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TRANSFORMING AFRICAN AQUACULTURE: EMPHASIZING FISH GUT MICROBIOTA AMIDST TECHNOLOGICAL SHORTFALLS

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Abstract: Technology, characterized as a strategic design to mitigate uncertainty in the causal relationship between action and outcome, comprises both hardware and software components (Rogers and Shoemaker, 1992). This definition encapsulates the essence of technological advancements, particularly within the aquaculture sector, where these innovations hold the promise of transformative opportunities for rural communities (Chattopadhyay, 2017).

This study delves into the intricate dynamics of technology integration in aquaculture, focusing on its potential to revolutionize rural economies and foster sustainable development. The juxtaposition of traditional farming practices and cutting-edge technologies presents a unique opportunity to bridge existing gaps and enhance the overall efficiency and productivity of aquaculture operations. The inherent challenges associated with embracing new technologies in resource-constrained environments require a nuanced understanding of the socio-economic factors influencing adoption patterns.

The study considers the implications of technological integration for industry innovation, economic growth, and the empowerment of rural populations engaged in aquaculture activities. The findings are expected to inform policies and strategies that foster sustainable technology adoption, ultimately contributing to the advancement of aquaculture practices and the well-being of communities dependent on this vital sector.

Keywords: Aquaculture Technology, Rural Innovation, Sustainable Development, Technology Adoption, Rural Empowerment

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INTRODUCTION

Technology is defined as a design for instrumental action to reduce uncertainty in the relationship between cause and effect (Rogers and Shoemaker, 1992). It comprises two components: hardware and software. In the aquaculture sector, technological advancements have presented greater opportunities for rural populations (Chattopadhyay, 2017). Despite the prevalence of lowtech farming operations in developing countries, embracing advanced farming technologies remains a challenge. Effective integration of modern technologies into aquaculture production can serve as a platform for industry innovation (Chattopadhyay, 2017).

The intestinal microbiota is recognized as a vast and intricate ecosystem within the body, constituting a "superorganism" (Amenyogbe et al., 2021). As indicated by existing literature, environmental factors, physiological state, and genetic factors can induce changes in the intestinal microbiota of fishes (Yang et al., 2021; Jin et al., 2017). Variations in the feeding habits of aquatic animals contribute to differences in fish intestinal microbiota (Ma et al., 2019a). The recent deficiency of modern technology for studying fish intestinal microbiota in sub-Saharan Africa has led to subpar fish production. Furthermore, studying fish microbiota holds significant implications for human health, as many fish species are vital food sources in Africa and globally.

The literature shows that several studies have utilized various modern technologies to investigate fish intestinal microbiota (Chen et al., 2019; Liu et al., 2019; Jiang et al., 2019; Parshukov et al., 2019; Zhang et al., 2020). These modern technologies aid in the identification, visualization, and characterization of microbial communities within the fish gut. There is a compelling need for advanced technologies in Africa to facilitate the study of fish intestinal microbiota, a pivotal field of research. To provide a comprehensive overview of disruptive and emerging technologies that could revolutionize aquaculture, this review briefly outlines and discusses how the absence of these technologies impacts African aquaculture research, specifically focusing on fish intestinal microbiota research. The present study offers crucial information and opens doors for technology innovators and businesses interested in the sector to invest in Africa.

COMPOSITION OF FISH INTESTINAL MICROBIOTA

The intricate and dynamic intestinal microbial ecosystem within animals plays a crucial role in nutrient absorption. Previous studies have demonstrated the benefits of fish intestinal microbiota for the host's nutrition, physiology, and immune processes (Llewellyn et al., 2014; Ma et al., 2019b). The utilization of metagenomics in aquatic organisms, whole-genome sequencing of the gastrointestinal microbiome, and the analysis of information related to microbiota's abundance, species, structure, composition, and function hold immense significance. These approaches contribute not only to controlling fish growth and development and preventing diseases but also to overcoming the limitations of traditional culturing methods. In both freshwater and marine fish intestinal microbiota, major bacterial genera such as Proteus, Bacteroides, and Firmicutes have been identified (Rimoldi et al., 2018). Additionally, Vibrio, Achromobacter, Alteromonas, and Flavobacterium are prevalent in marine fish (Egerton et al., 2018). The presence of different bacterial strains in these fish classes can potentially be attributed to the more complex habitats and diverse diets associated with these environments, as suggested by Skrodenytė-Arbačiauskienė et al. (2008).

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THE ROLE OF MICROORGANISMS IN THE DIGESTION OF DIET

According to literature, feed intake, metabolism and digestion in mammals are all regulated by microbes within the gastrointestinal tract (GIT) (Fetissov, 2017; Read and Holmes, 2017). The existence of interaction between GIT microbiota and neurotransmitters, such as serotonin (Yano et al., 2015), norepinephrine and catecholamines dopamine, affects the release and function of gastrointestinal hormones, motility, and feeding behaviour of the host (Strandwitz, 2018). The digestion and host diet are greatly significant when studying the functional interactions of fish diets and their intestinal microbial communities (Clements et al., 2014). Several herbivorous fishes of freshwater, such as grass carp, do not depend on the cellulolytic activity of bacteria but instead released huge amounts of plant materials swiftly via their gut and recoup the proteins and soluble sugars that are released via their pharyngeal teeth activities (Gangadhara et al., 2004). The pharyngeal apparatus helps to regulate the flow of food through the digestive system, ensuring that it is properly broken down and absorbed. The gut is responsible for the absorption of nutrients and the elimination of waste products. In grass carp, the gut is relatively long, which allows for more complete digestion of the fibrous plant material that they consume (Wu et al., 2021). Marine herbivorous fish differ from a range of freshwater herbivorous fish species in the sense that, marine herbivorous fish species depend on gut microorganisms for the transformation of inassimilable algal elements, such as mannitol, to metabolize their beneficial short chain fatty acid (White et al., 2010). On the other hand, omnivorous and herbivorous freshwater species exhibit shorter gut transit periods and minimal short chain fatty acid levels in their guts (German et al., 2010). However, only a few pieces of literature support gastrointestinal fermentation, supplying the most important components of day-to-day energy requirements for freshwater fish species and cellulose as a key substrate for the gut microbiota of freshwater fish species. This does not relegate the significance of gut microorganisms for their nutritional value in fish species. The gut microbiota has been shown to facilitate the formation of lipid droplet and uptake of fatty acid in the liver and intestinal epithelium of zebrafish (Semova et al., 2012). As of now, the role of microorganisms in the digestion of diet is still not completely elucidated. More studies are still needed to completely understand the role of these microbes in the digestion of diet.

