

## Editorial

# Molecular Genetics: A New Domain in the Field of Environmental Microbiology

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Molecular Genetic techniques have made new innovations in environmental microbiology by opening an approach for speedy throughput methods for an autonomous evaluation culture & the utilization of biological association existing in complicated ecosystems such waste water/waste water polluted soil & sludge [1]. The microbial community of soil is comparatively diversified with sturdy amount of prokaryotic variety. Different types of genes are present in the form of microbial culture and involved in the degradation of several toxic pollutants. In the present status the cultivation of diversity by traditional technology is quite less. The function of molecular genetics technology for the study of bacterial or fungal or algal inhabitants in contaminated sites devoid of the requirement for the growth of microbe which has a remarkable applicability in the finding of newly discovered and unidentified micro-organisms present in the microbial diversity offers a tremendous opening for microbial degradation of toxic contaminants present in the soil. Metagenomic DNA amplification with polymerase chain reaction combination, biological population and profiling techniques of catabolic genes identification are means to explicate the structure, powers and connections of microbial populations through environmental bioremediation [2]. The main purpose of the paper presents an impression of the various advantageous applicability of molecular techniques in the microbial degradation and remediation of hydrocarbons and supplementary toxic pollutants present in environmental society and an impression of up to date movement in the developing area of Environmental Biology. Environmental Microbiology has the impending to reasonably yet proficiently restore contaminated environments, but be short of knowledge about the factors that organize the amplification and metabolic process of microbial population in environmentally polluted sites frequently confines its accomplishment. Yet, speedy advance improvement in the appreciative understanding of biological treatment is on the perspective. Scientists have the talent to culture microorganisms which are imperative in environmental bioremediation strategy and may assess their physiology by using a grouping of genomic enabled

experimental and modeling. Now, newly applied environmental genomic methods propose the option for comparable studies on the uncultured organisms. Combination models that can predict the activity of microorganisms that contribute to the bioremediation with existing geochemical and hydrological models should transform bioremediation of mainly empirical science into practice.

During ancient times, the finding and investigation of microbes in the ecosystem has been made principally by bacterial culture methods. As extensively accounted, the purpose of this technology led to the segregation of bacterial inhabitants existing in the waste water and in the soil. In stipulations of profitable bioremediation and organization of an event of bioremediation methodology was only of inadequate significance because of the duration of time necessary for insulation; repeatedly when a drop of hydrocarbonoclastic organisms was observed, bioremediation has already stalled. Advancements in genomic approaches of independent culture have exceedingly improved our perception of the ecosystem and variety of microbial society. The disjointing or the recognition of trivial divergences in precise DNA sequences can furnish imperative knowledge concerning the structure of microbial population and variety of microbial cultures containing significant genes. Numerous fingerprints performances have been built up and utilized in circumstances of microbial ecosystem, as an environmental bioremediation. Advanced Molecular genetics practices endow with a fingerprint outline or sketch of the identified diversity based on the nucleic acid separation of distinctive species [3]. The general approach of bacterial communities consists of first, the nucleic acid extraction: either DNA and/or RNA, the subsequent augmentation of genes coding for 16S rRNA and the third analysis of polymerase chain reaction yield by DNA fingerprinting technology. To create banding patterns of known molecular fingerprint, diverse amplified yield can be separated by a method of electrophoresis. Modification in the molecular fingerprint may have an analysis methodology to identify the microbial community structure in space and time. Molecular Genetics exercises of independent culture have freshly unraveled the complexities of microbial populations, functions and interactions polluted hydrocarbons sites. These exercises were applied to scrutinize the evolution of environmental bioremediation of hydrocarbons and associated toxic contaminants and eternally increased appreciably recognition of the microbiological treatment of such pollutants as a result of the application of molecular based techniques on nucleic acids. In current years, the study of genetic expression proteins biosynthesis has materialized to complete the analysis of the microbial community DNA base [4]. Therefore, metagenomics propose an important assurance to advance the prediction of in situ microbial responses, activities and dynamics for oil / bioremediation of pollutants.

The function of molecular genomic technologies enabled the examination of environmental bioremediation is obviously in its

beginnings. There are abundant technological concerns to be resolved before some of the innovative approaches, such as the sequencing of the genome environment and tables, or multispecies consortia of *in silico* modeling, can be widely used in such area. Though, for bioremediation to progress as a science there is a robust necessity for ample understanding of the apposite links can provide. The eventual goal of this research study is the linkage patterns of growth and microbial metabolism in impure ecosystems with open geochemical and hydrological models to accurately envisage the assisted microbial innate attenuation of contaminants or the likely outcome of approach designed to hasten the bioremediation.

## References

1. Hansel CM, Fendorf S, Jardine PM, Francis CA. Changes in bacterial and archaeal community structure and functional diversity along a geochemically variable soil profile. *Appl Environ Microbiol.* 2008; 74: 1620-1633.
2. Li X, Luo Q, Wofford NQ, Keller KL, McInerney MJ, Wall JD, et al. A molybdopterine oxidoreductase is involved in H<sub>2</sub> oxidation in *Desulfovibrio desulfuricans* G20. *J Bacteriol.* 2009; 191: 2675-2682.
3. Markowitz VM, Chen IM, Palaniappan K, Chu K, Szeto E, Grechkin Y, et al. The integrated microbial genomes system: an expanding comparative analysis resource. *Nucl Acids Res.* 2010; 38: 382-390.
4. Nielsen JL, Christensen D, Kloppenborg M, Nielsen PH. Quantification of cell-specific substrate uptake by probe-defined bacteria under *in situ* conditions by microautoradiography and fluorescence *in situ* hybridization. *Environ. Microbiol.* 2003; 5: 202-211.