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Pathogens of major concern in fish: A review

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Abstract

Fish in the wild and in aquaculture facilities are both vulnerable to infection caused by a phylogenetically diverse group of pathogenic bacteria. Treatment and control options based on drugs and vaccines are insufficient, inefficient, or impractical. The traditional approach to studying fish pathogenic bacteria was to look at individual or small groups of virulence factors. Considered one of the fastest expanding animal - based food sector in the world, and it is expected to grow even more to feed the world's growing population. Existing and re-emerging diseases, on the other hand, are impeding fish and shellfish cultivation as well as yield. Many diseases lack vaccination protocols, and the overuse of antibiotics and some other chemicals is a major concern. This review reveals the implications of microbiota to mitigate (re-)emerging diseases in aquaculture and describes insights into the diversity and functions of fish bacterial communities revealed by next-generation sequencing.

Keywords: Aquaculture, fish diseases, bacteria and pathogens

Introduction

According to the United Nations Food and Agricultural Organization (FAO), the world's food and feed supply will need to increase by 70% by 2050 to support the growing human population. Aquaculture is currently the world's fastest growing animal food sector. However, several emerging diseases caused by viruses, bacteria, fungi, oomycetes, amoebas, and other ectoparasites are limiting fish and shellfish production. Antibiotics are typically used to treat bacterial fish diseases [1]. Beneficial bacteria introduced through into aquaculture environment, also known as probiotics, are regarded as a highly promising and long-term strategy for disease mitigation in fish. To date, a variety of potential probiotics, including bacteria, bacteriophages, fungi, and yeasts, have been investigated for use in aquaculture [2, 3]. Microorganisms are normally found on fish outer surface such as skin and gills, including inside the fish in regions including the digestive tract and internal organs such as the kidney, liver, and spleen. Fish and fish products, particularly undercooked or raw products, have been linked to outbreaks of bacterial pathogens, biotoxins, histamine, viruses, and/or parasites. Fish have really been recognised as reservoirs of pathogenic bacteria associated with human diseases such as *Mycobacterium* spp., *Streptococcus iniae*, *Photobacterium damsela*, *Vibrio alginolyticus*, *Vibrio vulnificus*, *Vibrio parahaemolyticus*, *Vibrio cholerae*, *Erysipelothrix rhusiopathiae*, pathogenic *Escherichia* *Clostridium botulinum*, *Clostridium perfringens*, *Campylobacter jejuni*, *Delftia acidovorans*, *Edwardsiella tarda*, *Legionella pneumophila* and *Plesiomonas shigelloides* are among the bacteria found [4]. Natural fish microflora generally reflects the microbial communities of the surrounding waters. It is hard to estimate why so many microorganisms are usually associated with fish because it is heavily dependent on the nature of sample examined and the isolation protocol used. In fact, standard culture-dependent methods can only recover 1 to 10% of total bacteria in a given sample. This problem has yet to be addressed using more precise, molecular-based methods. Bacteria numbers are typically high in gastrointestinal tracts and gills, though these are influenced by water quality and feed. Fish from clean and cold waters have lower bacterial counts than fish from eutrophic and/or warm waters. Both scenarios, however, may contain potential human pathogens.

Microflora

Gram-negative genera such as *Acinetobacter*, *Flavobacterium*, *Moraxella*, *Shewanella*, and *Pseudomonas* dominate the autochthonous bacterial flora of fish. Members of the Vibrionaceae (*Vibrio* and *Photobacterium*) and Aeromonadaceae (*Aeromonas* spp.) families are also common aquatic bacteria found in fish flora.

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Bacillus, *Micrococcus*, *Clostridium*, *Lactobacillus*, and *Coryneforms* are also present in varying proportions [5].

Pathogens: Growth and Survival

Endogenous chemical compounds, algal toxins, human viruses, bacteria, and higher parasites all pose some risk when eating fish. Bacterial risks are among those that increase after the fish is captured. There are only a few human bacterial pathogens capable of causing primary infections or disease and of persisting in the aquatic environment. Even fewer are capable of growing on live fish. The remaining few bacteria pose a significant risk when consuming raw seafood such as sushi or oysters, but these risks are significantly reduced with proper cooking [5,6]. Only two pathogenic bacteria species can be said to occur naturally in fish. These are *Clostridium botulinum* type E and *Vibrio parahaemolyticus*. Furthermore, agricultural run-off or polluted water can pollute in-shore species, particularly molluscan filter feeders, with pathogenic microorganisms or viruses. Cases of contamination of seafood with organisms such as *S. typhi*, *Vibrio spp.*, and *Campylobacter* have been reported in filter feeding mollusks such as mussels [7].