EFFECT OF FOOD FACTORS ON FISH INTESTINAL MICROBIOTA

With the continuous development of high-throughput sequencing technologies, the effects of feed components on the composition of farmed fish gut microbiota will be more precise. The structural and compositional analysis of fish intestinal microbiota can reflect the information of their habitat and diet. Currently, there are many research fields of microbial meta-genomics (Fjelheim et al., 2007). There are often marked microorganisms in the gut for different feeding habit of fish, which digest and absorb different types of nutrients (Navarrete et al., 2008). It has been indicated that there is a significant relationship between the host's food preference and the composition of intestinal microbiota (Mikaelyan et al., 2015). The composition of intestinal microbiota in different feeding habit of fish is different due to different factors such as degradation of cellulose, protein, and chitin. The fish feeding habits are categorised into three groups: herbivores, carnivorous, and omnivorous. The major nutritional sources of *herbivores* fish are plants, which are rich in cellulose and polysaccharide. The degradation of cellulose depends on various cellulases, but fish cannot produce cellulase by themselves. Therefore, cellulose utilisation only depends on the decomposition and absorption by intestinal microbiota (Bairagi et al., 2002). The diversity of intestinal microbiota of carnivorous fish is slightly lower than that of *phytophagous* and filter feeding fish, which might be due to their single feeding preference. The microorganisms involved in cellulose metabolism are also found in the intestinal microbiota of carnivorous fish species like *Bacillus thuringiensis* and *Bacillus citrate*, but they are in less abundance. The intestinal microbiota of two types of carnivorous fishes, including Mandarin fish (*Siniperca chuatsi*) and Mongolia (*Culter alburnus*), were compared to those of *phytophagous* fishes. The results showed that the protease-producing *Halomonas* and *Fusobacterium* were the predominant bacteria in both carnivorous fish. The enzymatic activity analysis showed higher activity of trypsin and lower activity of cellulase in carnivorous fishes, while the herbivorous fishes showed opposite results. Furthermore, another study reported predominant cellulase-producing *Paenibacillus* in herbivorous fish but not in carnivorous fish (Liu et al., 2016). This may be because the filter-feeding omnivorous fish feed on the common young plants and filters out the individual microphytoplankton, organic debris, and bacterial aggregates expanding the feeding species, requiring complex intestinal microbiota for decomposition and absorption.

EFFECTS OF FATS, PROTEINS AND CARBOHYDRATES ON FISH INTESTINAL MICROBIOTA

Due to the shortage of animal protein sources, especially that of fish meal, the fish industry generally improves the fat contents in feed to play "protein-saving effect" and replaces fish oil with vegetable oil to reduce costs to promote the rapid growth of fish. At the same time, it has many adverse effects, such as excessive accumulation of fat and immune damage to fish (Xing et al., 2013), and affects the composition and structure of intestinal microbiota (Sheng et al., 2018). In the formation of lipid droplets, sclerenchyma tissues play a crucial role, while *Bacteroides* and *Proteus* cannot increase the number of lipid droplets. When the Salmon (*Salmonidae*) were fed with polyunsaturated fatty acids (linoleic acid and linolenic acid) or high unsaturated fatty acids (HUFAs) in diet, the number of *Lactobacilli* in the intestine and faeces among the fish in the linolenic acid group and HUFA group increased significantly (Bagi et al., 2018; Falcinelli et al., 2017; Ringø et al., 2016).

The problem of substitution for protein sources in aquatic feeds, especially the replacement of fish meal with plants-based protein sources, animal by-products, as a protein source, has become a hot topic for scientists worldwide (Acar et al., 2019, 2018). The effect of replacing fish meals on their intestinal health, primarily intestinal microbial balance, needs to be studied.

Sphingomonas was the dominant bacterial group when soybean proteins were used as a substitution for the protein source (Ringø et al., 2016). To sum up, the current studies, based on pure culturing technology, show that the use of soybean proteins as a substitution for protein source does not significantly alter the microecological balance of fish intestine, and to a certain extent, leads to the formation of the anaerobic state in the intestine, thereby providing resistance to the invasion of pathogenic bacteria (Ringø et al., 2016). Therefore, it can be utilised as a good substitution for protein source in a fish meal (Ringø et al., 2016).

In terms of glucose metabolism, the fish are considered to be born with "diabetes" and are intolerant to high glucose concentrations (Jiang et al., 2011). Scientists try to explain this from the perspective of evolution (Jiang et al., 2011) and molecular biology (Jiang et al., 2011). The fish industries also try to reduce the feed cost by increasing carbohydrates content or adding different sugar sources in fish feed (Sulaiman et al., 2020; Zhou et al., 2013). However, the interactions of different carbohydrates sources with intestinal microbiota in the fish gut and their effects on the metabolism of fish carbohydrates are still not known (Sulaiman et al., 2020; Jiang et al., 2011). The use of different carbohydrates sources for energy metabolism by intestinal microbiota, critical roles of different bacterial groups in intestinal microbiota, and the low ability of fish to utilise carbohydrates as an energy source due to the lack of some bacterial groups are not clear, which are needed to be studied in detail.

Effects of additives on fish intestinal microbiota and host nutrition metabolism

Amino acids, vitamins, and minerals are essential nutrients for the body's metabolism. Most bony fish cannot synthesize these nutrients by themselves. They rely on exogenous factors to meet the body's growth, development, and metabolism needs (Zhai et al., 2017). In recent years, the influence of probiotics and prebiotics on the intestinal microbiota of fish has changed the developmental direction of aquaculture from an increase in quantity to an improvement of quality (Nyman et al., 2017). Meanwhile, there has been rapid development in scientific research and industry related to probiotics and prebiotics. At present, probiotics, which are mainly used in aquatic fish feed, include *Lactobacillus, Bacillus, Clostridium bifermentans*, and yeast. The common prebiotics includes fructo-oligosaccharide, galactooligosaccharides, dextran, mannan and xylooligosaccharides. The lactic acid bacteria and yeast are currently the most widely used probiotics in aquaculture (Merrifield et al., 2013; Ahire et al., 2019; Abdelrahman et al., 2017; Giorgia et al., 2018).

