

MARINE MICROORGANISMS AS A SOURCE OF NOVEL PROBIOTICS

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Abstract

Probiotics from marine microorganisms become available in improved health effects upon consumption. Probiotic is a term now used to refer to ingested microorganism related to health and positive impacts to animals and humans. Probiotics have varied benefits since they are sources of nutrients, which supply enzymes to facilitate improved digestion and enhance the immune system response against pathogenic bacteria. Disease outbreaks typically afflict the aquaculture industry, limiting financial benefit and causing livestock losses. Therefore, antimicrobials are typically used to manage disease. However, there have been growing movements to implement different approaches to aquaculture enterprises' disease control. This has made it easier to introduce probiotics into aquaculture operations, which has reduced the use of antibiotics at a good rate. Because of the limited effectiveness of experiments with terrestrial bacteria, probiotics derived from marine microorganisms offer a more innovative and superior option for applications. Streptomyces and the newly identified bacteria have potential probiotic qualities and have a bright future in aquaculture.

Key words: probiotics, aquaculture, enzymes, nutrient sources, marine

1. INTRODUCTION

Because aquatic fish live in harsh conditions, such as hydrothermal vents or deep, dark trenches, they have evolved a variety of unique physiological and biochemical adaptations. Another important source of distinct and varied natural bioactive chemicals with both medicinal and commercial utility is marine habitats. Marine-derived drugs with a variety of biological activity, including peptides and antibodies, now have 15 clinical licenses. Several more are in different stages of clinical research. Both novel antimicrobials and alternatives to antibiotics are desperately needed today [2]. Human health is seriously threatened by antimicrobial resistance (AMR) on a global scale. In 2019 alone, an estimated 4.95 million deaths were ascribed to AMR[3]. While multidrug-resistant infections are becoming more common and traditional antibiotic medicines are becoming less effective, new antibiotic-based treatments have only slowly emerged in recent decades[11].

The fish gut microbiome, a known source of helpful microorganisms and maybe therapeutic chemicals, clearly does not reflect this status[4]. Fish gut microbiota bioprospecting is becoming more popular as a way to find novel bioactive substances that may have uses in aquaculture and medicine[10]. Important biological functions of fish gut microbiota include immune system regulation, stress response, pathogen and infection defines, and digesting

[16]. A recent study looked at the progress made in understanding the unique functional roles of gut bacteria in marine fish[12]. Class II bacteriocins are either cyclic or unaltered, while class I bacteriocins undergo significant post-translational modification[15]. For example, class I lanthipeptides are made up of individual β -methylanthionine and/or lanthionine residues that undergo significant post-translational modification to produce distinctive (methyl)lanthionine rings.

2. REVIEW OF LITERATURE

In general, bacteriocins affect the target cells' cell membrane. They can effectively disrupt negatively-charged target cell membranes due to their hydrophobic nature and overall net positive charge. Despite having different modes of action, bacteriocins generally cause holes in cell membranes that allow substances from inside the cell to leak out, destabilizing the membrane potential and ultimately killing the cell. Alternatively, they can obstruct cellular functions by attaching to specific cellular receptors. Both broad-spectrum and narrow-spectrum bacteriocins have antibacterial properties. Broad-spectrum bacteriocins work against a variety of bacterial species, just like traditional antibiotics do. The ability to treat infections for which the etiological pathogen is unknown is one benefit of this. Nevertheless, it can seriously alter the diversity of commensal gut microbiota and increase the likelihood of antibiotic-resistant strains and chronic illnesses linked to the gut. Only particular genera or even species are affected by narrow-spectrum bacteriocins. This characteristic can be used to develop precise medicines that target disease species without endangering beneficial bacteria [5].

generated by *Bacillus thuringiensis*, for example, was found to be more efficient than conventional antibiotics at reducing *Clostridium difficile* in a distal colon tract without significantly altering the total microbial diversity. Because of their wide spectrum of antibacterial action, thermostability, and substantial potential for bioengineering and the creation of variations with added-value properties, bacteriocins are therefore attractive substitutes for conventional antibiotics. But ongoing advancements in culture-independent technology, including metagenomic sequencing, are making it possible to investigate this microbial niche in greater detail. Marine microbes are the least accessible and least understood due to the size of the marine ecosystem, which increases the usefulness of employing culture-independent metagenomic analysis[6]. Fish gut microbiota in the ocean is a virtually untapped source of new antimicrobials. Marine fish have a diverse microbial population in their guts, with bacteria predominating and numbers ranging from colony forming units (CFU) to fungi, viruses, and archaea[13].

During the fish larval stage, this community begins to take shape, with early colonizers coming from the egg surface, surrounding water, and first feeding. Abiotic and biotic variables, such as host phylogeny, trophic level (diet), ambient salinity, and, to a lesser extent, environmental pH and temperature, then affect the richness of the fish gut microbiome. A significant and unique position in the marine environment is occupied by the gut microbiome of fish. Research has shown that the microorganisms in the stomachs of marine fish can differ from those in the surrounding waters and may even include species that are rarely, if ever, found in the surrounding water.

