

Microbiome and Antimicrobial Resistance: A Mini Review

Sunny Mandal¹, Sudhish Mishra², and Prabir K. Mandal^{3*}

¹Department of Cell Biology, Microbiology, and Molecular Biology, College of Arts and Sciences, University of South Florida, USA ²Translational Science and Molecular Medicine, Michigan State University, USA ³Biology Program, Edward Waters College, Jacksonville, USA

*Corresponding Author: Prabir K. Mandal, Biology Program, Edward Waters College, Jacksonville, USA

ABSTRACT

The microbiome is the genetic information which provides the blueprints and instructions for the vast array of bacteria, viruses, and fungi that live in and on our bodies. Ubiquitous in nature, antimicrobial resistance (AMR) has existed long before the golden age of antimicrobials. While antimicrobial agents are beneficial to combat infection, their widespread use contributes to the increase in and emergence of novel resistant microbes in virtually all environmental niches. When acquired by pathogens however, AMR becomes a serious public health threat worldwide. Our ability to combat the threat of emerging resistance relies on accurate AMR detection methods and the development of therapeutics that function despite the presence of antimicrobial resistance.

Keywords: Antibiotic resistance; microbiome; genome; resistome; metagenomics;

INTRODUCTION

In the modern era of antibiotics, which began in 1928 in the staphylococcal plate contaminated with Penicillium notatum in Alexander Fleming's laboratory, clinicians have used antibiotics therapeutically and prophylactically to save millions of lives. In addition to our own cells and genomes, humans are hosts to a vast community of microbes. This microbiota are indispensable contributors to host physiology, acting in a symbiotic relationship with the host (Van Opstal and Bordenstein, 2015). The establishment of the indigenous microbiota starts as soon as the amniotic membranes rupture and subsequently involves a succession of bacterial populations waxing and waning as the diet changes and the host develops. Antimicrobials are defined as drugs with activity against microorganisms such as bacteria, viruses, fungi and parasites. Antimicrobials have been widely used in the poultry industry, for therapeutic purposes, disease prevention and growth promotion. It is now accepted that use of antibiotics in farms selects for drug resistant organisms which can then spread from farm to humans through consumption of contaminated food (Hawkey, 2008). Antibiotic use alone has saved many lives once life threatening infections can now be treated effectively and operations that would have been dangerous in the past, can now be performed safely. It has been estimated that the use of antibiotics has extended our life expectancy by an average of 20 years.

Antimicrobial resistance is increasingly widespread, largely due to human influence. The increasing prevalence of antibiotic resistance in clinically relevant pathogens has emerged as a major health crisis around the world (WHO, 2014). Antibiotic resistance is also prevalent in the indoor environment, where humans spend up to 90% of their time. Microbes in the indoor environment, referred to as the indoor micro biome, have been identified as an important source of antibiotic-resistant infections Hartmann et al., 2016). There are genetic and biological mechanisms of antibiotic resistance. Genetic resistance is related to the ability of DNA in microorganisms. The major mechanisms of genetic transfer are transformation, conjugation, and transduction. The spread of antibiotic resistant genes (ARG) is exacerbated by the widespread use of antimicrobial chemicals, which are prevalent in building materials and products personal care (Halden, 2014). However, microbes can become resistant to the drugs that were once able to target them,

rendering them ineffective. Antibiotic resistance develops in bacteria through genetic mutation.

The development and spread of antibiotic resistance among bacteria is considered a universal threat to human, animal and environmental health. The use of antibiotics heavily disrupts the ecology of the human microbiome i.e., the collection of cells, genes, and metabolites from bacteria, eukarvotes, and viruses that inhabit the human body (Langdon, Crook, Dantas, 2016). Water is one of the most important bacterial habitats on Earth, is a major way of dissemination of microorganisms in nature and has been recognized as a significant reservoir of antibiotic resistance. The diversity of microbiome contributes to normal growth and development, including normal maturation of immune system (Hooper, Littman, the Macpherson, 2012). As our understanding of the microbiome has developed, the collection of antimicrobial resistance genes within a bacterial population has been defined as the resistome. Previously treatable communicable diseases such as malaria, tuberculosis (TB) and other serious bacterial infections are now untreatable in some parts of the world.

The mechanisms of AMR include the production of enzymes that deactivate or inhibit the antimicrobials, the altered membrane permeability so the antibiotics cannot penetrate into the cell wall of the bacteria, alterations to the antimicrobial target sites, and the alterations to metabolic pathways that compensate for antibiotic effects.