A couple of studies showed that the addition of short chain fructooligosaccharides and xylooligosaccharides to fish feed did not alter the diversity of intestinal microbiota in Norwegian sea bass (*Sparus aurata*) and European sea bass, but significantly increased the abundance of lactic acid bacteria (Guerreiro et al., 2018; Dawood et al., 2016). Therefore, it is of great significance for the aquaculture industry to isolate fish-derived probiotics from the intestines of fish, fed with different diets and different environmental conditions, and carry out relevant taxonomy and basic biology studies.

The active components in plant extracts include glycosides, acids, polyphenols, polysaccharides, terpenes, flavonoids and alkaloids. A study on Rainbow trout showed that the addition of cresol or thymol decreased the abundance of anaerobic bacteria in the fish intestine, along with the decrease in the abundance of lactic acid bacteria (Hagi et al., 2004).

INTESTINAL MICROBIOTA AND GUT IMMUNITY IN FISH

The gut microbiota of fish plays a vital role in the inhibition of pathogenic microorganisms. The dominant microbial species in their intestinal tract protect the host from infection and invasion of environmental pathogens. Some intestinal microbial species also promote the proliferation of intestinal epithelial cells and immune system response (Stagaman et al., 2017). Environmental pressures, such as pollution, hypoxia, and sudden temperature variations, can damage the host's immune system, which can lead to the invasion of pathogens, thereby altering the composition of intestinal microbiota. The changes in the structure of the intestinal microbiota of fish are not the only factors for adapting and improving their immune ability, but also some chemical elements (antibiotics, pollutants, pesticides, insecticides) entering the digestive tract of animals have a significant impact on the composition of intestinal microbiota (Navarrete et al. 2008).

Even though a symbiotic relationship exists between the host's metabolism and gut microbiota, the interactions of host-microbiota at the functional level, particularly in the wild species, are still not precise (Tarnecki et al., 2017). Most of the studies regarding the assembly practices and interactions of host-microbiota are laboratory-based studies that typically use model species that have been tamed in laboratory environments for generations (Tarnecki et al., 2017; Eichmiller et al., 2016). Nonetheless, the interactions of fish gut microbiota and other organisms have many features, and these laboratory-based studies might not satisfactorily represent these interactions in wild-type animals. Therefore, the enhanced understanding and knowledge of the natural microbiota of healthy animals and their mode of interaction with hosts and other environmental factors are still of utmost significance.

OTHER TECHNOLOGIES, RESEARCH METHODS AND STRATEGIES IN AQUACULTURE

The rapid development of aquaculture has been promoted by applying science and introducing cutting-edge technologies (Figure 1) over the past five to six decades (Yue and Shen, 2021). Scientific and technological advances have benefited almost every aspect of aquaculture. Aquaculture species can now be diversified due to improved reproductive technologies (Yue and Shen, 2021; Weber and Lee, 2014).

Using quantitative genetics, selective breeding has resulted in significant improvements in more than 60 culture species of aquaculture (Gjedrem and Robinson, 2014). The cost of feed has been reduced and the feed conversion rate (FCR) has been improved when feed formulations are optimized depending on the species of fish and their nutritional needs (Yue and Shen, 2021). Kelly and Renukdas (2020) noted that disease management technologies had reduced disease occurrence in aquaculture. Aquaculture has grown tremendously as a result of these early innovations, but the challenges are formidable as the world population continues to grow (FAO, 2020). Aquaculture can be further developed sustainably and profitably (FAO, 2020). The aquaculture industry is experiencing rapid growth through the development and introduction of cutting-edge technologies (Ab Rahman et al., 2017). Global seafood production and profitability will be significantly enhanced by emerging and disruptive technologies. Among these technologies are digital technology, genome editing, genomic selection, offshore farming, recirculating aquaculture systems, solar energy, and oral vaccines (Yue and Shen, 2021; Aich et al., 2020; Houston et al., 2020). Africa is lagging behind due to unavailability of most of these technologies. Hence there is an urgent need for inventors, investors and governments to quickly invest in these areas in the continent.

Several characteristics of aquaculture species that are economically significant can be improved through genomic selection (GS) and genome editing (GE). Aquaculture genetic improvement will be substantially accelerated if GS and GE are combined with advanced conventional breeding strategies and matured biotechnologies (Yue and Shen, 2021). In another vain, increasing feed consumption and reducing feed loss can substantially reduce total production costs when the feeds are fed in accordance with hunger status (Su et al., 2020; Li et al., 2020). There is an ongoing effort in Europe to develop a platform that can detect and monitor chemicals, harmful algae bloom, pathogens, and toxins, using an automated and integrated system (Johnston, 2018). The aquaculture industry in the African continent will be able to maintain an ideal environment for fish through sensors in water collaborating with cloud management and mobile connectivity to ensure optimal feeding for growth and feed conversion. Real-time sensors will be crucial to detect pathogens in water; measure stress levels in individual fish in the future (Yue and Shen, 2021). It is possible to draw inspiration from Stanford researchers' studies on measuring stress and overall health using wearables that detect cortisol (Parlak et al., 2018).

