

Focus on Metagenomics

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In recent years, metagenomics and microbiome investigations have expanded to nearly every corner of biology enabling the detailed study of microbial function in nearly any sample type collected from environmental soils to human-related samples. These studies include scores of recognized microbiome projects including the two well-known flagship ventures: the Human Microbiome Project and the Earth Microbiome Project. Numerous other ongoing endeavors are expanding these investigations into novel areas, including the microbiome of the built environment, the extreme microbiome project, metagenomics of world mass transit system (Meta-Sub), and even space microbiome projects, to name a few. All of the studies aim to characterize the mixed biologic community composition through massively parallel DNA/RNA sequencing; though they vary significantly based on techniques from sample collection to sequencing approach and in depth and type of data analysis. At the present time, there are no required experimental methods to conduct a microbiome or metagenomics experiment, but rather investigators adjust based upon the hypothesis and type of sample that is studied. The most commonly used and economically feasible technique for microbiome analysis is

16S rDNA sequencing. However, the number of studies that sequence ALL DNA in a sample (shotgun metagenomics) continues to grow as sequencing becomes less costly and information content is realized (antibiotic resistance, functional pathways, mobile genetic elements, genetic variation, host genotyping). Regardless of the technical protocols used in these studies, microbiome and metagenomics is one of the fastest growing fields in science today and offers society numerous potential benefits that range from new drug discovery, to disease prevention and surveillance, curing of diseases, improved food production, and understanding the intricacies of climate change.

Recognizing this rapid growth, the Association of Biomolecular Resource Facilities (ABRF) responded by establishing the first ever research group devoted to microbiome and metagenomics in 2014 and since has become the Association's largest research group which focuses on developing and evaluating new approaches for metagenomics. Additionally, to recognize the excitement and enormous potential of microbiome research in general, *The Journal of Biomolecular Techniques* has devoted this special issue to highlight this new and growing area of science.

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