3. MATERIALS AND METHODS

A thorough analysis of the composition of the fish gut microbiome has already been completed. Research on the variety of fish microbiomes was first limited to culturable microorganisms. By being linked to particular symbiotic functional processes, like the production of bioactive enzymes, they were proposed to contribute to stomach digestion. To determine the bacterial component of this community, 16S rRNA sequencing data has been used in most investigations on the gut microbiota of marine fish. Nonetheless, a recent study looked at whole-metagenome shotgun sequencing data from many deep-sea species in the northern Atlantic Ocean (Atlantic). The nutrient cycle in pelagic and deep-sea sediment depends on these two types of planktonic archaea, which are among the most prevalent in marine habitats. The digestive tract of fish has been regarded as a vital home for types of archaea in the ocean, especially the obligate anaerobic Euryarchaeotic[7].

Viruses are the most prevalent organisms on Earth, and this is also true in the ocean. the approximate quantity of viruses in one milliliter of saltwater. Because of their diversity and the factors influencing their microbiome diversity, it has been difficult to identify a "core microbiome" inside marine fish. Additionally, fish gut microbiota members might be temporary. Instead, functional diversity has been proposed as a potential more important factor than taxonomic/phylogenetic variety. Furthermore, the majority of these investigations demonstrated that a significant percentage of operational taxonomic units (OTUs) could not be assigned to genus level taxonomically. This suggests that the gut microbiomes of marine fish are unique and offer a wealth of opportunities for biodiscovery. Additionally, the gut microbiota of marine fish controls host functions like metabolism, reproduction, stress and immunological responses, and digesting.

Because of its hydrophobic properties and structural similarity to bacteriocins that resemble defensin, BaCf3 was predicted to target the cell membrane. This was confirmed by microscopic analysis of *Bacillus* circulant target cells after exposure, which revealed damage to the cell membrane and intracellular material leaking. was also discovered to have anti-cancer and anti-biofilm properties[8]. This work is one of the first to isolate a new bacteriocin from a deep-sea fish's intestines. More importantly, when subjected to low temperatures (4 °C) and high pressure and heat treatments (autoclaving), it maintains its antibacterial properties[17].

Both compounds exhibited broad-spectrum action, targeting fungus and both gram-positive and gram-negative bacteria[14]

They were found to be more similar to eukaryotic AMPs than bacterial peptides once their chemical structure was established. Additionally, recent in vitro and genomic screening investigations have demonstrated the antibacterial efficacy of novel fish-derived *Bacilli*. Actinobacteria are also commonly found in marine habitats, and it is known that those that live alongside higher organisms like fish, mollusks, and sponges produce a broad spectrum of bioactive metabolites with various biological properties. An effective antibiotic against *Bacillus anthracis*, the causative agent of anthrax, is a strong antibacterial generated by an actinomycete acquired from marine sources. *Streptomyces* isolates from maritime sediment were screened, and anthramycin was found.

4. RESULT AND DISCUSSION

One application for sea-derived bacteriocins is to cure fish diseases in aquaculture by substituting them for antibiotics. Fish and fish products are valuable, globally traded commodities because millions of tons of them are consumed annually, either directly as food, fishmeal, or for fish oil. Commercial fish disease outbreaks have a significant impact on global supplies, the economy, and public health. Marine fish-derived bacteriocin genic isolates are provoking tremendous attention to the aquaculture sector to be exploited as probiotics.