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By combining drones with artificial intelligence (AI) and cloud computing, the aquaculture industry can reduce costs and improve operations (Yue and Shen, 2021;
Chen et al., 2020). The use of artificial intelligence (AI) in aquaculture is increasingly being studied and applied by science-based research institutes and start-ups (Razman et al., 2020; Evensen, 2020). A shorter period of time can be devoted to increasing aquaculture production using AI since it reduces labor-intensive aspects of aquaculture (Yue and Shen, 2021). The use of feeders, monitoring water quality, and harvesting and processing of fish are just a few examples (Jothiswaran et al., 2020). It is critical that aquaculture production and marketing data be shared between fish farms and big aquaculture companies (Yue and Shen, 2021).
Virtual Reality (VR) can be applied to teaching and education in the aquaculture industry (Ferreira et al., 2012). The use of VR has been used, for instance, to inspire young people to become more interested in aquaculture in Norway (Prasolova-Førland et al., 2019). As social media have become more relevant to the food industry, the aquaculture industry can hook onto this platform to increase its production (Dupont et al., 2018). Predictive models can be generated using internet of things (IoT) and machine learning with data collected over time. Making better and more precise decisions using these predictive models will enable early warnings of potential risks. In the African aquaculture industry, the IoT and big data solutions can revolutionize productivity, sustainability, and profitability and make it simpler and safer to manage risks.
Figure 2 shows a recirculating aquaculture system (RAS) in which fish are farmed in controlled conditions (Badiola et al., 2018). As a result of RAS, less water is used, biosecurity is improved, and yield is higher or enhanced. However, the technology faces several challenges, including insufficient knowledge, high energy requirements, high initial investments, and difficulty removing bacteria from the RAS once they enter (Xiao et al., 2019; Badiola et al., 2018). Several research projects have been conducted on improving recirculating loops and waste treatment, as well as using renewable energy to reduce energy costs (Badiola et al., 2018). On RAS farms, however, only high-value product species will likely be profitable due to current knowledge and technologies (Yue and Shen, 2021). Fish farmers should work with fish scientists and engineers to effectively design each RAS system component to reduce costs.

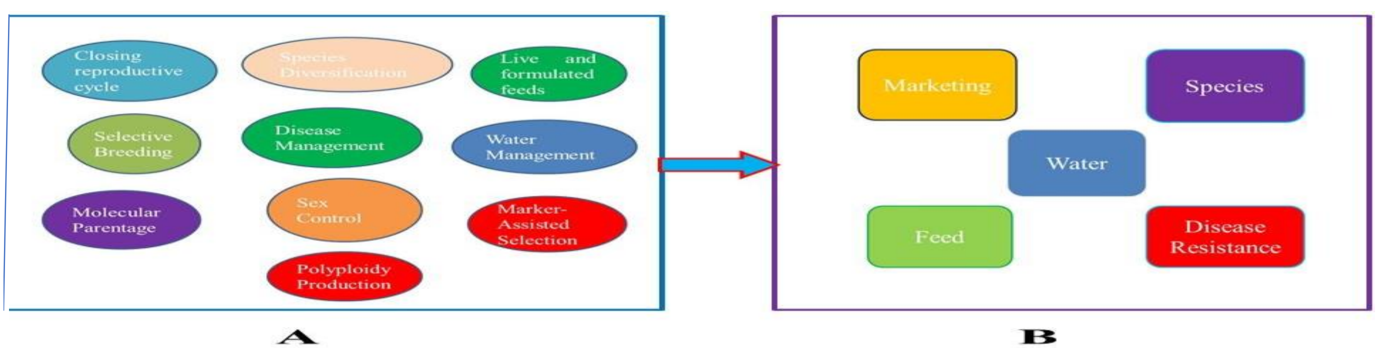

Figure 1. As a result of aquaculture technologies, aquaculture production have increased rapidly (A) Technologies applied to aquaculture. Different technologies are used in different parts of the world with different methods (B) A key component of increasing aquaculture production.
Source: Yue and Shen (2021).

Figure 2. An image of a recirculating aquaculture system (RAS). Several offshore aquaculture systems exist, including cage aquaculture, submersible cages, vessel aquaculture, and fish farms permanently moored in deep water. Additionally, tank-based recirculating aquaculture systems, vertical aquaponics, multistory vertical tanks, and desert tanks are among recirculating aquaculture systems (RAS).
Sources: https://www.aquacultureid.com/recirculating-aquaculture-system/

AFRICAN PERSPECTIVES

There has been much advancement made into studying the fish gut microbiota, but there is still much more to be done especially on fish species from the African continent. For instance, the extent to which the microbiota is involved in feeding, immune responses, digestion, and metabolisms, thereby contributing to the sustenance and general health of fish, is still not completely elucidated (Egerton et al., 2018). One technology used in analysing the role of microorganisms in digestion is metagenomics. Metagenomics involves the direct sequencing of DNA extracted from an environmental sample, allowing for the identification and characterization of all microorganisms present in the sample, regardless of whether they can be cultured (Wu et al., 2021; Egerton et al., 2018). In the context of aquaculture, metagenomics can be used to analyse the microbial communities present in fish gut samples and to identify the functions of these communities in the digestion of feedstuffs (Wu et al., 2021). Another technology used in studying the gut microbiome of fish is microbial culturing. This involves the isolation of individual microorganisms from a sample and their subsequent identification and characterization through various biochemical and molecular techniques. This method has the advantage of allowing for the isolation and study of individual microorganisms. However, this technique is known to miss significant portion of the microbial diversity present in the sample (Wu et al., 2020). Researchers have also developed culture-independent methods, which include molecular techniques such as polymerase chain reaction (PCR), denaturing gradient gel electrophoresis (DGGE), and next-generation sequencing (NGS) (BisiJohnson et al., 2017; Sullam et al., 2012). PCR is a technique that amplifies a specific region of DNA, allowing for the identification of microorganisms through the sequencing of their DNA. DGGE is a technique that separates PCR-amplified DNA fragments based on their melting properties, allowing for the identification of different microbial populations in a sample. NGS is a high-throughput sequencing method that can identify a vast array of microorganisms in a sample (Bisi-Johnson et al., 2017). This technology involves the use of molecular probes to target specific microbial taxa within the gut microbiota. Microbiome profiling allows the identification and quantification of specific microbial groups, such as beneficial probiotic or pathogenic bacteria that may significantly impact fish health and productivity. Finally, metabolomics is another technique used in the analysis of the role of microorganisms in digestion. Metabolomics involves the analysis of the small molecules produced by the metabolic processes of microorganisms. This technique can provide insight into the metabolic pathways involved in the digestion of feedstuffs and help identify potential biomarkers for monitoring the health of fish in aquaculture (Bereded et al., 2020).

Techniques such as next-generation sequencing and metagenomics have shown promise in this regard, but they require specialized equipment and expertise that is often lacking in African research institutions. While the role of microorganisms in African aquaculture is increasingly recognized, the need for advanced technologies for analyzing microbial communities remains a significant obstacle.