Bacterial Pathogens of Fish

Despite the fact that pathogenic species representing the majority of existing bacterial taxa have now been implicated in diseases, only a low amount of pathogens are responsible for significant economic losses in cultured fish around the world.

Vibrios

Vibrio bacteria are primarily pathogenic to brackish and marine water fish. They are, however, reported in some studies in freshwater species. Vibriosis is found all over the world and causes significant economic losses in the aquaculture industry. Vibriosis, one of the most serious bacterial diseases affecting fish, bivalves, and crustaceans, is primarily caused by pathogenic *Vibrio anguillarum*, *Vibrio harveyi* (Syn. *V. carchariae*), *Vibrio ordalii*, and *Aliivibrio salmonicida* (formerly *Vibrio salmonicida*) [8-12]. The identification of pure isolates from infected tissues is required for diagnosis. Isolation of *V. cholerae* from fish is common and should not be cause for concern as long as the isolate is not of the O type. Stress and crowding are two preventive measures. Coldwater vibriosis (Hitra disease), a serious problem in salmonid sea farming, is characterised by high mortality, drug resistance, and stress mediation. *Aliivibrio salmonicida* is the causative agent. Avoidance is difficult due to the prevalence of members of this family in marine environments. In the salmonid industry, preventive vaccination with formalin-killed *Vibrio* is used. The results of sensitivity testing should be used to direct antibiotic therapy.

Coldwater vibriosis is caused by *Aliivibrio salmonicida* (formerly *Vibrio salmonicida*) in fish population such as farmed Atlantic salmon (*Salmo salar*), sea-farmed rainbow trout (*Oncorhynchus mykiss*), and captive Atlantic cod (*Gadus morhua*). *In vivo*, the Gram-negative bacterium causes tissue degeneration, hemolysis, and sepsis. *Aliivibrio salmonicida*'s genome sequencing demonstrated a mosaic structure affected by massive intrachromosomal alternations, gene acquisition, deletion, and duplication of

DNA within the chromosomes or between chromosomes as well as the plasmids [13-14].

Vibrios are common in aquatic habitats, and these bacteria have been found on the skin, gills, and intestinal tracts of fish and shellfish. In comparison to water and sediment samples, fish intestines had a higher number of *V. vulnificus* and *V. parahaemolyticus*. Other factors, such as water salinity and temperature, may influence *Vibrio spp.* prevalence in fish and aquatic environments. Bacteria were found more frequently in warm water and water with a lower salinity. *V. parahaemolyticus* is commonly associated with molluscan shellfish; but even so, a higher incidence of such bacteria has been evidenced in fish, with the pathogen being detected in much more than 50% of tested freshwater fishes in Vietnam, Malaysia, and Indonesia. *Vibrios* are most commonly found in marine fish, but they have also been observed in freshwater fish. In a Malaysian study, for example, 24% of catfish and 40% of red tilapia samples were contaminated with *V. parahaemolyticus* [19-20]. In conclusion, *Vibrio spp.* are found in both marine and freshwater fish and are widely distributed in aquatic environments. These bacteria can contaminate fish and fish products as a result of improper handling, long-term transportation, evisceration, and cross-contamination from raw materials. *Vibrio spp.* can multiply in food, and the level of bacteria in the final product can rise to the point where it poses a health risk to consumers.

Aeromonads

Aeromonas hydrophila and many other motile aeromonads are some of the most common bacteria in a wide range of aquatic areas around the world, including bottled water, chlorinated water, well water, sewage, and heavily polluted waters, and therefore are frequently linked to serious disease in cultivated and feral fishes, amphibians, reptiles, and birds. Aeromonads are also considered major source of human pathogens. The biological, biochemical, and immunogenic heterogeneity of members of that community has complicated determining the aetiology of diseases caused by aeromonad infections [15-16]. *Aeromonas salmonicida*, the causal agent of furunculosis in salmonid and nonsalmonid fish, is a non-motile, Gram-negative bacterium; furunculosis is a major disease in both wild and cultured fish stocks, causing significant losses to the aquaculture sector worldwide [17-18].

Clostridium botulinum

Clostridium botulinum is a *Clostridium* species that is commonly associated with foodborne botulism. *C. botulinum* is widely distributed in nature and can be found in soil and water. Botulism is caused by *C. botulinum*, which produces botulinum neurotoxin. Botulinum neurotoxins are classified into eight types (A, B, C, D, E, F, G, and H). Botulism in humans is caused by types A, B, E, F, and H, whereas botulism in animals is caused by types C and D. Until now, Type G has not been linked to any botulism cases. *C. botulinum* ability to form spores aids in its survival in the environment. The presence of *C. botulinum* in water sediments and fish could be affected by a combination of factors, including geographical location, fish species feeding habits, sample types, and detection method. *C. botulinum* was discovered in a variety of water sediments and fish samples [21-25].

