



Antimicrobial Resistance in Human Microbiota: Insights and Implications

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DESCRIPTION

Antimicrobial-Resistant Bacteria (ARB) in human microbiota pose a significant challenge to public health. While many bacteria in the human body contribute to health and homeostasis, some can harbor resistance genes that may transfer to pathogenic bacteria, complicating infections and treatments. This paper reviews the presence and risks of antimicrobial-resistant bacteria within the human microbiota, particularly in the gut, skin and respiratory tract. Understanding the mechanisms of resistance development and spread in normal flora is important to reducing risks and guide effective treatments.

Human microbiota is a diverse and complex community of bacteria that inhabit various parts of the body, such as the gut, skin and respiratory tract. These bacteria play essential roles in digestion, immunity and protection against pathogens. However, due to factors like antibiotic overuse, some bacteria in the normal flora have developed resistance to antimicrobial agents. This resistance is concerning because it can spread to pathogenic bacteria, increasing the risk of hard-to-treat infections. Investigating the presence and implications of antimicrobial-resistant bacteria within human flora is essential to manage and prevent antimicrobial resistance.

The gut hosts trillions of bacteria that aid in digestion and nutrient absorption. However, it is also a significant reservoir of Antimicrobial-Resistant Genes (ARGs) due to frequent exposure to antibiotics from medical treatment and diet. Common resistant bacteria in the gut include *Escherichia coli*, *Enterococcus* and *Klebsiella* species. Resistant strains of these bacteria can harbor genes that are easily transferred to pathogens through Horizontal Gene Transfer (HGT), a process facilitated by plasmids, transposons and other mobile genetic elements. This gene transfer can increase the prevalence of multidrug-resistant pathogens.

The skin harbors various bacteria, such as *Staphylococcus* and *Corynebacterium* species, that play a role in protecting against harmful microorganisms. However, strains of *Staphylococcus*

aureus, including Methicillin-Resistant *Staphylococcus aureus* (MRSA), are increasingly common. The resistance genes in MRSA strains can be transferred to other bacteria or pathogenic *Staphylococcus* strains, posing a significant threat in healthcare settings. The skin's exposure to environmental bacteria and frequent use of topical antimicrobials contributes to the development of resistance.

The respiratory tract hosts a range of bacteria, including *Streptococcus pneumoniae* and *Haemophilus influenzae*, which can be opportunistic pathogens. Antibiotic resistance in these bacteria is worrisome because respiratory infections are common and can lead to serious health complications. *Streptococcus pneumoniae*, for example, has developed resistance to multiple antibiotics, including penicillin, making infections more challenging to treat. The spread of resistant bacteria in the respiratory tract can also facilitate outbreaks, particularly in crowded places and healthcare facilities.

Spontaneous genetic mutations can render bacteria resistant to specific antibiotics. Transfer of resistance genes occurs *via* transformation, conjugation and transduction, enabling resistant genes to spread among different bacterial species. Overuse and misuse of antibiotics create selective pressure, allowing only resistant bacteria to survive and proliferate. This selective pressure is particularly prevalent in environments with repeated exposure to antimicrobials, such as healthcare settings. The presence of antimicrobial-resistant bacteria in the human microbiota has significant implications for public health:

When pathogenic bacteria acquire resistance genes from normal flora, infections become harder to treat, requiring alternative or more potent antibiotics. Resistant strains reduce the effectiveness of standard antibiotics, leading to a reliance on last-resort drugs that may have more side effects or limited availability. Resistant bacteria from human microbiota can spread to others through direct contact or environmental contamination, exacerbating the global resistance crisis and reduce the impact of resistant bacteria in human microbiota, several strategies should be considered:

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Reducing unnecessary antibiotic prescriptions and avoiding antibiotics in livestock can help limit selective pressure for resistance. Developing non-antibiotic therapies, such as bacteriophages or probiotics, can provide alternatives to traditional treatments. Regular monitoring of resistance patterns in human microbiota can help detect emerging threats and guide treatment policies.

CONCLUSION

Antimicrobial-resistant bacteria in the human microbiota present an evolving threat with implications for public health.

Understanding the mechanisms of resistance acquisition and the role of normal flora in spreading resistance genes is important. Efforts to monitor, prevent and control resistance must involve prudent antibiotic use, alternative therapies and effective surveillance to reduce the risk of resistant infections originating from normal human flora.