

Microbial species and drug resistance evaluation in aquacultures using genomics and in addition to genome analysis

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SUMMARY

Due to the rising demand for human nutrition and a lack of wild fishery resources, aquaculture has experienced a significant expansion in terms of production and economic value over the past few decades. Therefore, sustainable aquaculture production is one of the European Union's top priorities in the 2030 agenda. However, the expansion of fish farming has resulted in an increase in the use of antibiotics to combat illness and a rise in the risk of outbreaks. The selective pressure generated by these drugs creates the ideal conditions for the emergence of antimicrobial resistance hotspots in aquaculture facilities. Refers to a collection of contemporary technologies such as genomics, metagenomics, transcriptomics, proteomics, culturomics, and metabolomics. These techniques have received increasing acclaim because of their capability to decipher novel biological science mechanisms. Metagenomics makes it possible to study microbial genomes in specific environments. In aquaculture, microbial diversity, microbial functions, and antibiotic resistance genes could all be studied with the help of metagenomics. The high-throughput technologies used in aquaculture studies of microbial diversity and antimicrobial resistance will be discussed in detail in this review.

Keywords: Aquaculture; Bacterial communities; Antibiotic resistance; Microbial metagenomics

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INTRODUCTION

The need to feed an expanding global population of 9.8 billion people in a safe and adequate manner by 2050 has increased the importance of the aquaculture industry. Aquaculture is quickly becoming the primary source of seafood for human consumption, making it the animal food production industry with the fastest growth rate in the world. Over the past few decades, a significant expansion of aquaculture has been driven by the decline in wild fishery stocks, rising human populations, a persistent demand for seafood, and international trade in terms of production and economic value. Aquaculture's production of fish accounts for nearly half of all fish consumed worldwide, necessitating intensive and semi-intensive production techniques. Nine of the ten nations with the highest levels of aquaculture species diversity are in Asia, with China leading the pack by a significant margin. Egypt, which raises Nile tilapia (*Oreochromis niloticus*), and Norway and Chile, which primarily raise Atlantic salmon (*Salmo salar*), are the largest aquaculture producers outside of Asia [1].

On the other hand, employing intensive or semi-intensive methods for the production of fish leads to a greater concentration of animals in small spaces, which significantly raises the likelihood of contracting infectious diseases. Accordingly, antimicrobials are right now used to forestall and treat sickness flare-ups, and the substances that are broadly utilized in hydroponics are equivalent to those that are authorized to treat and forestall irresistible illnesses in people and animals. Quinolones (such as oxalonic acid, flumequine, and enrofloxacin), tetracyclines (such as oxytetracycline), and phenicols (such as florfenicol), which are mostly given as food, are the antibiotics that are used most frequently in aquaculture to control bacterial fish disease [2].

Horizontal gene transfer (HGT), and mutagenesis even at sub-inhibitory concentrations. The identification of the factors influencing AMR rise and spread in creature production, such as hydroponics, will enhance the capacity to control opposition in the space of food production, the climate, and general health due to the associations of epidemiological pathways between people, creatures, and the environment [3].

The majority of studies have focused on antimicrobial-resistant bacteria. However, it is common knowledge that, particularly in complex matrices like aquaculture environments and sediments; the majority of the bacterial population is non-cultivable, requiring the use of techniques

that are culture-independent. High-throughput genomic technologies offer innovative approaches to environmental health monitoring, such as metagenomic surveillance of antibiotic resistance determinants (ARDs). This review focuses on how omics can be used to evaluate determinants of antibiotic resistance in aquaculture.

Bacterial cell (such as its physicochemical properties and the presence of efflux pumps, for example), the antibiotic compound being destroyed by enzymes that break it down or the cell not having the target molecules. Schmieder and Edwards identified at least four well-known mechanisms that contribute to antibiotic resistance in bacteria: i) the antibiotic being altered or inactivated; ii) a modification to the antibiotic's target site that makes it less able to bind; iii) modifying metabolic pathways to avoid antibiotics' effects; and (iv) decreased the accumulation of antibiotics within the cell by either increasing active efflux or decreasing permeability to antibiotics [4].

The ability of bacteria to adapt to changes in their environment and to defend themselves against toxic substances is crucial to their evolution. Additionally, the effective transmission of a specific bacteria's genetically determined resistance to its clonal expansion and/or other bacterial species is made easier by mobile genetic elements like plasmids, transposons, and integrons. Because of the coordinated activity of genetic/heritable elements and phenotypic traits, it has been determined that a wide range of metabolic functions are necessary for the emergence and spread of antimicrobial resistance [5].

