also decreased with temperature during Low Rains. Intestinal *Haplorchis* spp. responded to COD during the Short Rains and to pH during the Low Rains, reflecting their adaptability to fluctuating conditions. Comparable patterns have been reported in Asian aquaculture, where rainfall-driven nutrient loading promoted helminth infections (Pham Thi et al., 2023).

The study identified significant inter-species variability in resistance to amoxicillin and erythromycin among bacterial isolates from fish farms in Uasin Gishu County. Fisher's exact test revealed this variation to be statistically significant ($p = 0.0005$), emphasizing non-uniform resistance profiles across taxa. Resistance rates exceeded 35–50% in *E. coli*, *A. hydrophila*, and *Streptococcus* spp., as visualized in the heatmap (Figure 4.19).

This inter-species variability is likely driven by several factors, such as horizontal gene

transfer (HGT), which facilitates the spread of resistance genes among environmental bacteria. This process is particularly potent in complex ecosystems like aquaculture, where microbial communities interact within shared water systems. As described by (Sun et al., 2025), the persistence and mobility of antibiotic resistance genes (ARGs) in livestock and poultry settings can lead to their accumulation in the environment via effluent, manure, and runoff, eventually reaching aquatic systems through integrated farming practices.

Data from poultry and pig farms also provide compelling parallels. (Gudda et al., 2024), documented antibiotic residues in 25.8% of chicken compost samples and 23.1% of pig-manure-fertilized soils, with trimethoprim concentrations exceeding safety thresholds. Resistance risk increased with flock size and antibiotic use intensity, suggesting significant environmental loading of antimicrobials even in terrestrial systems linked to aquaculture via water runoff and integrated farming.

Although no antibiotics are currently used directly for treating fish in the surveyed farms, the integration of fish farming with crop and livestock production introduces potential indirect exposure routes. Antibiotics used in livestock and horticulture can contaminate fishponds via manure fertilization, irrigation runoff, or drainage from nearby fields, thereby exerting selective pressure on aquatic microbiota. This aligns with the "One Health" perspective, emphasizing the interconnectedness of human, animal, and environmental health in driving resistance dynamics (Alhaji et al., 2024).

In contrast, resistance patterns for Cotrimoxazole, Doxycycline, Streptomycin, and Ciprofloxacin showed no statistically significant inter-species variation. These antibiotics exhibited generally low resistance percentages and clustered near the origin in the PCA biplot (Figure 4.20), suggesting limited contribution to the observed variance in bacterial re-

sistance profiles. This may indicate either conserved bacterial targets or limited environmental exposure to these drugs in the study area. Ciprofloxacin, in particular, demonstrated the highest uniformity, possibly due to its mechanism of targeting essential and highly conserved bacterial enzymes such as DNA gyrase and topoisomerase IV (Rajesh et al., 2025; Vezeau & Kahn, 2025)

The PCA analysis further clarified relationships among antibiotics and bacterial species. The principal component loading vectors for Amoxicillin and Erythromycin showed strong discriminatory power along the first two dimensions, effectively separating resistant species such as *E. coli*, *A. hydrophila*, and *V. harveyi* from the rest. The clustering of other species near the origin suggests shared susceptibility profiles and minimal variance in resistance to the other tested antibiotics.

These findings underscore the need for enhanced antimicrobial stewardship in aquaculture, even in contexts where antibiotics are not directly applied. Proactive monitoring of environmental exposure routes, integrated with species-specific susceptibility data, is essential for preventing the emergence and dissemination of resistance. Educational outreach to farmers about indirect antibiotic pathways and implementation of biosecurity practices can serve as effective preventative strategies.

CHAPTER SIX

CONCLUSIONS AND RECOMMENDATIONS

6.1 Conclusions

The study revealed a high diversity of both beneficial and pathogenic bacterial species in fish farms across Uasin Gishu County, with *E. coli*, *P. aeruginosa*, and *A. hydrophila* being the most prevalent, particularly in gills and intestines.

The study demonstrated co-occurrence of bacterial and parasitic infections in aquaculture systems, influenced by environmental conditions, pond types, farm management practices, and seasonal changes. Notably, *E. coli*, *P. aeruginosa*, and various Vibrio species co-occurred in critical fish organs, while nematodes, monogeneans, and protozoans exhibited tissue-specific infestations, particularly in poorly managed farms and during warmer months.

