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SOIL MICROBIAL DIVERSITY FOR BIO PROSPECTING

S. C. Wijayaratne

Department of Botany, Faculty of Applied Sciences, University of Sri Jawardenapura.

chandrani_wijeya@yahoo.com

Microbes have been living on this planet since more than three billion of years ago. But, it was only after the discovery of symbiotic, non-symbiotic aerobic nitrogen fixing and sulphate reducing bacteria from soil by Beijerinck (1888-1901), the role of microorganisms in ecosystem was well recognized. His work contributed greatly to understand the critical role of microorganism in elemental cycling, which gave insight into their involvement in energy and nutrient exchange in the ecosystem. Subsequently, with the discovery of antibiotics by Alexander Fleming in 1928 and later with various technological advancements, a renaissance in microbiology came about especially in areas of bioprospecting.

It is difficult to correctly estimate the total number of microorganisms present in the biosphere. However, approximate calculations suggest that 4-6 x 10^{30} prokaryotes inhabits the earth(1)but the proportion of microorganisms, which can be cultured, is estimated to be only 0.1% or at most 10% of the total population in the biosphere. Major revolutionary advancement in biological sciences that came about in the last few decades have facilitated exploitation of microorganisms to obtain various biochemicals, ranging from food to pharmaceuticals, to use them in a variety of bioprocesses for the benefit of man. Almost all of these microbial products or processes have been developed essentially from cultivable microorganisms.

Currently there is a global drive to promote industrial biotechnology for a sustainable economic future in modern industrial societies. White biotechnology as it is now referred to, originating partly or fully from microorganisms, has its roots in ancient human history and its products are already part of everyday life from vitamins, medicines, biofuel, bioplastics to enzymes in detergents or dairy or bakery products (2). However, the handful of known microbes is unable to fulfill all of the future requirements of the human society. It has been well established that some of the unique abilities of microorganisms *viz.* production of pharmacologically active secondary metabolites, decomposition of recalcitrant materials such as lignocellulosic plant cell walls, are due to the activities of microorganisms that live in consortia or by microorganisms that inhabit unique niches, some of which are difficult to establish *in vitro*. As such, microbiologists besides surveying hitherto unexplored unique ecosystems, *viz.* extreme environments, endophytic environments, should also use cultivation independent methods to detect and make use of uncultivable microbes to satisfy future requirements. To meet these challenges, already various methods have been adopted: mimicking natural habitats for growth, single cell micro-encapsulation and heterogenous expression of biosynthetic genes that encode secondary metabolites through cloning. A novel method to study microbial systems at the ecosystem level (eco-systems biology) is to characterize complete microbial ecosystems by combining metagenomics (also referred to as environment and community genomics), meta-transcriptomics and meta-metabolics facilitated by faster and low cost novel gene sequencing technologies, which do not require the cloning of DNA fragments before sequencing as in conventional sequencing (3). In metagenomic studies, the focus is on 16S ribosomal RNA sequences, which are relatively small and often conserved within the species. These new technologies can provide a cultivation-independent assessment of the largely untapped genetic reservoir of soil microbial communities.

Cellulose is nature's most abundant biopolymer, and long has been recognized as a potential source of sugars for biofuel production. Use of recalcitrant biomass, such as lignocellulosic plant cell walls, is a vast and potential resource for new biocatalytics (enzymes) for various industrial processes, including the production of biofuels. For prospecting novel enzymes from an isolated metagenomic DNA, two complementary approaches can be used: function-based screening of expression libraries and sequence-based gene searches. In the former, metagenomic expression libraries are constructed and screened for target enzyme activities while for the latter, target genes are cloned after being amplified from metagenomic DNA by using polymerase chain reaction with conserved sequences as primers (3). Thus, these molecular methods would pave the way to access boundless realms of microbial biodiversity and also give the way to the reality of tapping this biodiversity for the benefit of man.

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Elena Nardini *et .al.*Microbial Biodiversity and Molecular Approach, JRC Scientific and Technical Report, Aquatic microbial world and biodiversity: Molecular Approach to improve the knowledge, EUR 24243 ENISBN 978-92-79-14990-0, ISSN 1018-5593, DOI 10.2788/60582,Luxembourg