



Genomic Tools for the Surveillance and Investigation of Foodborne Disease and Enteric Zoonoses

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Deadline for manuscript
submissions:

closed (31 July 2022)

Message from the Guest Editor

Whole-genome sequencing (WGS) is rapidly replacing traditional typing methods that provide limited information and are usually pathogen-specific. By offering the highest resolution possible, genomic-based microbial typing tools can be used for pathogen tracking, outbreak control and source attribution, in addition to provide an all-in-one test for species identification, serotyping, resistance profiling and virulence detection useful for pathogen diagnostics and treatment decisions. However, WGS raises several challenges in terms of data extraction and its conversion to clinical and epidemiological information which include bioinformatic tool development, interpretation guideline definitions, harmonization and societal acceptance. This last challenge is covered by GE3LS by investigating economic, legal and societal questions at the intersection of genomics and society. In the last few years, several methods have been developed for phylogenetic analysis based on single nucleotide polymorphism (SNP) or allelic (cgMLST or wgMLST) variation applied on the core- or the whole- genome.





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Message from the Editor-in-Chief

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