Commentary

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British Journal of Research
ISSN 2394-3718

2017
Vol.4 No.5:35

DOI: 10.21767/2394-3718.100035

Metagenomics: The Revolution in the Biomedical World

Rituparna De*

Department of Radiation Sciences, Umea University, Sweden

***Corresponding author:** Rituparna De, Ph.D, Visiting Researcher, Department of Radiation Sciences, Umea University, Sweden, Tel: +46700059384; E-mail: rituparna.de@umu.se

Received Date: November 24, 2017; **Accepted Date:** December 27, 2017; **Published Date:** December 31, 2017

Citation: De R (2017) Metagenomics: The revolution in the biomedical world. Br J Res Vol. 4 No 5: 35.

Abstract

Metagenomics has revolutionised almost every area in biomedical sciences and its industrial applications are enormous. It has found potential applications starting from discovery of novel microbes and microbial products to successfully establishing pragmatic link between diseases like cancer and inflammatory disorders and the microbiome.

Keywords: Metagenomics; Microbialmeta genomics; Viral metagenomics; Uncultured microbes; Cancer; Microbiome

Commentary

Metagenomics has revolutionized current research in the world of biomedical sciences and industry. The discovery of new microbes and different microbial products bypassing culture methods was a major breakthrough of the late 20th and early 21st centuries. The earliest applications of metagenomics was in the discovery of enzymes and antibiotics of microbial origin [1] and its benefits are being recognized every day. Metagenomics is the genomic analysis of uncultured microorganisms [2]. Rondon et al. used the term “metagenome” to denote the compound genome of the whole microbiota, in the soil [3]. Screening of metagenomic libraries has changed our understanding of microbial ecology and given us new insight into gene cataloguing as it has opened up avenues to access the enormous diversity of the microbial world and vast gene pools and study their significance in various metabolic processes and in immune defense [4], by overcoming the constraints of culture-based approaches.

Metagenomics has paved a promising pathway for researchers seeking novel information about the diversity of the microbial world and enriching their understanding about vital processes of life. The most potential applications of metagenomics has been in the discovery of microbes from different niches of the biosphere and which has helped immensely in advancing our understanding about the etiology of diseases and also in the origin of epidemic strains.

The human virome has been understudied and one of the stupendous applications of metagenomics has been in the discovery of viruses, many of which are extremely abundant and have not been cultivated in the laboratory. Most of these are significant in health and disease. For example, the discovery of the crAssphage, the most abundant human-associated virus is a striking example of the applications of metagenomics in the discovery of viruses [5]. A recent study by Yutin et al., reported the discovery of the bacteriophage family that comprises viruses related to the crass-phage [6]. Most of these viruses are associated with bacteria from the human gut belonging to phylum Bacteriodetes which includes some of the most abundant bacteria in the human gut and in other habitats [6]. The same group has done an extensive in silico analysis of genomic and metagenomics databases to analyse and predict the functions of the phage proteins [6].

Metagenomics is finding applications even in the social scenario. Some researchers are making endevours to introduce the concept to the general populace. The community library of Hackuarium, a non-profit organization presented to ctizens the targeted metagenomic profile of 39 bottled beers from 5 countries, based on internal transcribed spacer (ITS) sequencing of fungal species [7]. This report highlights the application of this cutting-edge technology for identification of microbial content in bottled beer and shows its prospective commercial applications [7].

Metagenomics have been previously used to distinguish microbiome among ethnic groups [8]. A recent interesting systematic and successful application of the technology has been in identifying distinct enterotypes among three different populations comprising 48 Han Chinese, 48 Kazaks, and 96 Uyghurs on the basis of 16s RNA gene, metagenomes of the gut microbiota and genome-wide association of the host genomes. This study which showed a clear classification of the gut microbiota of these 192 subjects into two distinct enterotypes, namely, Bacteroides and Prevotella has helped in throwing light on the genetic basis of the microbiome [9]. Metagenomics has proved to be a very useful tool in establishing link between the microbiome and cancer [10].

On the whole, metagenomics, the novel technology has benefitted the scientific world immensely. Right from solving compex etiology of diseases to finding novel biomarkers to enhance the prognosis and diagnostics of life threatening diseases it has contributed by providing valuable insight and solutions.

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This article was originally published in a special issue, entitled: **"Global Research on Different Scope"**