

Review on Translational Metagenomics

Dr. Luigina Guasti*

Department of Internal Medicine, University of Insubria, Varese, Italy

***Corresponding author:** Dr. Luigina Guasti, Department of Internal Medicine, University of Insubria, Varese, Italy, E-mail: Luigina.Guasti@uninsubria.it

Received date: September 08, 2021; **Accepted date:** September 22, 2021; **Published date:** September 29, 2021

Citation: Guasti L (2021) Review on Translational Metagenomics. *Transl Biomed* Vol.12 No.9:191

Introduction

The increasing threat of antimicrobial resistance poses one of the greatest challenges to modern medicine. The collection of all antimicrobial resistance genes carried by various microorganisms in the human body is called the human resistome and represents the source of resistance in pathogens that can eventually cause life-threatening and untreatable infections. A deep understanding of the human resistome and its multilateral interaction with various environments is necessary for developing proper measures that can efficiently reduce the spread of resistance. However, the human resistome and its evolution still remain, for the most part, a mystery to researchers. Metagenomics, particularly in combination with next-generation-sequencing technology, provides a powerful methodological approach for studying the human microbiome as well as the pathogenome, the virolome and especially the resistome. The increasing numbers of infections caused by Multi-Drug Resistant (MDR) bacteria have developed into a global and acute public health crisis. The implementation of antimicrobial stewardship programs as well as the development of novel anti-infectives has become a primary focus of public health and research activities in order to reduce the burden of infections caused by MDR pathogens. New mechanisms mediating antimicrobial resistance against antibiotics in the “last line of defence” are steadily reported from all over the world, leaving us only limited therapeutic options for treating serious infections. It is important to understand that human beings can be the vessel in which antimicrobial resistance is born or by which it is spread. The human body harbours at various sites a complex microbial ecosystem and represents a vast reservoir for

antimicrobial resistance genes (ARGs), referred to in their totality as the human “resistome”.

Functional metagenomics and the human resistome

In this review, we present an overview of current knowledge on the human resistome. We also outline how metagenomics may be used to characterize the human resistome and how newly acquired insights can be rapidly transferred to clinical microbiology and infection control for practical implementation. We call this approach translational metagenomics. Conventional approaches used to determine antimicrobial resistance in bacteria usually rely on a culture-based methodology and focus almost exclusively on human pathogens. Since only a minority of bacterial organisms can be cultured. The primary strength of functional metagenomics is its ability to detect novel and highly divergent ARGs on a large scale. New ARGs have been discovered every year in the last decade, reflecting a relentless global evolution of a magnitude we have yet to comprehend. Therefore, efforts to detect novel ARGs must be one of the major goals of research if we are to limit the danger of resistance. Humans are born with microbiota, which have accompanied us through our life-span. There is an important symbiotic relationship between us and the microbial communities, thus microbial communities are of great importance to our health. In this review, we summarize frontiers in metagenomic research, including new concepts and methods. Then, we focus on the applications of metagenomic research in medical researches and clinical applications in recent years, which would clearly show the importance of metagenomic research in the field of translational medicine.