



antibiotics



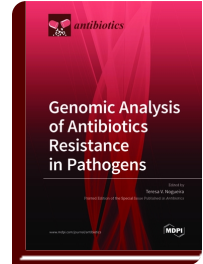
Special Issue Reprint

Genomic Analysis of Antibiotics Resistance in Pathogens

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The emergence of antibiotic-resistant pathogens currently represents a serious threat to public health and the economy. Due to antibiotic treatments in humans and veterinary medicine, prophylactic use and environmental contamination, bacteria are today more frequently exposed to unnatural doses of antibiotics and their selective effect.

Antibiotic resistance can be encoded on chromosomes, plasmids, or other mobile genetic elements in bacteria. It may also result from mutations that lead to changes in the affinity of antibiotics for their targets or in the ability of antibiotics to act on bacterial growth or death. Exposure of bacteria, bacterial populations, and microbial communities to antibiotics at different concentrations shapes their genomic dynamics, as does the mobilisation and spread of resistance determinants. It is, therefore, essential to understand the dynamics and mobilisation of genes encoding antibiotic resistance, in human, animal, plant, and environmental microbiomes, through genomic and metagenomic approaches and bioinformatics analyses.

This Special Issue gathers research publications on the horizontal transfer of antibiotic-resistance genes, their dissemination and epidemiology, their association with bacterial virulence, between bacterial genotypes and their phenotypes, and other related research topics.



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