



Genetic Background of Antimicrobial Resistance

Guest Editor:

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Message from the Guest Editor

Dear Colleagues,

The increasing prevalence of antimicrobial resistance (AMR) is a significant threat to global health. The widespread use of antibiotics in human healthcare and animal disease control is increasingly shortening the time it takes for resistant strains to develop. The background of the phenotypic appearance of AMR is determined by genetic factors such as antimicrobial genes (ARGs) and single-nucleotide polymorphisms, among others. While ARGs often occur with significant sequential variability, the effect of this diversity on AMR is less explored. Moreover, little is known about the structural properties of the genome that determine ARG expression. Due to these genomic features, the antimicrobial resistance potential is not necessarily activated phenotypically. A crucial point in the research on AMR spread is the identification of genetic factors that facilitate the horizontal gene transfer of ARGs between bacteria. Within the range of possible MGEs, the significance of plasmid and phage environments is beyond question.





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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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