

Special Issue on
From Microbial Genomics to Metagenomics

CALL FOR PAPERS

Next-generation sequencing technology is revolutionizing the practice of microbial science and provides an unprecedented view on microbial diversity. Current sequencing technologies allow us to intensively investigate complex microbial ecosystems, such as the human gastro-intestinal (GI) microbiota, consisting of over 3 million genes from mainly gram-positive bacteria.

Genomic comparisons of different bacterial genera and species have helped to reveal the evolutionary origins of virulence and niche specification. Comparative analyses that compile the genomes of different strains from the same or different species—into what is called a “pan-genome”—have revealed the gene content within an entire species or genera is much more than that of a single strain or species. Moreover, this sort of study has aided the understanding of one of the dominant genetic forces behind bacterial evolution, namely, the concept of lateral gene transfer between microorganisms.

Steady advances in sequencing technologies have allowed light to be shed on the genetics of microbial interactions, for example, via the comparative metagenomic and metatranscriptomic analyses of bacterial communities. Metagenomics has been one of the most rapidly growing fields. The metagenomics approach provides an extraordinary view on the diverse microbial world in different environments, such as within human and animal body sites, marine and other water bodies, soil, and air. Metagenomic and metatranscriptomic analyses of bacterial communities can shed light on the genetics of microbial interactions and have been widely used by researchers in many disciplines such as ecology, energy, agriculture, biotechnology, and medicine. As a rapidly growing field, comparative genomics/metagenomics also presents many challenges that need to be addressed.

This special issue aims to provide an insight into this comparative/metagenomics research. Researchers are invited to submit both original research papers and review articles on studies of different microbial environments and systems using the comparative genomics or metagenomics approach. Submissions concerning novel computational/statistical methods/algorithms for handling comparative or metagenomics data are also welcomed.

Potential topics include but are not limited to the following:

- ▶ Comparative/pan-genomics of various bacteria species
- ▶ Functional genomics of commensal and pathogenic bacteria
- ▶ Microbial metagenomics and metatranscriptomics
- ▶ Gut microbiome genomics and metagenomics
- ▶ Viromics- viral metagenomics
- ▶ Genomics and metagenomics in microbial ecology
- ▶ Computational methods for next-generation sequencing data analysis

Authors can submit their manuscripts through the Manuscript Tracking System at <https://mts.hindawi.com/submit/journals/ijg/fbgm/>.

Papers are published upon acceptance, regardless of the Special Issue publication date.

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