The water quality parameters varied significantly across farms, ponds, and seasons, with Turbo Farm Farm showing the highest bacterial contamination and suboptimal water quality.

The study demonstrated that water quality parameters, including temperature, DO, COD, BOD, TDS, pH, and nitrate concentrations, significantly influenced the presence of bacterial and parasitic pathogens in aquaculture systems. Elevated COD, BOD, and nitrates were positively correlated with the proliferation of harmful microorganisms and parasites, while higher temperatures and DO levels generally had a suppressive effect on their presence.

There was significant species-level variation in antibiotic resistance among fish farm

bacterial isolates in Uasin Gishu, with highest resistance observed to amoxicillin and erythromycin. The results suggest indirect antibiotic exposure, likely from integrated livestock-crop systems, is driving resistance. In contrast, ciprofloxacin, doxycycline, streptomycin, and cotrimoxazole remained largely effective.

6.2 Recommendations

1. Regularly monitoring of key water quality parameters like oxygen, pH, temperature, nitrates, COD and BOD for early detection of changes, allowing timely corrective actions to maintain healthy pond conditions.

2. Adopt proper waste and feed management practices by avoiding overfeeding, removal of uneaten feed, and regular cleaning of ponds to reduce organic buildup that encourages bacterial and parasitic growth.

3. Improve pond design and control environmental inputs by preventing runoff or wastewater inflows while regulating fertilizers to reduce nutrient overload.

4. To address the emerging antibiotic resistance in aquaculture environments, this study recommends enhanced farmer education on indirect exposure pathways, strict waste management practices, responsible antibiotic use across sectors, and further research into resistance mechanisms and environmental transmission routes.

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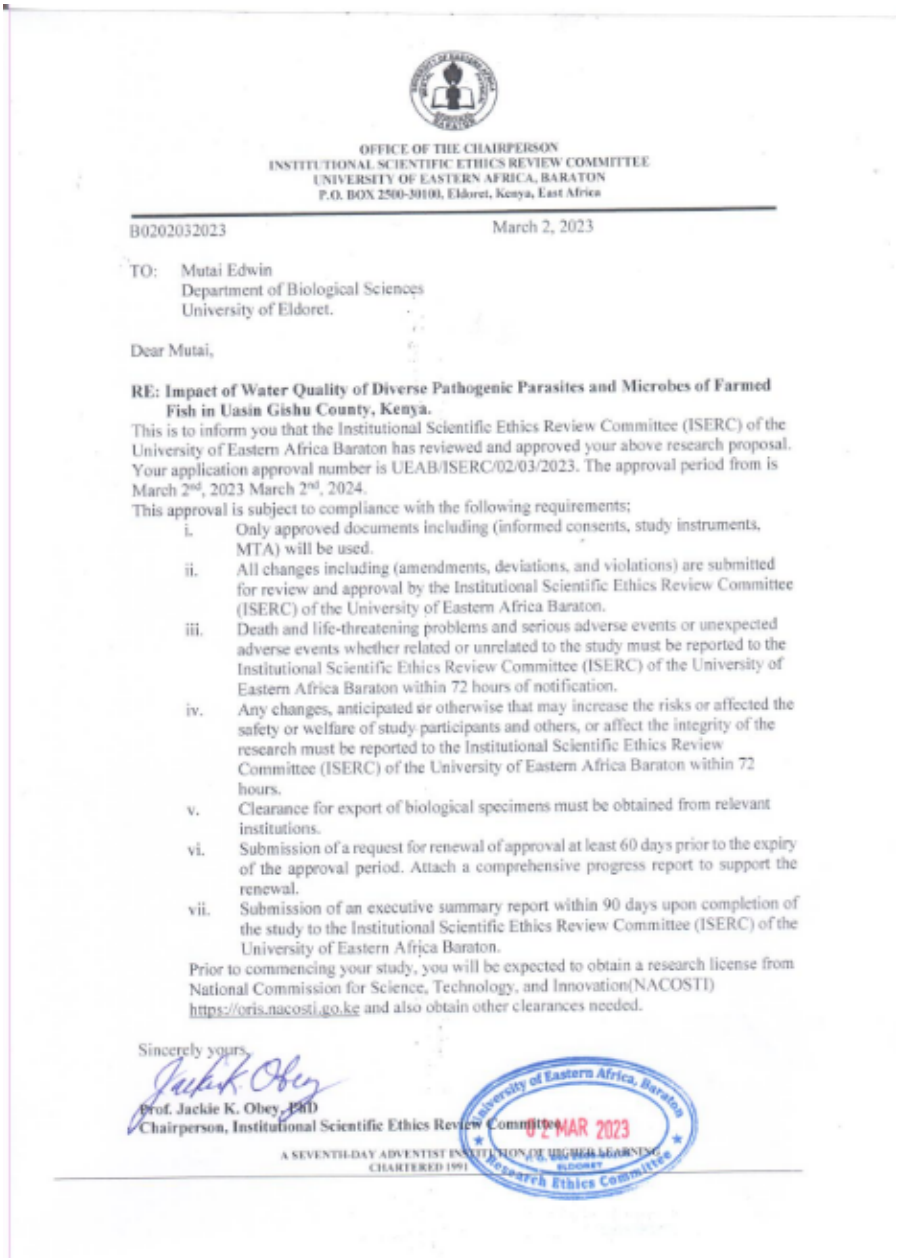
APPENDICES

