



# **Current Trends in Experimental and Computational Approaches to Combat Antimicrobial Resistance**

Madangchanok Imchen<sup>1</sup>, Jamseel Moopantakath<sup>1</sup>, Ranjith Kumavath<sup>1\*</sup>, Debmalya Barh<sup>2</sup>, Sandeep Tiwari<sup>3</sup>, Preetam Ghosh<sup>4</sup> and Vasco Azevedo<sup>3</sup>

<sup>1</sup> Department of Genomic Science, School of Biological Sciences, Central University of Kerala, Kasaragod, India, <sup>2</sup> Centre for Genomics and Applied Gene Technology, Institute of Integrative Omics and Applied Biotechnology, Purba Medinipur, India, <sup>3</sup> Laboratório de Genética Celular e Molecular, Departamento de Biologia Geral, Instituto de Ciências Biológicas, Universidade Federal de Minas Gerais, Belo Horizonte, Brazil, <sup>4</sup> Department of Computer Science, Virginia Commonwealth University, Richmond, VA, United States

### **OPEN ACCESS**

#### Edited by:

Mehdi Pirooznia, National Heart, Lung, and Blood Institute (NHLBI), United States

#### Reviewed by:

Lenwood Scott Heath, Virginia Tech, United States Patrick Munk, Technical University of Denmark, Denmark Andrew C. Pawlowski, Harvard Medical School, United States

\*Correspondence:

Ranjith Kumavath RNKumavath@gmail.com; RNKumavath@cukerala.ac.in

#### Specialty section:

This article was submitted to Computational Genomics, a section of the journal Frontiers in Genetics

Received: 20 May 2020 Accepted: 01 September 2020 Published: 06 November 2020

## Citation:

Imchen M, Moopantakath J, Kumavath R, Barh D, Tiwari S, Ghosh P and Azevedo V (2020) Current Trends in Experimental and Computational Approaches to Combat Antimicrobial Resistance. Front. Genet. 11:563975. doi: 10.3389/fgene.2020.563975 A multitude of factors, such as drug misuse, lack of strong regulatory measures, improper sewage disposal, and low-guality medicine and medications, have been attributed to the emergence of drug resistant microbes. The emergence and outbreaks of multidrug resistance to last-line antibiotics has become quite common. This is further fueled by the slow rate of drug development and the lack of effective resistome surveillance systems. In this review, we provide insights into the recent advances made in computational approaches for the surveillance of antibiotic resistomes, as well as experimental formulation of combinatorial drugs. We explore the multiple roles of antibiotics in nature and the current status of combinatorial and adjuvant-based antibiotic treatments with nanoparticles, phytochemical, and other non-antibiotics based on synergetic effects. Furthermore, advancements in machine learning algorithms could also be applied to combat the spread of antibiotic resistance. Development of resistance to new antibiotics is guite rapid. Hence, we review the recent literature on discoveries of novel antibiotic resistant genes though shotgun and expression-based metagenomics. To decelerate the spread of antibiotic resistant genes, surveillance of the resistome is of utmost importance. Therefore, we discuss integrative applications of whole-genome sequencing and metagenomics together with machine learning models as a means for state-of-the-art surveillance of the antibiotic resistome. We further explore the interactions and negative effects between antibiotics and microbiomes upon drug administration.

Keywords: antibiotic resistance, multidrug resistance, whole genome sequence, metagenomics, next generation sequencing, nanoparticles

# INTRODUCTION

Microorganisms are ubiquitous in nature and play crucial roles in the body's biochemical functions. Despite their importance, opportunistic and pathogenic microbes have evolved to bypass the immune system. Gram-negative bacteria in particular are of clinical importance, as they produce metabolites, such as endotoxin and lipopolysaccharide, which are major causes of infection

1