



Genomic Characterization of Antimicrobial Resistance and Evolution Mechanism of Bacteria

Guest Editors:

Dr. Daniel Gyamfi Amoako

1. Department of Pathobiology, University of Guelph, Guelph, ON, Canada
2. Antimicrobial Research Unit, College of Health Sciences, University of KwaZuluNatal, Durban 4000, South Africa

Dr. Linda Bester

1. College of Health Sciences, University of KwaZulu-Natal, Durban, South Africa
2. Department of Biochemistry and Microbiology, University of Venda, Thohoyandou, South Africa

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Message from the Guest Editors

In the ever-evolving battle against antimicrobial resistance (AMR), our understanding of the genomic landscape of bacteria and their mechanisms of evolution has become pivotal. In bacteria, resistance to antibiotics is determined by genetic factors such as chromosomes, plasmids or other movable genetic elements. Although antimicrobial resistance genes (ARGs) typically exhibit significant sequence variability, such as the impact of different concentrations of antibiotics on their genomic dynamics, the impact of this diversity on AMR is still unclear. Therefore, understanding the dynamic changes and mobilization of antibiotic resistance genes in humans, animals, plants and environmental microorganisms through genomics and metagenomics methods is crucial.

This Special Issue seeks to foster a comprehensive understanding of the genetic underpinnings of bacterial antimicrobial resistance and the evolutionary dynamics that underlie these adaptations.

Dr. Daniel Gyamfi Amoako

Dr. Linda Bester





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Editor-in-Chief

Prof. Dr. Nicholas Dixon

School of Chemistry and
Molecular Bioscience, University
of Wollongong, Wollongong, NSW
2522, Australia

Message from the Editor-in-Chief

There are very few fields that attract as much attention as scientific endeavor related to antibiotic discovery, use and preservation. The public, patients, scientists, clinicians, policy-makers, NGOs, governments, and supra-governmental organizations are all focusing intensively on it: all are concerned that we use our existing agents more effectively, and develop and evaluate new interventions in time to face emerging challenges for the benefit of present and future generations. We need every discipline to contribute and collaborate: molecular, microbiological, clinical, epidemiological, geographic, economic, social scientific and policy disciplines are all key. *Antibiotics* is a nimble, inclusive and rigorous indexed journal as an enabling platform for all who can contribute to solving the greatest broad concerns of the modern world.

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