



Systems Biology of Genomes and Metagenomes: From Simple to Complex

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More than 98% of the microbes from different environments are unknown mainly due to their unculturability. Whole genome sequencing of three such so far unculturable microbes from termite and mammalian gut has provided valuable clues about their distinctive features. The important feature of these microbes is their symbiotic lifestyle with their respective hosts and the loss of essential genes for survival as a result of genome reduction due to which they remain unculturable. Since many of these environments harbor a complex mixture of several species, extraction of genomic DNA of a single microbe is a daunting task. Recently, metagenomic sequencing has emerged as a powerful culture-independent approach for exploring the complexity and diversity of microbial genomes in their natural environments. The scale of metagenomic sequencing has been dramatically boosted by the availability of 'next generation' sequencers which have made sequencing even more high-throughput, less expensive, and, most importantly, cloning and culturing independent. Previously we performed metagenomic sequencing of the gut of thirteen Japanese individuals, including infants. The most apparent outcome of this analysis was the identification of species and functional enrichment of human gut microbiome. This study also provided important clues for metagenomic sequencing related projects important for human health which are of my special interest. The biggest challenge in metagenomic sequencing projects is the high-throughput computational analysis of the gigantic data produced. Some of the expected important outcomes of such analyses are the identification of the novel genomes, genes and biochemical pathways regardless of whether complete genome sequences can be assembled or not. Such studies will be especially useful to understand the systems biology of the complex environments.