



Adaptive Evolution of Bacterial Pathogens in Response to Antibiotic Therapy

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Message from the Guest Editor

Dear Colleagues,

Bacterial pathogens have developed numerous methods to circumvent antibiotic therapy and cause long-term infections. In many instances, adaptations that occur during infection are pleiotropic and affect physiology, host-immune interactions, and pathogenesis.

Next-generation genome sequencing provides a technical platform to map and characterize adaptive mutations that are selected for during infection. The current Special Issue focuses on new mechanisms that alter treatment efficacy, immune responses, and/or bacterial virulence for the common nosocomial 'ESKAPE' pathogens (*Enterococcus faecium*, *Staphylococcus aureus*, *Klebsiella pneumoniae*, *Acinetobacter baumannii*, *Pseudomonas aeruginosa*, and *Enterobacter* spp), as well as for less-typical pathogens that may infrequently cause long-term human disease.





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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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