Additives in fish feed have been a topic of concern due to their potential impact on fish intestinal microbiota and host nutrition metabolism (Smorodinskaya et al., 2022; Sánchez-Alonso et al., 2020). Understanding these effects is crucial to improving aquaculture productivity and sustainability (Smorodinskaya et al., 2022; SánchezAlonso et al., 2020). Recent technological advancements have enabled the analysis of the fish intestinal microbiota and host metabolism at the molecular level. Advanced molecular techniques such as Next-generation sequencing, metabolomics, Metagenomic and metatranscriptomic approaches allow for identifying and quantifying microbial communities and their gene expression patterns, and host metabolism and nutrient utilization and their interactions with the diet respectively (Sánchez-Alonso et al., 2020; Liu et al., 2021). These techniques will provide insights into the functional roles of these communities in digestion, nutrient absorption, and disease resistance in African aquaculture and will provide a comprehensive understanding of the complex interactions between fish, their gut microbiota, and the feed additives. However, the African aquaculture industry still needs access to specific technologies.

Understanding how different feed ingredients and formulations impact the gut microbiota of African aquaculture species is essential for developing sustainable and cost-effective aquaculture practices. Understanding the effects of additives on fish intestinal microbiota and host metabolism is crucial to improving aquaculture productivity and sustainability in Africa. Advancements in technology will enable a better understanding of these complex interactions, providing opportunities for developing effective strategies to mitigate negative impacts and optimise fish growth and health. The intestinal microbiota and gut immunity play critical roles in fish health and production. Their analysis using various technologies can lead to the development of effective strategies for sustainable aquaculture in Africa.

CONCLUSIONS

Utilizing the fish's gut microbiota holds unlimited potential for the fish aquaculture industry to enhance the growth and development of cultured species. Technological innovations are essential for the expansion of aquaculture. Aquaculture is on the cusp of a revolution thanks to several innovative and disruptive technologies. It is no secret that the aquaculture sector tends to be slow in adopting cutting-edge technologies. However, individuals within the field are realizing that recent technological advancements could revolutionize certain aspects of aquaculture on a small scale and in a sustainable manner. Innovative and disruptive technology significantly lags behind the available technology, and the application of these technologies in aquaculture is not widespread (Yue and Shen, 2021).

Incorporating different technologies into aquaculture systems is a complex process. To make aquaculture more sustainable and profitable in Africa, these technologies must be effectively integrated. To achieve this, fish farmers, fish scientists, economists, software developers, and engineers must collaborate. In order to integrate disruptive technologies into the aquaculture sector, government agencies in Africa need to fund multidisciplinary research projects, while aquatic farming investors, venture capital firms, and extension services can support young start-ups. The aquaculture industry in Africa stands to become significantly more resourceful due to emerging and disruptive technologies. Moreover, these technologies will create new business and employment opportunities for young individuals in Africa. The sustainability of aquaculture must be enhanced through effective management to prevent these emerging technologies from undermining it (Yue and Shen, 2021; FAO, 2020). By presenting essential information, the current study enables technology inventors and businesses interested in the sector to invest on the African continent and advance aquaculture research.

CONFLICT OF INTERESTS

The authors have not declared any conflict of interests.

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REFERENCES

Ab Rahman A, Hamid UZA, Chin TA (2017). Emerging technologies with disruptive effects: A review. Perintis eJournal 7:111-128.

Abdelrahman H, ElHady M, Alcivar-Warren A, Allen S, Al-Tobasei R, Bao L, Beck B, Blackburn H, Bosworth B, Buchanan J (2017). Aquaculture genomics, genetics and breeding in the United States: Current status, challenges, and priorities for future research. BMC Genomics 18:191. https://doi.org/10.1186/s12864-017-3557-1.

Acar Ü, Kesbiç OS, Yılmaz S, Karabayır A (2018). Growth performance, haematological and serum biochemical profiles in rainbow trout (*Oncorhynchus mykiss*) fed diets with varying levels of lupin (*Lupinus albus*) meal. Aquaculture Research 49(7):2579-2586. doi:10.1111/are.13724

Acar U, Kesbic OS, Yilmaz S, Kesbic FI, Gultepe N (2019). Gibel carp (Carassius auratus gibelio) meal as an alternative major protein in feeds for rainbow trout juveniles (Oncorhynchus mykiss). Turkish Journal of Fisheries and Aquatic Sciences 19(5):383-390. doi:10.4194/1303-2712-v19_5_03

Ahire JJ, Mokashe NU, Chaudhari BL (2019). Effect of dietary probiotic *Lactobacillus helveticus* on growth performance, antioxidant levels, and absorption of essential trace elements in goldfish (*Carassius auratus*). Probiotics Antimicrobial Proteins 11(2):559-568. doi: 10.1007/s12602-018-9428-5.

Aich N, Nama S, Biswal A, Paul T (2020). A review on recirculating aquaculture systems: Challenges and opportunities for sustainable aquaculture. Innovative Farming 5(2020):17-24. Retrieved from http://www.innovativefarming.in/index.php/IF/article/view/109.

Amenyogbe E, Huang JS, Chen G, Wang WZ (2021). Probiotic Potential of Indigenous (*Bacillus* sp. RCS1, *Pantoea agglomerans* RCS2, and *Bacillus cereus* strain RCS3) Isolated from Cobia Fish (*Rachycentron canadum*) and Their Antagonistic Effects on the Growth of Pathogenic *Vibrio alginolyticus, Vibrio harveyi, Streptococcus iniae*, and *Streptococcus agalactiae*. Frontiers in Marine Science 8:672213. doi: 10.3389/fmars.2021.672213.

Badiola M, Basurko OC, Piedrahita R, Hundley P, Mendiola D (2018). Energy use in Recirculating Aquaculture Systems (RAS): A review.

Aquacultural Engineering 81:57-70. doi: 10.1016/j.aquaeng.2018.03.003

Bagi A, Riiser ES, Molland HS, Star B, Haverkamp THA, Sydnes MO, Pampanin DM (2018). Gastrointestinal microbial community changes in Atlantic cod (*Gadus morhua*) exposed to crude oil. BMC Microbiology 18:1-14. doi:10.1186/s12866-018-1171-2

Bairagi A, Ghosh KS, Sen SK, Ray AK (2002). Enzyme producing bacterial flora isolated from fish digestive tracts. Aquaculture International 1(2):109-121. doi:10.1023/a:1021355406412.