DISCUSSION

It is recognized that one of the most important public health threats worldwide is antimicrobial resistance. The incidence of antibiotic-resistant infections is rising sharply. In 2015, antibioticresistant pathogens were estimated to cause over 50,000 deaths a year in Europe and the USA. Some estimates suggest that deaths attributable to antimicrobial resistance may rise from the current estimate of 700,000 lives per year to ten million lives annually by 2050. With whole metagenome sequencing, it is now possible to monitor the development of antibiotic resistance in entire microbial communities. Antimicrobial healthcare resistance increases costs substantially in many countries. Despite the increase in knowledge of antibiotic resistance in host-associated microbiomes and the existence of high-profile antibiotic-resistance pathogens in the build environment, we still know very little about the indoor resistome.

Antibiotic resistance is manifested through a number of different mechanisms including target alteration, control of drug influx and efflux, and through highly efficient enzymemediated inactivation. One of the challenges in studying the evolution and prevalence of resistance is the massive use of antibiotics in the clinic and in agriculture over the past seven The mechanisms of antibiotic decades. modification and inactivation are evidence of highly specific evolutionary adaptations. Our microbial genomes have a tremendous capacity for rapid adaptations which can influence health and disease. Therefore, in order to better understand the basis of many modern diseases a deeper insight into our interactions with our microbes is required. Future advances in DNA sequencing technologies are likely to facilitate high-throughput characterization of the resistome by metagenomic sequencing.

AMR is a major public health threat globally and cause elevated healthcare costs. To tackle AMR, a global public awareness campaign and innovation fund is needed. Incentives for the development of new treatments will increase production of much needed innovative antimicrobials. Also, diagnostic technology needs to be improved to ensure antimicrobials are used appropriately; needs improved hygiene and sanitation; vaccines and other alternative treatments should be promoted; and reduce the unnecessary use of antimicrobials in agriculture.

CONCLUSION

Rapidly emerging resistant bacteria threaten the extraordinary health benefits that have been achieved with antibiotics. This crisis is global, reflecting the worldwide overuse of these drugs and the lack of development of new antibiotic agents to address the challenge. Antibioticresistant infections place a substantial health and economic burden on the U.S. health care system and population. Over the past several years, the invisible microbial world has taken center stage thanks to DNA sequencing methods that enable researchers to detect bacteria and other organisms that can't be grown in culture. Science strives to cover advances that reveal the specific ways in which the microbiota influences the physiology of the host, both in a healthy and in a diseased state and how the microbiota may be manipulated, either at the organismal or molecular level, to improve the health of the host. What's hot right now is extending the role of microbes in human biology and recognizing that viruses, too, have an impact, and

Microbiome and Antimicrobial Resistance: A Mini Review

understanding how specific microbes and their products contribute to healthy and diseased states. Antimicrobial resistance poses significant challenges for current clinical care. Modified use of antimicrobial agents and public health interventions, coupled with novel antimicrobial strategies, may help mitigate the effect of multidrug-resistant organisms in the future. Coordinated efforts to implement new policies, renew research efforts, and pursue steps to manage the crisis are greatly needed.

REFERENCES

- Hawkey P M (2008). The growing burden of antimicrobial resistance. Journal of Antimicrobial Chemotherapy, 62(Suppl 1), S1-S9.
- [2] World Health Organization (2014). Antimicrobial resistance: global report on surveillance. World Health Organization, Geneva, Switzerland.

- [3] Hartmann E M, Hickey R, Hsu T, Betancourt Roman C M, Chen J, Schwager R, Kline J, Brown G Z, Halden R U, Huttenhower C, Green J L (2016). Antimicrobial Chemicals Are Associated with Elevated Antibiotic Resistance Genes in the Indoor Dust Microbiome. Environ SciTechnol, 50, 9807-9815.
- [4] Halden R U (2014). On the need and speed of regulating triclosan and triclocarban in the United States. Environ SciTechnol, 48(7), 3603-3611.
- [5] Van Opstal E J, Bordenstein S R (2015). MICROBIOME. Rethinking heritability of the microbiome. Science, 349, 1172-1173.
- [6] Hooper L V, Littman D R, Macpherson A J (2012). Interactions between the microbiota and the immune system. Science, 336, 1268-1273.
- [7] Langdon A, Crook N, Dantas G (2016). The effects of antibiotics on the microbiome throughout development and alternative approaches for the therapeutic modulation. Genome Medicine, 8, 39.