



Molecular Mechanisms and Epidemiology of Antimicrobial Resistance in Foodborne Bacteria

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DESCRIPTION

Foodborne bacteria are microorganisms that can cause infections or intoxications in humans through the consumption of contaminated food or water. Some of the most common foodborne bacteria are *Escherichia coli*, *Salmonella*, *Campylobacter*, *Listeria*, and *Vibrio*. Foodborne bacterial infections can cause various symptoms, such as diarrhea, vomiting, fever, abdominal pain, and sometimes more serious complications, such as sepsis, meningitis, or hemolytic uremic syndrome.

Antimicrobial Resistance (AMR) is the ability of bacteria to survive or grow in the presence of antimicrobial agents that are intended to kill or inhibit them. AMR is a major public health concern, as it reduces the effectiveness of available treatments and increases the risk of treatment failure, morbidity, mortality, and healthcare costs. AMR can also spread from bacteria to bacteria, from animals to humans, and from food to humans, posing a threat to food safety and security. The molecular mechanisms of AMR in foodborne bacteria involve various genetic elements and processes that confer resistance to different classes of antimicrobials.

Some of these molecular mechanisms

Mutation: Mutation is a change in the DNA sequence of a gene that can alter the structure or function of a protein. Mutation can cause resistance to antimicrobials by modifying the target site of the antimicrobial (e.g., Deoxyribonucleic acid gyrase or topoisomerase for Fluoroquinolones), reducing the uptake or increasing the efflux of the antimicrobial (e.g., porins or pumps for β -lactams or tetracyclines), or increasing the expression of an intrinsic resistance gene (e.g., ampC for cephalosporins).

Horizontal Gene Transfer (HGT): Horizontal gene transfer is the movement of genetic material between bacteria that are not related by descent. HGT can occur through three main mechanisms: transformation (uptake of free DNA), transduction (transfer of Deoxyribonucleic Acid (DNA) by bacteriophages), and conjugation (transfer of DNA by plasmids or other mobile

elements). HGT can cause resistance to antimicrobials by introducing new resistance genes or gene clusters into a bacterial genome. These genes can encode enzymes that inactivate or modify the antimicrobial (e.g., β -lactamases, aminoglycoside-modifying enzymes, or methyltransferases), proteins that protect the target site of the antimicrobial (e.g., ribosomal protection proteins for tetracyclines), or proteins that alter the metabolism or physiology of the bacterium (e.g., efflux pumps or regulators).

Gene amplification: Gene amplification is the increase in the number of copies of a gene within a bacterial genome. Gene amplification can cause resistance to antimicrobials by increasing the expression of a resistance gene or a gene involved in bacterial survival or growth. For example, gene amplification can increase the production of an enzyme that degrades or modifies the antimicrobial (e.g., β -lactamases), a protein that confers tolerance to the antimicrobial (e.g., heat shock proteins), or a metabolite that counteracts the antimicrobial (e.g., folate for sulfonamides).

The epidemiology of AMR in foodborne bacteria involves the distribution and determinants of AMR among different populations, sources, and regions.

Factors that influence antimicrobial resistance epidemiology

Antimicrobial use: Antimicrobial use is one of the main drivers of AMR selection and dissemination. Antimicrobials are widely used in human and veterinary medicine, as well as in agriculture and aquaculture, for therapeutic, prophylactic, or growth-promoting purposes. The misuse or overuse of antimicrobials can increase the exposure and pressure on bacteria to develop and maintain resistance. Moreover, the residues of antimicrobials in food products, animal waste, or environmental samples can also contribute to AMR emergence and spread.

Food production and processing: Food production and processing are important stages in the food chain where AMR can be introduced or transmitted. Food production involves various practices and conditions that can affect AMR in food

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animals and plants, such as animal husbandry, feed composition, hygiene measures, biosecurity protocols, vaccination programs, or pest control methods. Food processing involves various steps and technologies that can affect AMR in food products, such as slaughtering, cutting, washing, cooking, freezing, drying, fermenting, packaging, or irradiating.

Food consumption and handling: Food consumption and handling are critical points where AMR can be transferred from food to humans. Food consumption involves various factors that can affect AMR exposure and infection risk, such as dietary habits, preferences, patterns, frequency, quantity, quality,

diversity, or safety. Food handling involves various practices and behaviors that can affect AMR contamination and cross-contamination, such as storage conditions, temperature, time, cleanliness, sanitation, or hygiene.

In conclusion, AMR in foodborne bacteria is a complex and multifaceted phenomenon that involves molecular mechanisms and epidemiological factors that determine the occurrence and spread of AMR among different sources and hosts. A better understanding of these aspects can help in developing and implementing effective strategies for the prevention and control of AMR in foodborne bacteria.