In the Baltic Sea, studies of marine sediment samples revealed a very high prevalence of *C. botulinum* type E, up to 100 percent. As a result, the Baltic Sea area's sea bottom sediment could be considered an important reservoir for *C. botulinum* type E. Hielm *et al.* (1998a) [23] studied the incidence and type dispersion of *C. botulinum* in Finnish trout farm sediments and fish harvested from the farms. The fish samples selected for the study came from four different species: rainbow trout (*Oncorhynchus mykiss*), lake trout (*Salmo trutta lacustris*), sea trout (*Salmo trutta trutta*), and whitefish (*Salmo trutta trutta*) (*Coregonus lavaretus*). *C. botulinum* type E was found in 68 and 15% of the 125 sediment samples and 165 fish intestine samples tested, respectively. Types A, B, and F were not found in trout farm sediment or fish samples. According to the findings of their study, the design of fish farms can influence the presence of *C. botulinum* in fish farm sediment.

Finally, the predominance of *C. botulinum*, primarily type E, in aquatic environments raises the possibility that fish may harbour multiple types of *C. botulinum* and become a cause of foodborne botulism. *C. botulinum* in fish has been linked to contact with contaminated water environments as well as ingestion of *C. botulinum* spores from sediments or contaminated feed. *C. botulinum* in fish can endanger public health, especially when improper handling during fish processing or inadequate thermal treatment fails to kill all *C. botulinum* spores in the final product.

Edwardsiella

Although *Edwardsiella ictaluri* is usually associated with ailment in channel catfish, it also is responsible for the high fatalities in zebrafish in both research labs and aquarium fish. This is an obligate bacterium that can be passed on through contact with infected fish, water, or faeces. Infected zebrafish show clinical signs of disease such as skin haemorrhaging, pale gills, lethargy, and splenomegaly. Bacteria are commonly found in high numbers on histopathology in the spleen, anterior and posterior kidneys, nares, and forebrain. It can be isolated on conventional culture media, but it grows slowly. *Aeromonas spp.* co-infections are common; *Aeromonas spp.* are fast growers and therefore can easily outgrow *E. ictaluri*.

Edwardsiella tarda and *E. ictaluri* are important pathogens of fish. Both of these are Gram-negative motile rods with cytochrome oxidase negative that ferment glucose and produce acid and gas. Biochemically, the two species differ in that *E. tarda* produces both indol and hydrogen sulphide, whereas *E. ictaluri* produces neither. Furthermore, serologically, the two species do not cross-react. *E. tarda* has been isolated from a variety of warm water and cold water fishes, whereas *E. ictaluri* was only confined from just few warm water fish species. *E. tarda* causes systemic hemorrhagic septicemia in fish, which includes swelling skin lesions and also ulcer and necrosis in internal tissues such as liver, kidney, spleen, and musculature. It can infiltrate and keep increasing in epithelial cells and macrophages to undermine the host's immune system and survive in the fish [26-27].

Mycobacteria

Mycobacteriosis is a related to chronic, systemic, granulomatous disease that affects aquarium fish and cultivated food fish, especially those raised in intensive environments. Low dissolved oxygen, low pH, and high

organic load are all predisposing environmental factors found in recirculating aquaculture systems. The proper use of ultraviolet light to disinfect system water reduces number of bacteria and could be a valuable tool for infection control in exhibit organisms. The pathogenic bacteria could be any Mycobacterium species, including *M. chelonae*, *M. marinum*, and *M. fortuitum*. Syngnathids (sea horses) are especially vulnerable, but the disease can affect any fish. *Mycobacterium marinum*, *Mycobacterium fortuitum*, *Mycobacterium chelonae*, and *Mycobacterium avium* have already been isolated from wild and cultured fish having suffered from mycobacteriosis in various parts of the world [28-30].

Conclusions

The number of bacteria species implicated in fish diseases has steadily increased. *Vibrio*, *Aeromonas*, *Flavobacterium*, *Yersinia*, *Edwardsiella*, *Streptococcus*, *Lactococcus*, *Renibacterium* and *Mycobacterium* are the most common pathogenic bacterial species found in fish. However, there are increasing indications which the pathogens spectrum, as well as the geographic and host range of fish pathogens, is expanding, resulting in the emergence of new pathogens. In contrast to human and animal medicine, fish diseases present unique and daunting challenges. It is almost certain that the genetic analysis information will result in paradigm shifts in bacterial pathogenesis, as well as new perspectives on the evolutionary and adaptive strategies of aquatic bacteria, as well as how they colonise and establish in larger ecological niches as well as new host species. Furthermore, identifying key virulence factors in pathogenic strains should aid in the development of effective drugs and treatments to combat major pathogenic bacteria of fish.

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