

Metagenomics: A New Opportunity for Enzyme Engineering

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Editorial

In the past few years, developments in genomics such as metagenomics provide a new paradigm to look at microbes, and researches on microbial communities are transforming the way we seek for solutions to biomedical, energy and environmental questions.

The relationship between microbiota and human physiology has largely been neglected until the Human Microbiome Project and other microbiome projects were initiated. Analysis of these metagenomic data indicates that metabolic pathways of these microbiome are closely related to many human health problems such as obesity, diabetes, inflammatory bowel disorder and cancers. It is expected that by perturbing metagenome composition in our gut, we will be able to treat these diseases. Metabolites from gut microbiome can be potential drugs to interact with human body through blood, and microbial metabolic pathways can be potential drug targets for medical intervention. Large-scale metagenome projects provide us the opportunity to discover these diseases related microbiomes, metabolites and metabolic pathways. A recent study characterized some drug-like antibiotics produced by biosynthesis gene clusters, which is widely distributed in genomes and metagenomes of human microbiome. Furthermore, many of our currently used drugs were originally discovered in microbes. Meanwhile, approximately 10 million genes were cataloged from human gut microbiome, 500 times

more than the number of human genes, which is a vast repository for screening drugs and druggable targets, and the genes involved in these pathways will be idea targets for enzyme engineering. The potential medical landscape of these microorganisms extends far beyond what we can expect.

Moreover, metagenomics are also very useful in the field of bioenergy production, catalyzing the conversion of biomass into biofuels in more cost-effective way. In rumen animals and insects like ant, microbial communities are known to facilitate cellulosic biomass decomposition in an effective way, and by mean of metagenomics, genes associated with biomass-degrading have been recovered. With detailed study, the mechanism behind this biochemical process can be harnessed for industrial-level biomass degradation. Recent study on human microbiome showed that the pathway for fatty acid synthesis commonly found in *E. coli* from human gut can be redirected towards propane biosynthesis, which can be subsequently geared for microbial platform for biofuel production.

Around 95~99% of the microorganisms are unculturable, which was an untapped area before. Now, metagenomic approaches provide powerful tool to explore the diversity and depth of various microbial community in a high-throughput way. With more and more microbiome projects undergoing, applications from microbiome research could totally revolutionize human well-being in many ways.