Bereded NK, Curto M, Domig KJ, Abebe GB, Fanta SW, Waidbacher H, Meimberg H (2020). Metabarcoding Analyses of Gut Microbiota of Nile Tilapia (*Oreochromis niloticus*) from Lake Awassa and Lake

Chamo, Ethiopia. Microorganisms 8(7):1040. doi:10.3390/microorganisms8071040

Bisi-Johnson MA, Obi CL, Ekpo MH, Umeobika UC (2017).

Metagenomics and metabolomics analyses of African catfish (*Clarias gariepinus*) guts reveal the presence of microorganisms and their metabolic potentials. PLoS One 12(11):e0187667.

Chattopadhyay NRV (2017). Induced fish breeding: a practical guide for hatcheries. Academic Press.

Chen H, Li C, Liu T, Chen S, Xiao H (2019). A Metagenomic Study of Intestinal Microbial Diversity in Relation to Feeding Habits of Surface and Cave-Dwelling Sinocyclocheilus Species. Microbial Ecology 79(2):299-311. doi:10.1007/s00248-019-01409-4.

Chen HY, Cheng SC, Chang CC (2020). Semantic scene modeling for aquaculture management using an autonomous drone. In International workshop on advanced imaging technology (IWAIT) 2020. International Society for Optics and Photonics 1151521.

Clements KD, Angert ER, Montgomery WL, Choat JH (2014). Intestinal microbiota in fishes: what's known and what's not. Molecular Ecology 23(8):1891-1898. doi:10.1111/mec.12699.

Dawood MAO, Koshio S, Ishikawa M, Yokoyama S, El Basuini MF, Hossain MS, Nhu TH, Dossou S, Moss SA (2016). Effects of dietary supplementation of *Lactobacillus rhamnosus* or/and *Lactococcus lactis* on the growth, gut microbiota and immune responses of red sea bream, *Pagrus major*. Fish and Shellfish Immunology 49:275285. doi: 10.1016/j.fsi.2015.12.047.

Dupont C, Cousin P, Dupont S (2018). IoT for aquaculture 4.0 smart and easy-to-deploy real-time water monitoring with IoT, In 2018 global internet of things summit (GIoTS) (pp. 1–5). IEEE.

Egerton S, Culloty S, Whooley J, Stanton C, Ross RP (2018). The Gut Microbiota of Marine Fish. Frontiers in Microbiology 9:873.doi: 10.3389/fmicb.2018.00873

Eichmiller JJ, Hamilton MJ, Staley C, Sadowsky MJ, Sorensen PW (2016). Environment shapes the fecal microbiome of invasive carp species. Microbiome 4:44.

Evensen T (2020). Fishy business: Closing the gap between data-driven decision-making (DDM) and aquaculture: An analysis of incumbents in the Norwegian aquaculture industry (NAI) and the use of big data for competitive advantage. http://hdl.handle.net/10400.14/29687

Falcinelli S, Rodiles A, Hatef A, Picchietti S, Cossignani L, Merrifield DL, Unniappam S, Carnevali O (2017). Dietary lipid content reorganizes gut microbiota and probiotic *L. rhamnosus* attenuates obesity and enhances catabolic hormonal milieu in zebrafish. Scientific Reports 7(1):5512. doi:10.1038/s41598-017-05147-w.

FAO (2020). The state of world fisheries and aquaculture 2020. Rome, Italy: Sustainability in action. Ferreira JG, Aguilar-Manjarrez J, Bacher C, Black K, Dong S, Grant J (2012). Progressing aquaculture through virtual technology and decision-support tools for novel management. In Global conference on aquaculture.

Fetissov SO (2017). Role of the gut microbiota in host appetite control: bacterial growth to animal feeding behaviour. Nature Reviews Endocrinology 13(1):11-25. doi: 10.1038/nrendo.2016.150.

Gangadhara B, Keshavanath P, Ramesha TJ, Priyadarshini M (2004). Digestibility of bamboo-grown periphyton by carps (*Catla catla, Labeo rohita, Cirrhinus mrigala, Cyprinus carpio, Ctenopharyngodon idella*, and *Tor khudree*) and hybrid red tilapia (*Oreochromis mossambicus* X *O. niloticus*). Journal of Applied Aquaculture 15(3-4):151-162.

German DP, Nagle BC, Villeda JM, Ruiz AM, Thomson AW, Balderas S C, Evans DH (2010). Evolution of herbivory in a carnivorous clade of minnows (Teleostei: Cyprinidae): Effects on gut size and digestive ph ysiology. Physiological and Biochemical Zoology 83(1):1-18. doi:

10.1086/648510.

Giorgia G, Elia C, Andrea P, Cinzia C, Stefania S, Ana R, Daniel ML, Ike O, Oliana C (2018). Effects of *Lactogen 13,* a New Probiotic Preparation, on Gut Microbiota and Endocrine Signals Controlling Growth and Appetite of *Oreochromis niloticus* Juveniles. Microbial Ecology 76(4):1063-1074. doi:10.1007/s00248-018-1177-1.

Gjedrem T, Robinson N (2014). Advances by selective breeding for aquatic species: A review. Agricultural Sciences 5:1152. DOI: 10.4236/as.2014.512125

Guerreiro I, Serra CR, Oliva-Teles A, Enes P (2018). Short communication: gut microbiota of European sea bass (*Dicentrarchus labrax*) is modulated by short-chain fructooligosaccharides and xylooligosaccharides. Aquaculture International 26(1):279288. doi:10.1007/s10499-017-0220-4.

Houston RD, Bean TP, Macqueen DJ, Gundappa MK, Jin YH, Jenkins TL, Selly SL, Martin SA, Stevens JR, Santos EM, Davie A (2020). Harnessing genomics to fast-track genetic improvement in aquaculture. Nature Reviews Genetics (7):389-409. doi: 10.1038/s41576-020-0227-y.

Jiang M, Xu M, Ying C, Yin D, Dai P, Yang Y, Ye K, Liu K (2019). The intestinal microbiota of lake anchovy varies according to sex, body size, and local habitat in Taihu Lake, China. MicrobiologyOpen 9(1):e00955. doi:10.1002/mbo3.955.

