Special Issue

Whole-Genome Sequencing of Pathogenic Bacteria - New Insights into Antibiotic Resistance Spreading 2.0

Message from the Guest Editor

Antibiotic resistance acquisition by pathogenic and opportunistic bacteria has become a major problem worldwide. However, the mechanisms of antibiotic resistance acquisition and spreading among different bacterial species cannot be easily revealed by the traditional phenotypic analyses. Whole-genome sequencing (short- and long-read) is currently attracting increased attention since it allows for accurately and rapidly obtain data regarding the presence of specific antibiotic resistance genes and their locations in a bacterial genome (chromosomal or plasmid). For this Special Issue, we therefore invite you to contribute original research and review papers describing the application of the whole-genome sequencing of bacterial pathogens for revealing antimicrobial resistance genes, comparing phenotypic and genomic resistance profiles, reconstructing plasmids, performing epidemiological surveillance, and elucidating the mechanisms and/or methods of the spreading and acquisition of antimicrobial resistance. Novel computational approaches and pipelines for performing such investigations are particularly welcome.

Guest Editor

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Deadline for manuscript submissions

closed (30 June 2023)

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Message from the Editor-in-Chief

"Microorganism" merges the idea of the very small with the idea of the evolving reproducing organism is a unifying principle for the discipline of microbiology. Our journal recognizes the broadly diverse yet connected nature of microorganisms and provides an advanced publishing forum for original articles from scientists involved in high-quality basic and applied research on any prokaryotic or eukaryotic microorganism, and for research on the ecology, genomics and evolution of microbial communities as well as that exploring cultured microorganisms in the laboratory.

Editor-in-Chief

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