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Short communication

Antimicrobial Resistance: In this article, Antimicrobial Peptides (Amps) are the Major Focus

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Abstract

A critical public health problem that jeopardizes our capacity to treat common diseases is antimicrobial resistance (AMR). A subpopulation of resistant bacteria can grow by natural selection when proteins are unregulated, which frequently causes AMR in bacteria. Finding these proteins is vital for comprehending how AMR arises in bacteria and for creating innovative therapies to counter the danger of AMR spreading widely. Through measuring the altering protein abundances brought on by antibiotic treatment, mass spectrometry-based proteomics, a potent technique for understanding the biochemical processes of biological systems, provides great insight into AMR mechanisms in bacteria. In this article, we outline a serial passaging technique for bacterial resistance evolution that uses quantitative proteomics to identify the unique proteomes of resistant bacteria. Antimicrobial peptides (AMPs) are the main subject of this article; however the method may be applied to any antimicrobial substance. Comparative proteomics of sensitive and resistant strains in response to AMP treatment discloses ways to withstand the bioactive substance and identifies the mechanism of action for new AMPs.

INTRODUCTION

Antimicrobial resistance (AMR) puts at risk the ability to effectively prevent and cure a wide spectrum of diseases brought on by bacteria, parasites, viruses, and fungi.

Antimicrobial resistance occurs when bacteria and fungi acquire the capacity to resist the medications created to destroy them.

Antimicrobial Resistance (AMR) is the result of bacteria, viruses, fungi, and parasites that have evolved through time and have ceased to react to antibiotics. This makes infections more difficult to cure and raises the risk of disease spread, serious illness, and death (Tanwar J et., 2014).

Antibiotics and other antimicrobial medications lose their effectiveness as a result of drug resistance, and infections become harder or impossible to cure.

DESCRIPTION

Antimicrobial resistance can develop over time spontaneously, typically as a result of genetic changes in the germs. There are many different types of germs in our bodies, some of which are beneficial bacteria that shield us from infections, others of which are nasty bacteria that spread disease through infections, and only a small number of which are drug-resistant (Dramé O et al., 2020). Antibiotics typically kill both harmful and beneficial bacteria when ingested, but they are unable to damage drug-resistant bacteria, which are then permitted to proliferate and take control. Some bacteria that are resistant to drugs pass on their gene to other bacteria, making the latter group of bugs resistant and exacerbating the issue. So, genetic change results in natural bacterial resistance to antibiotics (Dadgostar P et al., 2019). Antibiotic abuse and/or overuse in people and animals have significantly exacerbated the antimicrobial resistance issue. Sometimes viral diseases like the cold and flu, which may not need antibiotics at all, are treated with antibiotics. Once more, antibiotics are inhumanely administered to animals to promote development and/or prevent sickness in otherwise healthy animals. Additionally, antibiotics are excessively employed in agriculture and to preserve chicken products (Rodríguez-Baño J et al., 2021). AMR is brought on by such improper or

excessive antibiotic usage. Antibiotic manufacturing wastes and effluents pollute the ecosystems (air, soil, and water) and represent a serious problem for antimicrobial resistance during the production of antibiotics (both raw materials and finished products) in the pharmaceutical industries.

Currently, the expansion of AMR is the main worry. AMR may transmit from humans to humans and from animals (like poultry) to humans in two different ways. A person may choose to get care at home, in a hospital, a nursing home, or other inpatient facilities if they use antibiotics to treat an infection but unavoidably acquire resistant bacteria. Staying at home increases the risk of AMR spreading to family, friends, and ultimately the wider community (Reygaert WC, 2018). The infected individual distributes AMR to physicians, nurses, and other healthcare workers at hospitals or inpatient institutions, and then to the general public.

Animals (often poultry) that receive antibiotic treatment acquire drug-resistant bacteria in their digestive tracts, which they then pass on to humans when their meat is improperly handled and/or prepared. When vegetables and crops are grown using fertilizers or water that contains animal excrement and drug-resistant germs, these bacteria can spread to the vegetables and crops. Ultimately, when these vegetables and commodities are ingested, the drug-resistant germs spread to people (Angulo FJ et al., 2004).

CONCLUSION

Systems for detecting antimicrobial resistance are essential to maintaining public health. Monitoring initiatives like NARMS give the information required to prioritize and prioritize science-based ways to reduce the risks of foodborne illness brought on by the use of antibiotics in food-producing animals. Findings from NARMS have been crucial in regulatory actions, risk factor identification, and epidemic investigation. The NARMS programme is growing and identifying opportunities for development. Future improvements in integrated surveillance will be made possible by the development of next-generation DNA sequencing technology and improved data on the usage of antibiotics.

Researchers will comprehend the ecology of resistant microbes in the food supply more fully as the genotypic and phenotypic database and strain collections expand. In order to prioritize treatments to reduce or reverse resistance in zoonotic foodborne pathogens, public health professionals will be better armed as a consequence.

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Not applicable

CONFLICT OF INTEREST

None

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