Jiang Y, Xie C, Yang G, Gong X, Chen X, Xu L, Bao B (2011). Cellulaseproducing bacteria of *Aeromonas* are dominant and indigenous in the gut of *Ctenopharyngodon idellus* (Valenciennes). Aquaculture Research 42(4):499-505. doi:10.1111/j.1365-2109.2010.02645.x.

Jin YX, Wu SS, Zeng ZY, Fu ZW (2017). Effects of environmental pollutants on gut microbiota. Environmental Pollution 222:1-9.

Johnston I (2018). Biosensors for real-time monitoring of biohazards and disease in aquaculture, sensors in food and agriculture in Food and Agriculture 2018. Norwich, UK. 9.07.

Jothiswaran V, Velumani T, Jayaraman R (2020). Application of artificial intelligence in fisheries and aquaculture. Biotica Research Today 2(6):499-502.

Kelly AM, Renukdas NN (2020). Disease management of aquatic animals, aquaculture health management. Elsevier. eBook ISBN: 9780128133606

Li D, Wang Z, Wu S, Miao Z., Du L, Duan Y (2020). Automatic recognition methods of fish feeding behavior in aquaculture: A review. Aquaculture 528:735508. doi: 10.1016/j.aquaculture.2020.735508

Liu X, Shi H, He Q, Lin F, Wang Q, Xiao S, Dai R, Zhang Y, Yang H, Zhao H (2019). Effect of starvation and refeeding on growth, gut microbiota and non-specific immunity in hybrid grouper (*Epinephelus fuscoguttatus*♀×*E. lanceolatus*♂). Fish and Shellfish Immunology 97:182-193. doi: 10.1016/j.fsi.2019.11.055

Liu Y, Zhang Y, Wang Y, Chen Y (2021). Probiotics in Aquaculture: A Comprehensive Review. Aquaculture 531:735948.

Liu Z, Liu W, Ran C, Hu J, Zhou Z (2016). Abrupt suspension of probiotics administration may increase host pathogen susceptibility by inducing gut dysbiosis. Scientific Report

6(1):23214. doi:10.1038/srep23214.

Llewellyn MS, Boutin S, Hoseinifar SH, Derome N (2014). Teleost microbiomes: the state of the art in their characterization, manipulation and importance in aquaculture and fisheries. Frontiers in Microbiology 22(5):207.

Ma C, Chen C, Jia L, He X, Zhang B (2019a). Comparison of the intestinal microbiota composition and function in healthy and diseased Yunlong Grouper. AMB Express 9(1):1-11. doi:10.1186/s13568-019-0913-3.

Ma J, Bruce TJ, Jones EM, Cain KD (2019b). A Review of Fish Vaccine Development Strategies: Conventional Methods and Modern Biotechnological Approaches. Microorganisms 7(11):569. doi:10.3390/microorganisms7110569.

Merrifield DL, Shaw BJ, Harper GM, Saoud IP, Davies SJ, Handy RD, Henry TB (2013). Ingestion of metal-nanoparticle contaminated food disrupts endogenous microbiota in zebrafish *(Danio rerio)*. Environmental Pollution 174*:*157-163. https://doi.org/10.1016/j.envpol.2012.11.017.

Mikaelyan A, Dietrich C, Köhler T, Poulsen M, Sillam-Dussès D, Brune A (2015). Diet is the primary determinant of bacterial community structure in the guts of higher termites. Molecular Ecology 24(20):5284-5295. doi:10.1111/mec.13376.

Navarrete P, Mardones P, Opazo R, Espejo R, Romero J (2008). Oxytetracycline Treatment Reduces Bacterial Diversity of Intestinal Microbiota of Atlantic Salmon. Journal of Aquatic Animal Health 20(3):177-183. doi:10.1577/h07-043.1.

Nyman A, Huyben D, Lundh T, Dicksved J (2017). Effects of microbe- and mussel-based diets on the gut microbiota in Arctic charr (*Salvelinus alpinus*). Aquaculture Reports 5:34-40. doi:10.1016/j.aqrep.2016.12.003.

Parlak O, Keene ST, Marais A, Curto VF, Salleo A (2018). Molecularly selective nanoporous membrane-based wearable organic electrochemical device for noninvasive cortisol sensing. Science Advances 4(7):eaar2904. doi: 10.1126/sciadv.aar2904.

Parshukov AN, Kashinskaya EN, Simonov EP, Hlunov OV, Izvekova GI, Andree KB, Solovyev MM (2019). Variations of the intestinal gut microbiota of farmed rainbow trout, (*Oncorhynchus mykiss* Walbaum), depending on the infection status of the fish. Journal of Applied Microbiology 127(2):379-395. doi:10.1111/jam.14302.

Prasolova-Førland E, Forninykh M, Ekelund OI (2019). Empowering young job seekers with virtual reality. In 2019 IEEE conference on virtual reality and 3D user interfaces (VR) pp. 295-302.

Razman MAM, Majeed APA, Musa RM, Taha Z, Susto GA, Mukai Y (2020). Machine learning in aquaculture hunger classification. Singapore: Springer.

Read MN, Holmes AJ (2017). Towards an integrative understanding of diet– host–gut microbiome interactions. Frontiers in Immunology 8:538. doi: 10.3389/fimmu.2017.00538.

Rimoldi S, Terova G, Ascione C, Giannico R, Brambilla F (2018). Next generation sequencing for gut microbiome characterization in rainbow trout (*Oncorhynchus mykiss*) fed animal by-product meals as an alternative to fishmeal protein sources. PLoS ONE

13(3):e0193652. https://doi.org/10.1371/journal.pone.0193652.

Ringø EZ, Zhou Z, Vecino JG, Wadsworth S, Romero J, Krogdahl Å, Olsen RE, Dimitroglou A, Foey A, Davies S, Owen M (2016). Effect of dietary components on the gut microbiota of aquatic animals. A never-ending story? Aquaculture Nutrition 22(2):219-282. doi:10.1111/anu.12346.

Rogers EM, Shoemaker FF (1992). Communication of innovation: A cross-culture approach. Fourth Edition, Collier Macmillan Publishers, London.

Sánchez-Alonso I, Marín A, Delgado-Pertíñez M, Fernández-Palacios H (2020). Nutritional and Functional Improvement of Aquaculture Products through the Use of Additives. Marine Drugs 18(3):170.

