

Metagenomics: A New Approach for Microbial Identification

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Traditional microbiology focused on clonal cultures of single microorganism. However, it is now well established that majority of the microbes existing in the world could not be laboratory cultivated while playing essential roles in human life. Therefore, the newly emerged metagenomic method poses an important approach to explore the fantastic world of unculturable microorganisms. With the power of modern genomic techniques the metagenomic approach directly analyze the collective nucleotide contents of the entire microbial community (i.e. the metagenome), bypassing the need for isolation and lab cultivation of individual species [1].

Though firstly proposed as early as 1998 [2], the metagenomic method was easily applicable only after the advent of next-generation sequencing (NGS) technologies, which have dramatically improved the speed and cost-effectiveness of DNA sequencing since 2005. In addition, the fast development of NGS platforms fueled the wide application of metagenomics in biomedical studies in recent years as reflected from the exponential increase in the number of related publications available in PubMed [Figure 1].

Though most of the former metagenomic studies focused on characterization of bacteria communities using 16S rDNA, many recent studies employed shotgun metagenomic strategy for screening all microorganism especially potential viral agents of human diseases. Using metagenomic approach on human tissue samples, Feng and co-workers discovered a previously unknown polyomavirus associated with Merkel cell carcinoma [3], and Palacios et al. also identified a new arenavirus related to a cluster of fatal transplant-associated diseases [4]. Metagenomic approach was further demonstrated to be a powerful complement to current methods for clinical diagnosis in accurate and parallel identification of various known viruses as well as novel variants from fecal [5-7] and nasal [8,9] specimen. For more information on applications of metagenomics in virus discovery refer to the recent review by Mokili et al. [10].

Nevertheless, some associated techniques need substantial

improvements to facilitate further applications of metagenomic approach for microbial identification. Efficient methods for microbe enrichment are essential to circumvent the high human contamination as currently encountered in many studies. In addition, optimized bioinformatics tools for accurate binning, assembly and annotation from the metagenomic data are also urgently required.

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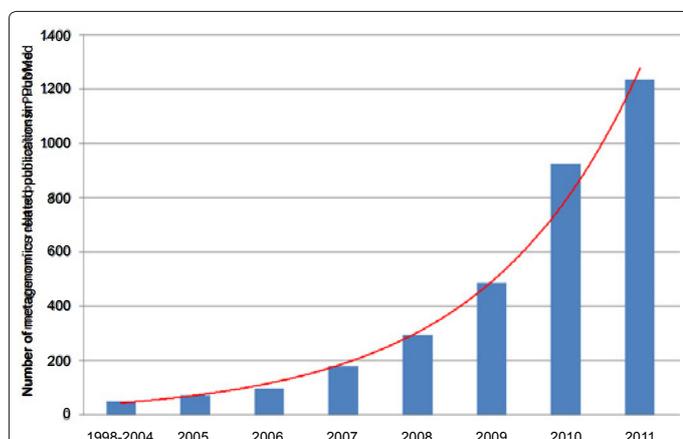


Figure 1. Fast growth of metagenomics related publications in PubMed (accessed at June 15, 2012). Keywords used for literatures search are 'metagenome OR metagenomic OR metagenomics'. An exponential trendline (red) was used to fit the data.

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