

ACTA SCIENTIFIC MICROBIOLOGY (ISSN: 2581-3226)

Volume 2 Issue 7 July 2019

Editorial

Environmental Microbiology

Iram Liagat*

Assistant Professor, Department of Microbiology, Government College University, Pakistan

*Corresponding Author: Iram Liaqat, Assistant Professor, Department of Microbiology, Government College University, Pakistan.

Received: April 22, 2019; Published: June 01, 2019

DOI: 10.31080/ASMI.2019.02.0260

Approximately, 5×10^{30} bacteria are present on Earth and in terms of biomass, its comparatively more than all existing plants and animals. Understanding the microbial interaction with environment is very necessary and led to establish discipline known as environmental microbiology. The discipline of microbiology was originated by Antony van Leeuwenhoek, a Dutch scientist of late- 17^{th} -century, making him the first microbiologist. He was the first person to explain tiny cells through drawings, prepared by inventing methods of grinding and polishing microscope lenses, thus enhancing magnification power by 270X. Microorganisms play essentially vital role in our daily lives. These may be eukaryotes (having true nucleus), such as protists and fungi, as well as prokaryotes (without a nucleus), for example, bacteria.

Many valuable and biotechnologically important microorganisms have been isolated from environments. These organisms have been the source of quality fermentation products including amino acids, secondary metabolites and with the ability to convert recalcitrant into simple biodegradable components. Limitation to isolate uncultured microorganisms has been overcome by revolution at molecular level using newer techniques such as metagenomics, single cell genomics and stable isotope probing, etc. This has led to the discovery of novel diverse having potential of pharmacologically active enzymes and products.

Metagenomics and single cell genomics have no doubtly changed the prevailing concept of bacterial and archaeal diversity in the environment using candidate phyla radiation (CPR) resulting into limited bacterial diversity of 25% only [1]. It relies on cloning of genes from all types of DNA of diverse organisms in complex systems. The CPR bacteria lack many universal genes and central metabolic pathways. In contrast, these possess many key value genes of enormous diversity, some important from biotechnology perspective but others indicate reductive evolution. These CPR bacteria are uncultivable due to symbiotic or parasitic association with other microbes for growth, which also explains why these could not be isolated successfully using culture media.

Another important recent development in the biosphere of environmental microbiology is the use of robust technique, known as stable isotopes probing (SIP). SIP has been refined for the study of all types of biomolecules, has been used to identify the key metabolites and microbes involved in diverse biological mechanisms. Use of this technique label the DNA of microorganisms with the heavy isotope, which is then collected get separated later using CsCl density gradient centrifugation method [2]. Accordingly, SIP is advantageous to identify the abundant target genes or those genes that are present at relatively less abundance due to unfavorable conditions in any environments for subsequent cloning or PCR amplification. In this way, a gene pool with novel target genes will be established which could lead to establish only novel microbes and their products from biotechnology perspective.

Bibliography

- 1. Castelle CJ and Banfield JF. "Major new microbial groups expand diversity and Alter our understanding of the tree of life". *Cell* 172 (2018): 1181-1197.
- 2. Hungate BA., *et al.* "Quantitative microbial ecology through stable isotope probing". *Applied and Environmental Microbiology* 81.21 (2015): 7570-7581.

Volume 2 Issue 7 July 2019

© All rights are reserved by Iram Liaqat.