



Antimicrobial Resistance and Food Safety: What Can We Learn from Genomics?

Guest Editor:

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Message from the Guest Editor

Antimicrobial resistance (AMR) is one of the major threats to public health in modern times. Foodborne infections largely contribute to transmitting antimicrobial resistant bacteria, and pose a challenge not only regarding classical foodborne infectious agents such as *Campylobacter*, but also gut microbiome mutualistic bacteria such as the *Bifidobacterium* and *Escherichia* species. The characteristics and dynamics of foodborne diseases and AMR emergence and transmission are becoming increasingly clear with the advancements in next-generation sequencing and third-generation sequencing. This Special Issue seeks research articles that use metagenomics and genomics approaches to elucidate the dynamics and mode of actions between AMR and foodborne infections. It also seeks to investigate how sequencing-based approaches can further explore such topics, beyond simply the diagnosis and description of infectious agents and their AMR profiles.





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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 disciples 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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