Appendix I: License for carrying out research from the Institutional Scientific Ethical Approval Committee University of Eastern Baraton, National Commission for Science, Technology & Innovation



OFFICE OF THE CHAIRPERSON
INSTITUTIONAL SCIENTIFIC ETHICS REVIEW COMMITTEE
UNIVERSITY OF EASTERN AFRICA, BARATON
P.O. BOX 2500-30100, Eldoret, Kenya, East Africa

B0202032023 March 2, 2023

TO: Mutai Edwin
Department of Biological Sciences
University of Eldoret.

Dear Mutai,

RE: Impact of Water Quality of Diverse Pathogenic Parasites and Microbes of Farmed Fish in Uasin Gishu County, Kenya.

This is to inform you that the Institutional Scientific Ethics Review Committee (ISERC) of the University of Eastern Africa Baraton has reviewed and approved your above research proposal. Your application approval number is UEAB/ISERC/02/03/2023. The approval period from is March 2nd, 2023 March 2nd, 2024.

This approval is subject to compliance with the following requirements;

i. Only approved documents including (informed consents, study instruments, MTA) will be used.
ii. All changes including (amendments, deviations, and violations) are submitted for review and approval by the Institutional Scientific Ethics Review Committee (ISERC) of the University of Eastern Africa Baraton.
iii. Death and life-threatening problems and serious adverse events or unexpected adverse events whether related or unrelated to the study must be reported to the Institutional Scientific Ethics Review Committee (ISERC) of the University of Eastern Africa Baraton within 72 hours of notification.
iv. Any changes, anticipated or otherwise that may increase the risks or affected the safety or welfare of study participants and others, or affect the integrity of the research must be reported to the Institutional Scientific Ethics Review Committee (ISERC) of the University of Eastern Africa Baraton within 72 hours.
v. Clearance for export of biological specimens must be obtained from relevant institutions.
vi. Submission of a request for renewal of approval at least 60 days prior to the expiry of the approval period. Attach a comprehensive progress report to support the renewal.
vii. Submission of an executive summary report within 90 days upon completion of the study to the Institutional Scientific Ethics Review Committee (ISERC) of the University of Eastern Africa Baraton.

Prior to commencing your study, you will be expected to obtain a research license from National Commission for Science, Technology, and Innovation(NACOSTI) https://oris.nacosti.go.ke and also obtain other clearances needed.

Sincerely yours,

Prof. Jackie K. Obey, PhD
Chairperson, Institutional Scientific Ethics Review Committee

University of Eastern Africa, Baraton
02 MAR 2023
Research Ethics Committee

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Appendix II: License for carrying out research from the National Commission for Science, Technology & Innovation

REPUBLIC OF KENYA

NATIONAL COMMISSION FOR SCIENCE,TECHNOLOGY & INNOVATION

Ref No: 494915

Date of Issue: 11/April/2023

RESEARCH LICENSE

This is to Certify that Mr.. Edwin Kipyegon Mutai of University of Eldoret, has been licensed to conduct research as per the provision of the Science, Technology and Innovation Act, 2013 (Rev.2014) in Uasin-Gishu on the topic: IMPACT OF WATER QUALITY ON DIVERSE PATHOGENIC PARASITES AND MICROBES OF FARMED FISH IN UASIN GISHU COUNTY, KENYA for the period ending : 11/April/2024.