Semova I, Carten JD, Stombaugh J, Mackey LC, Knight R, Farber SA, Rawls JF (2012). Microbiota Regulate Intestinal Absorption and Metabolism of Fatty Acids in the Zebrafish. Cell Host and Microbe 12(3):277-288. doi: 10.1016/j.chom.2012.08.003.

Sheng Y, Ren H, Limbu SM, Sun Y, Qiao F, Zhai W, Du ZY, Zhang M (2018). The Presence or Absence of Intestinal Microbiota Affects Lipid Deposition and Related Genes Expression in Zebrafish (*Danio rerio*). Frontiers in Microbiology 9:1124. doi:10.3389/fmicb.2018.01124.

Skrodenytė-Arbačiauskienė V, Sruoga A, Butkauskas D, Skrupskelis K (2008). Phylogenetic analysis of intestinal bacteria of freshwater salmon *Salmo salar and sea* trout Salmo *trutta trutta and* diet. Fisheries Science 74(6):1307-1314. doi:10.1111/j.14442906.2008. 01656.x .

Smorodinskaya S, Kochetkov N, Danilenko V, Bugaev O, Vatlin A, Abrosimova N, Antipov S, Kudryavtsev A,Klimov V (2022). Effects of Three Feed Additives on the Culturable Microbiota Composition and Histology of the Anterior and Posterior Intestines of Zebrafish (*Danio rerio*). Animals 12(18):2424. https://doi.org/10.3390/ani12182424

Stagaman K, Burns AR, Guillemin K, Bohannan BJ (2017). The role of adaptive immunity as an ecological filter on the gut microbiota in zebrafish. Isme Journal 11(7):1630-1639. doi:10.1038/ismej.2017.28.

Strandwitz P (2018). Neurotransmitter modulation by the gut microbiota. Brain Research 1693:128-133. doi: 10.1016/j.brainres.2018.03.015.

Su X, Sutarlie L, Loh XJ (2020). Sensors, biosensors, and analytical technologies for aquaculture water quality. Research P. 8272705.

Sulaiman MA, Kamarudin MS, Romano N, Syukri F (2020). Effects of increasing dietary carbohydrate level on feed utilisation, body composition, liver glycogen, and intestinal short chain fatty acids of hybrid lemon fin barb (*Barbonymus gonionotus* onio*Hypsibarbus wetmorei* male eiius wetmoreiliver glycog: 100250. doi: 10.1016/j.aqrep.2019.100250.

Sullam KE, Essinger SD, Lozupone CA, O’CONNOR MP, Rosen GL, Knight RO, Kilham SS, Russell JA (2012). Environmental and ecological factors that shape the gut bacterial communities of fish: a meta-analysis. Molecular Ecology 21(13):3363-3378. doi:10.1111/j.1365-294x.2012.05552.x.

Tarnecki AM, Burgos FA, Ray CL, Arias CR (2017). Fish intestinal microbiome: diversity and symbiosis unravelled by metagenomics. Journal of Applied Microbiology 123(1):2-17. doi:10.1111/jam.13415.

Weber GM, Lee CS (2014). Current and future assisted reproductive technologies for fish species. Current and Future Reproductive Technologies and World Food Productio. Springer. Advances in Experimental Medicine and Biology 752:33-76. doi: 10.1007/978-14614-8887-3_3.

White WL, Coveny A, Robertson J, Clements KD (2010). Utilization of mannitol by temperate marine herbivorous fishes. Journal of Experimental Marine Biology and Ecology 391:50-56.

Wu S, Wang G, Angert ER, Wang W, Li W (2020). Changes in gut bacterial community and morphology of grass carp in response to different diets. Aquaculture 528:735567.

Wu Z, Zhang Q, Lin Y, Hao J, Wang S, Zhang J, Li A (2021). Taxonomic and Functional Characteristics of the Gill and Gastrointestinal Microbiota and Its Correlation with Intestinal Metabolites in NEW

GIFT Strain of Farmed Adult Nile Tilapia (*Oreochromis niloticus*). Microorganisms 9(3):617. doi:10.3390/microorganisms9030617

Xiao R, Wei Y, An D, Li D, Ta X, Wu Y, Ren Q (2019). A review on the research status and development trend of equipment in water treatment processes of recirculating aquaculture systems. Reviews in Aquaculture 11(3):863-895. https://doi.org/10.1111/raq.12270.

Xing M, Hou Z, Yuan J, Liu Y, Qu Y, Liu B (2013). Taxonomic and functional metagenomic profiling of gastrointestinal tract microbiome of the farmede adult turbot (*Scophthalmus maximus*). FEMS Microbiology Ecology 86(3):432-443.

Yang TT, Liu Y, Tan S, Wang WX, Wang X (2021). The role of intestinal microbiota of the marine fish (Acanthopagrus latus) in mercury biotransformation. Environmental Pollution 277:116768. https://doi.org/10.1016/j.envpol.2021.116768.

Yano JM, Yu K, Donaldson GP, Shastri GG, Ann P, Ma L, Nagler CR, Ismagilov RF, Mazmanian SK, Hsiao EY (2015). Indigenous Bacteria from the Gut Microbiota Regulate Host Serotonin Biosynthesis. Cell 161(2):264-276. doi: 10.1016/j.cell.2015.02.047.

Yue K, Shen Y (2021). An overview of disruptive technologies for aquaculture. Aquaculture and Fisheries 7(2):111-

120. doi: 10.1016/j.aaf.2021.04.009

Zhai QX, Yu LL, Li TQ (2017). Effect of dietary probiotic supplementation on intestinal microbiota physiological conditions of Nile tilapia (*Oreochromis niloticus*) under waterborne cadmium exposure. Antonie van Leeuwenhoek 110(4):501-513.

Zhang Y, Wen B, Meng LJ, Gao JZ, Chen ZZ (2020). Dynamic changes of gut microbiota of discus fish (*Symphysodon haraldi*) at different feeding stages. Aquaculture 735912. doi: 10.1016/j.aquaculture.2020.735912.

Zhou CP, Ge XP, Liu B, Xie J, Miao LH (2013). Effect of High Dietary Carbohydrate on the Growth Performance and Physiological Responses of Juvenile Wuchang Bream, *Megalobrama amblycephala*. Asian-Australasian Journal of Animal Sciences 26(11):1598-608. doi: 10.5713/ajas.2012.12659.