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Molecular basis of antibiotic resistance: Challenges and strategies for combatting resistance

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Genet. Mol. Res. 23 (1): gmr34042
Received January 17, 2024
Accepted January 19, 2024
Published February 16, 2024

INTRODUCTION

Antibiotics have revolutionized medicine, saving countless lives since their discovery in the early 20th century. However, the emergence of antibiotic resistance threatens to undermine their efficacy, posing a significant global health challenge. Antibiotic resistance occurs when bacteria develop mechanisms to withstand the effects of antibiotics, rendering these drugs ineffective against infections. The molecular basis of antibiotic resistance is multifaceted, involving various genetic and biochemical mechanisms that enable bacteria to survive antibiotic exposure. Understanding these mechanisms is crucial for developing strategies to combat resistance and preserve the effectiveness of antibiotics.

DESCRIPTION

One of the primary mechanisms of antibiotic resistance is the modification or inactivation of the antibiotic target. Many antibiotics exert their effects by binding to specific targets within bacterial cells, such as enzymes or proteins involved in cell wall synthesis, protein synthesis, or nucleic acid replication. Bacteria can develop resistance by altering these targets through mutations or acquiring genes encoding modified enzymes that are no longer susceptible to antibiotic binding. For example, Methicillin-Resistant *Staphylococcus Aureus* (MRSA) produces a modified penicillin-binding protein that has reduced affinity for β-lactam antibiotics, conferring resistance to this class of antibiotics.

Another common mechanism of antibiotic resistance is the efflux of antibiotics from bacterial cells. Efflux pumps are specialized transport proteins that actively pump antibiotics out of the bacterial cell, reducing their intracellular concentration below the threshold required to exert antimicrobial activity. Bacteria can acquire resistance to multiple antibiotics by up-regulating efflux pump expression or acquiring mutations that increase pump efficiency. For instance, fluoroquinolone-resistant strains of Escherichia coli often overexpress efflux pumps, allowing them to expel fluoroquinolone antibiotics and maintain their survival.

Furthermore, bacteria can develop resistance through the enzymatic degradation or modification of antibiotics. Some bacteria produce enzymes, such as β-lactamases, which hydrolyze the β-lactam ring of β-lactam antibiotics, rendering them inactive. Additionally, bacteria can acquire genes encoding enzymes that chemically modify antibiotics, such as aminoglycoside-modifying enzymes that acetylate, phosphorylate, or adenylate aminoglycoside antibiotics, reducing their efficacy.

Horizontal gene transfer plays a significant role in the dissemination of antibiotic resistance genes among bacterial populations. Bacteria can exchange genetic material through processes such as conjugation, transformation, and transduction, allowing them to acquire resistance genes from other bacteria. This rapid spread of resistance genes contributes to the emergence of multidrug-resistant pathogens and complicates treatment options for infectious diseases.

The misuse and overuse of antibiotics accelerate the development and spread of antibiotic resistance. Inappropriate prescribing practices, failure to complete prescribed antibiotic courses, and the use of antibiotics in agriculture and animal husbandry contribute to the selective pressure that drives the evolution of resistant bacteria. Furthermore, the lack of new antibiotics in development exacerbates the problem by limiting treatment options for resistant infections.

Combatting antibiotic resistance requires a multifaceted approach that addresses both the clinical and public health aspects of the problem. Improved antibiotic stewardship practices, including judicious prescribing, surveillance of antibiotic use and resistance patterns, and education of healthcare providers and the public, are essential for preserving the effectiveness of existing antibiotics. Additionally, the development of new antibiotics and alternative therapies, such as bacteriophage therapy and immune-based treatments, is critical for combating resistant infections.

Enhancing infection prevention and control measures, such as improved sanitation, vaccination, and infection control practices in healthcare settings, can help reduce the transmission of resistant pathogens. Furthermore, innovative strategies, such as the use of combination therapy, which involves administering multiple antibiotics with different mechanisms of action to prevent the emergence of resistance, show promise in overcoming antibiotic resistance.

Research into the molecular mechanisms of antibiotic resistance continues to provide insights into the evolution and spread of resistant bacteria. Advances in genomic sequencing technologies allow for the rapid identification of resistance genes and the tracking of resistant strains. Moreover, the development of novel therapeutic approaches, such as CRISPR-based antimicrobials and phage-derived enzymes that target specific bacterial pathogens, offers new avenues for combatting antibiotic resistance.

CONCLUSION

The molecular basis of antibiotic resistance is complex and multifaceted, involving various genetic and biochemical mechanisms that enable bacteria to survive antibiotic exposure. Combatting antibiotic resistance requires a comprehensive approach that addresses the clinical, public health, and research aspects of the problem. By implementing effective antibiotic stewardship practices, investing in the development of new antibiotics and alternative therapies, and enhancing infection prevention and control measures, we can mitigate the impact of antibiotic resistance and ensure the continued efficacy of antibiotics in treating infectious diseases.