



Advances in Techniques and Analyses to Characterize Host-Specific and Environmental Microbiomes

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Message from the Guest Editors

Microbiome research has exponentially increased over the last two decades and provided insights into microbial community structure, genome composition, phylogenetic relationships, and functions in numerous (eco)systems. While efforts to advance microbiome research have primarily resulted from the application of 16S rRNA gene (16S), shotgun metagenomic, and metatranscriptomic sequencing within human-centric samples and analysis tools, there has been limited development of host-specific tools to provide greater taxonomic and functional information.

The present Special Issue welcomes studies characterizing host- and environmental-specific microbiomes (e.g., canine, vaginal, skin, and environmental) using specialized analysis tools. Submission of studies demonstrating comparison of results using different analytical techniques, such as bioinformatics techniques, databases, statistical tools, chemical extractions, analytical chemistry techniques, and microbial techniques, is encouraged. Articles presenting a novel bioinformatic tool or benchmarking an existing one for the analysis of host-specific microbiomes and those integrating additional omes are also welcome.





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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.

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