Microbial communities and antimicrobial resistance in aquacultures

The United Nations Environment Programme (UNEP) ranked environmental antibiotic resistance as the most pressing of six emerging issues in December 2017. Up to 75% of the antibiotics used in aquaculture may end up in the environment, it was mentioned. It was discovered that there is a strong positive correlation between the consumption of flumequine and florfenicol in aquafarms and the presence of their residues in samples of sediment and surface water, indicating that the antibiotics used in aquaculture can reach the environment that is close to water. In Europe, Japan, and North America, where only a few antibiotics have been approved, antibiotics are only used for therapeutic purposes in aquaculture. For instance, between 1987 and 2013, Norway's salmon production system saw a 99 percent reduction in the use of antibiotics thanks to the use of vaccines, sanitary practices, and scientific research [6].

Small-tank animal husbandry causes stock losses and other significant financial harm by putting animals under more stress and increasing the risk of infectious diseases. Fish farming has been proposed as a source of ARGs, and a significant connection has been accounted for between the event of ARGs and the centralization of anti-infection agents in hydroponics locales. This prompts the utilization of anti-microbials for both prophylactic and remedial purposes, advancing the choice and scattering of anti-toxin

obstruction qualities by various courses (food, feed, and climate) [7].

Technologies to address microbial communities

The foundation of conventional methods for the detection of antibiotic resistance is growth inhibition assays in broth or agar disc diffusion, which estimate the minimal inhibitory concentration (MIC) of particular antibiotics for each bacterial isolate. This method only allows for the study of a small number of bacterial isolates at a time, in contrast to the millions of bacterial species that can be found in aquaculture facilities and ecosystems that receive effluent. The refined time, which can take somewhere in the range of one to two days for quickly developing microorganisms to a little while for slow-developing species, is one more issue with culture-based frameworks [8].

Despite the development of quantitative PCR and microarray technologies, only a few well-studied antibiotic resistance-related genes are detected. They prevent wide-spectrum screening, so non-culturable species' true potential as reservoirs of antibiotic resistance is overlooked. The outbreak of next-generation sequencing can circumvent these limitations because it does not require culture or amplification. Because of these technologies, which offer a deeper comprehension of the genomic information of the majority of bacteria, new resistance genes can be discovered. Metagenomics extends beyond the study of a single genome. In addition to expediting the discovery of novel genes, the meta- (transcendent in Greek) strategy provides information regarding the presence, absence, or modification of antibiotic resistance-causing genes [9].

Aquatic resistomes

The more conventional target sequence polymerase chain reaction (PCR)-based amplification methods are insufficient for identifying and quantifying ARGs in microbial communities. High-throughput sequencing technologies have made it possible to study ARGs in a wide range of ecological settings thanks to metagenomics. Metagenomics, for instance, demonstrated a co-selection of virulence and resistance determinants in bacterial communities, particularly in the microbiomes of the human gut [10].

In order to aid in the identification and annotation of ARGs, numerous antibiotic resistance gene databases have been developed in recent years. A review of the existing antibiotic resistance gene data resources is provided by lists of some of the most recent antibiotic resistance gene data resources, such as Comprehensive Antibiotic Resistance Database (CARD 2020), Antibiotic Resistance Gene-Annotation (ARG-ANNOT), or Structured Antibiotic Resistance Genes (the SARG) with a hierarchical structure (ARGs type-subtype-reference sequence) ARGs-OAP.

CONCLUSION

Due to the rise in human activities, antibiotics are now a significant contaminant of the habitat, particularly the aquatic and aquaculture environments. As a result, it is

possible for them to become part of the human food chain. Because some of these antibiotic residues may be of critical importance to human health, bacteria that share resistance to these antibiotics should be kept under epidemiological control. In addition to being a promising instrument for studying the diversity of microbial communities in aquatic environments, metagenomics has emerged as a useful method for assessing the variety of antimicrobial

resistance characteristics present in a microbiome. On the other hand, culturomics, a method that combines automation equipment with high-throughput bacterial culture methods, is bringing back some old microbiology trends. Overall, we might want to emphasize that large-scale examination is a very useful method for studying unstructured ocean conditions and microbial networks, and that its application should be unlimited.

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