news digest #032

Seafood contamination by *Vibrio* spp.: Fueled by climate change?

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Climate change is expanding the reach of pathogenic bacteria, allowing them to thrive and emerge in new regions. This affects the spread of infectious diseases, food safety, and public health. For instance, Vibrio bacteria are moving into temperate regions, causing a rise of infections. The growing presence of antimicrobial resistance genes in *Vibrio* spp. found in seafood is a significant concern. Hence, rapid identification systems, such as the MALDI Biotyper®, are essential for effective microbial surveillance.

One of the less visible yet significant effects of climate change is the shift in ecological niches that favor bacterial growth. Changes in temperature, humidity, and other environmental factors are enabling the geographic expansion of various microorganisms, including pathogenic bacteria relevant to human, animal, and environmental health.

The consequences can be severe, leading to increased bacterial proliferation in already colonized areas and the emergence of pathogens in new regions where they were previously absent. This shift directly impacts the spread of infectious diseases, food safety, and public health.

A concrete example is the expansion of *Vibrio* bacteria, part of the Vibrionaceae family. These primarily flagellated microorganisms inhabit aquatic environments, particularly marine waters and river mouths. They are typically more concentrated in waters with temperatures above 20°C and moderate salinity.[1] *Vibrio* species are commonly associated with various organisms, including fish, seabirds, algae, corals, crustaceans, mollusks, and mammals.[2]

Recent studies have highlighted how global warming is contributing to the spread of *Vibrio* species into temperate areas previously unsuitable for their growth.[3]

This has led to an increase in gastrointestinal infections and septicemia associated with contact to pathogenic *Vibrio* species, particularly due to the consumption of raw or undercooked seafood and shellfish, such as oysters.

Some pathogenic species in this family are responsible for two major diseases in humans: cholera and vibriosis. The latter is a gastrointestinal infection that can be self-limiting in healthy individuals, lasting only a few days. However, in immunocompromised individuals, it can develop into a severe and potentially fatal condition.[3]

Beyond the infection risk, another growing concern, according to the latest EFSA assessment, is the presence of antimicrobial resistance (*AMR*) genes, including those conferring resistance to last-resort antibiotics, in *Vibrio* spp. isolates from seafood.[4] The presence of these genes is alarming due to its potential impact on public health.

Given the increasing economic damages, especially in aquaculture and public health, due to the rising prevalence of these bacteria, it is essential to have rapid, effective, and cost-efficient identification methods at hand. To address this necessity, many food and environmental laboratories nowadays are favoring mass spectrometry-based tools such as MALDI-TOF MS (Matrix-Assisted Laser Desorption/Ionization Time-Of-Flight Mass Spectrometry), particularly the MALDI Biotyper, over culture-dependent methods or genomic sequencing techniques.

While culture-based techniques are simple to perform and require relatively accessible laboratory equipment, they have significant drawbacks, including long turnaround times. Additionally, these methods demand considerable resource investments (time and reagents) for each sample. The accuracy of many commercially available test systems is limited by the high phenotypic variability of *Vibrio* species. Furthermore, these techniques are often subject to operator-dependent interpretations (e.g., visually detected color variations) and require skilled personnel with in-depth knowledge of these bacteria's biology.[5]

Whole genome sequencing (WGS), combined with average nucleotide identity (ANI), also represents a high-resolution method for bacterial identification, characterization, and surveillance. However, despite its high accuracy, WGS is not always practical for rapid identification. The turnaround time for a complete analysis can take several days, making it less suitable for situations requiring immediate results.[6]

Unlike these methods, MALDI-TOF MS technology allows bacterial identification within minutes from colony material, significantly reducing turnaround times and operational costs. Recent studies using the MALDI Biotyper system highlight that the instrument provides high accuracy in identifying *Vibrio* species, thanks to the continuous expansion of its reference libraries, currently covering more than 4,700 species.[5,6]

Bruker's MALDI Biotyper system also goes beyond microbial identification, enabling the detection of specific antibiotic-resistance markers through a dedicated software module. This feature allows for the identification of *cfiA*-positive Bacteroides fragilis, *bla*KPC-positive *Enterobacteriaceae* such as *Klebsiella pneumoniae* and methicillin-resistant *Staphylococcus aureus* (MRSA) isolates.

Building on its established success in different types of microbiology labs, the MALDI Biotyper is now gaining more and more popularity in environmental and food laboratories for microbiological surveillance.

References

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