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Genetics of Antimicrobial Resistance

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Deadline for manuscript
submissions:

closed (20 May 2021)

Message from the Guest Editors

Antimicrobial Resistance is an increased risk for human health, due to the intensive use of antimicrobial compounds on agricultural applications and livestock industries. The spread of AR genes along the food chain is an important health risk factor that needs to be deeply studied. Moreover, recent studies on AR genes spread along wastewater or coastal sea water samples have shown the prevalence of such genes in natural environments due to human activities.

Whole genome and metagenome sequencing technologies, including NGS and software for NGS data analysis, have notably increased the capacity to detect and study ARGs on isolated bacteria and environmental samples. These technologies also allow one to determine the genomic environment of such ARGs, including mobile element regions, favoring the execution of more accurate risk assessments. Furthermore, transcriptomic and metatranscriptomic approaches have allowed one to obtain a wider knowledge of the genetic regulation of AR on isolated bacteria.

We welcome researchers across the world to contribute their high-quality manuscripts covering all the aspects related to the genetics of antimicrobial resistance.



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Special Issue



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Message from the Editor-in-Chief

Genes is central to our understanding of biology, and modern advances such as genomics and genome editing have maintained genetics as a vibrant, diverse and fast-moving field. There is a need for good quality, open access journals in this area, and the *Genes* team aims to provide expert manuscript handling, serious peer review, and rapid publication across the whole discipline of genetics. Starting in 2010, the journal is now well established and recognised. Why not consider *Genes* for your next genetics paper?

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