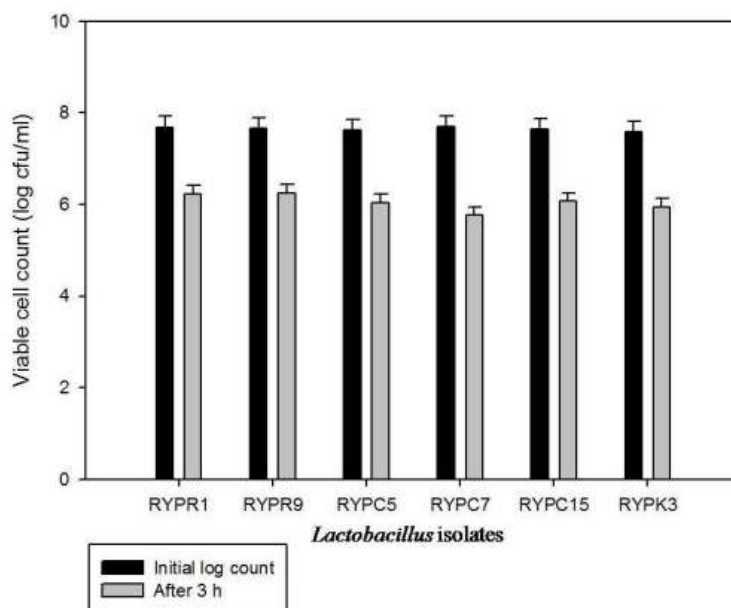


Figure 1: Survival of isolates to SSDP

For example, it was demonstrated that, in addition to its capacity to create bacteriocin, *Enterococcus lactis* RS5 had a number of essential traits of probiotic strains, such as low pH, protease digestion, and resistance to bile salts. examined the probiotic potential of the bacteria that were first identified from Olive flounder's intestine. The in vitro expression of the genes involved in bacteriocin biosynthesis and the culture of the producer bacteria present two challenges in the biodiscovery of bacteriocins from marine microbial communities.

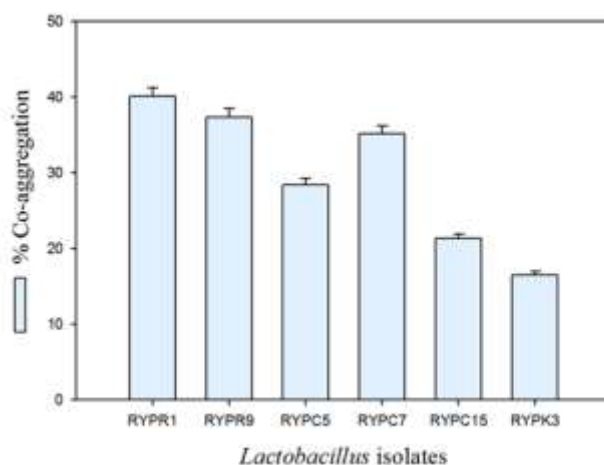


Figure 2: Co-aggregation percent of selected isolates

A number of variables should be taken into account, including temperature, dissolved oxygen content, and environmental pressure, as these generate. For the manufacture of antimicrobials, selected or modified medium are often required, along with extended incubation times of days or even weeks. They noted that replacement of carbon, nitrogen, and salt sources, and pH change had different influences upon antimicrobial activity.

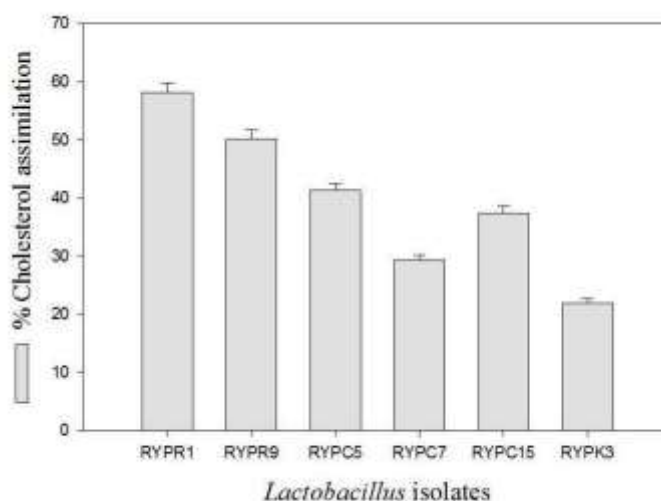


Figure 3: Percent cholesterol assimilation of selected isolates.

Additionally, after growing on solid agar for two days, the strain produced bioactive metabolites; however, this did not occur after incubating in broths for more than ten days. Furthermore, the presence of particular signalling molecules in their native habitat may be necessary for the growth of some marine bacteria. Culture-independent and metagenomics-based techniques, including genome mining, metabolomics, metagenomic library construction, and next-generation sequencing, are increasingly being used to analyse microbial populations. These technologies remove the sampling bias of culturable microbiota and provide a more complete picture of these microbial populations.

5. CONCLUSION

Obtaining novel bioactive compounds is urgently needed as the need for new antimicrobial medicines to combat antibiotic resistance grows. The diversity of marine organisms and their biomolecules is influenced by a multitude of factors, which add to the marine ecosystem's vastness. This also holds true for the marine fish gut microbiota, which is now recognized to include a variety of antibiotic compounds, such as bacteriocins. Important characteristics of marine life, such as high salinity, hydrostatic pressure, and a wide temperature range, influence the structural and functional diversity of marine antimicrobial compounds, or bacteriocins, which often set them apart from their terrestrial counterparts. Although it is currently difficult, figuring out the true variety of the

microorganisms found in marine fish gut microbiomes and the bioactive substances they produce can be crucial to realizing the promise of this niche. Marine fish gut bacteriocins are byproducts of probiotic strains and can be utilized directly or indirectly to prevent illness and preserve food. Although access and technological limitations have prevented a comprehensive examination of the gut microbiome of marine fishes' full bio prospective potential, it represents a potential goldmine of novel bacteriocins and other antimicrobials.

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