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494915

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See overleaf for conditions

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Appendix III : Field Observations and Laboratory Procedures in the Identification of Bacteria and Parasites

Eye Infection

Final Ulcers

Furuculonsis Eye Infection

Fish Measurement

Laboratory Identification of parasites and Isolation of bacteria

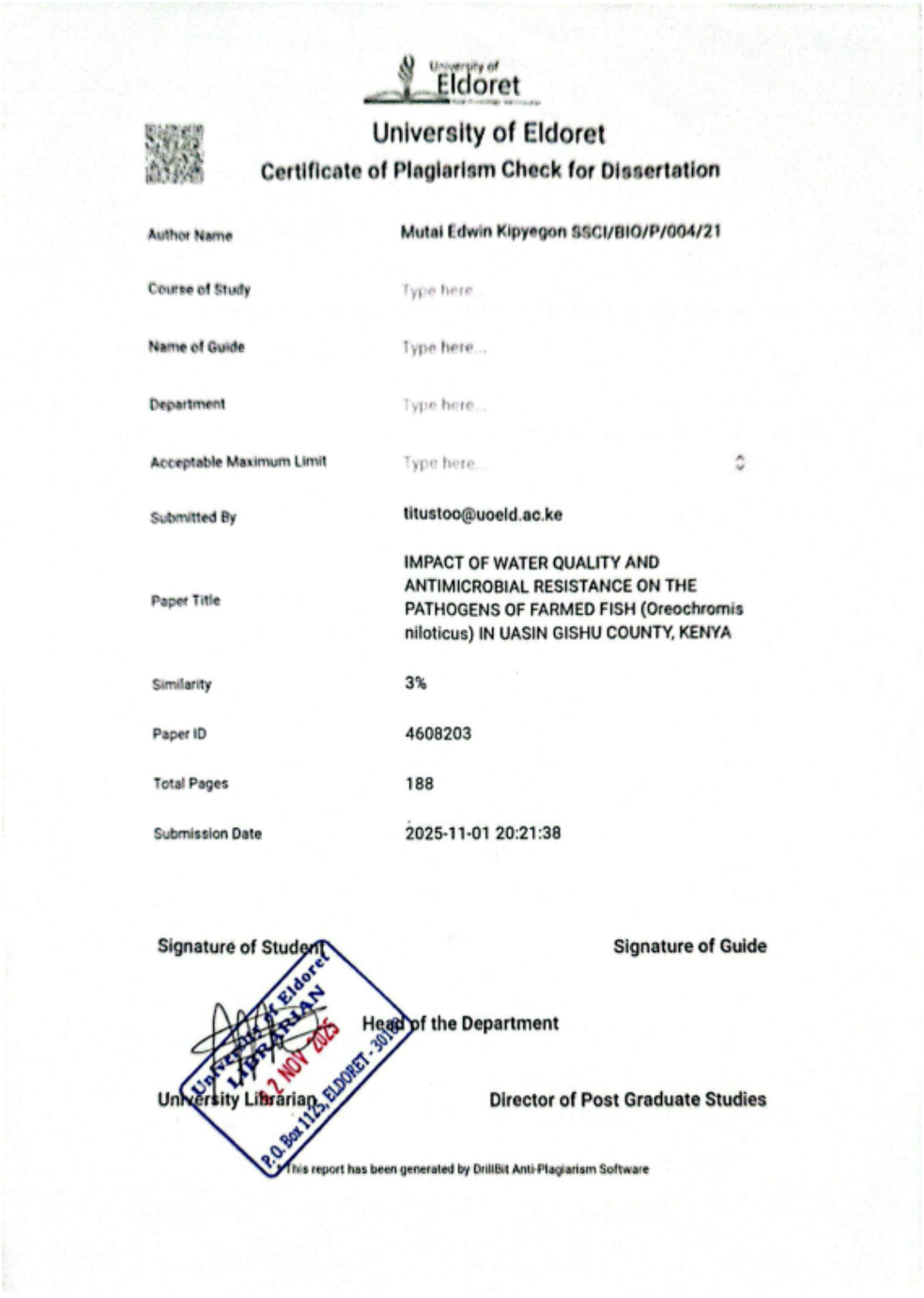
Appendix IV : Laboratory Analysis of water samples and Field observations

Laboratory analysis of water samples

Fish Measurement

An Earthen Liner Pond with the Culture Fish

Appendix V: Similarity Report



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