Microbial Diversity and Degradation of Pollutants

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Extensive use of chemical substances has now become a global environmental issue. The ideal chemical substance is expected to serve, only its indented use. When it becomes unwanted, the contamination of the environment ensues. Harmful effects of a chemical substance set in the process of pollution. The cost effective choice to halt this process is decontamination through microbial functions. The microorganisms can use the chemical substances as sources of energy and nutrients in soils, which are an important sink for many pollutants. On a hectare basis, the microbial biomass is about 1000 to 10,000 kg in the surface soil alone, and these organisms represent a significant fraction of the living biomass on Earth [1]. With about 80% of global terrestrial Carbon stored in them, the soils support the carbon-based life immeasurably. In addition to utilizing natural substances, microorganisms have an extensive capacity to degrade synthetic substances. Actually, the microbiological properties are more sensitive than the chemical and physical properties of soils to the presence of pollutants. The ‘microbial infallibility hypothesis’ suggests that microorganisms will be found to degrade every chemical substance synthesized by any living organism [2]. Credence to this hypothesis is further advanced by the microbial capabilities to degrade many human-made, synthetic substances. But, the molecular complexity of some chemical substances makes their microbial degradation very demanding. Nevertheless, the microbial detoxification and degradation will continue to remain an effective biotechnological approach to clean up the sites contaminated with a variety of chemical pollutants.

Microorganisms are isolated, grown, and cultivated in the laboratory for many reasons. The cataloguing of microbial diversity has traditionally relied on their growth. Interestingly, the number of Colony Forming Units (CFUs) is generally found to increase, as the nutrient concentrations of medium decreases. The choice of media for microbial growth estimation may strongly affect the diversity of colonies obtained. Generally, the laboratory media contain high concentrations of nutrients, which are a billion to a trillion times more than what microorganisms find in their natural environment. Even after prolonged incubation of 1 to 6 months, many colonies of soil bacteria can still be present as micro-colonies. Such ‘self-limiting growth behavior’ is largely credited to the oligotrophic microorganisms. The microbial traits such as high surface-to-volume ratio, high-affinity uptake system for substrate, and the efficient shutdown of metabolism upon starvation are advantageous for their oligotrophic growth, for survival at low substrate levels in nature. Another interesting physiological group of microorganisms are anaerobic microorganisms. They require many components, about 33 in their media for cultivation in the laboratory. Changing any two components of the medium at the same time (increasing and decreasing their concentrations) would result in 2,112 different medium combinations to study. Such variations of any 22 components at a time would make about 1000 billion combinations [3]. The slowest-growing laboratory culture so far reported are that of anaerobic hydrocarbon degrading methanogenic consortium by Zengler et al. [4]. In the first year of its cultivation, the growth was inferred by detecting methane produced, and only after 3 years of incubation, the change in turbidity (optical density at 600 nm ∼0.1) was observed.

Microbial growth is dependent on the Gibbs free energy available, as well as the requirements of maintenance energy by the organism itself. Interestingly, the syntrophic cultures survive on maintenance of Gibbs free energies that are much lower than the theoretical values, even under the laboratory cultivation [5]. The energy input of soils is just enough for microbial division to occur once in every 16 h or more. For the subsurface microorganisms, the doubling times and resulting community turnover can be between 100 and 2000 years [6]. Goldfarb et al. [7] compared the relative growth rates of more than 2200 bacterial taxa across 43 divisions/phyla on organic substrates of increasing chemical recalcitrance. Taxa that increase in relative abundance with labile organic substrates are numerous (more than 500), while those with more chemically recalcitrant substrates are fewer (168). Only about 6% of detected taxa, including many Burkholderiales, increased in relative abundance with both labile and chemically recalcitrant substrates. Improving our understanding of the metabolic plasticity/rigidity and determining the microbial capabilities to utilize different types of substrates will enable us to better predict the consequences of pollution, and to select the means to improve the remediation efforts.

Compared to figures based on cultivation in laboratory media, the enumeration by microscopy raises the microbial counts by 100-1000 times. Majority of cells observed under the microscope will not form colonies on solid media. This phenomenon is referred to as “the great plate count anomaly” [8]. Distinguishing growth by microscopy can allow a detection of ~103 cells per ml. The application of flow cytometry which allows the screening of 5000 to 50,000 events per second can detect microbial growth better [9]. High-throughput approaches, such as the use of Giga Matrix can be applied for miniaturized culture volumes, allowing growth and screening of millions of cells in a highly compartmentalised format [10]. After a latency period, microbial species capable of using pollutants as energy sources and nutrients can be detected. Anyway, failure to detect some organisms does not imply that there will be no organism with the expected capabilities, but it is missed and has remained inaccessible so far.

The complex physical-chemical environment of soil coupled with an enormous diversity of microorganisms and their interacting processes makes it difficult to manipulate these microorganisms with the precision we would wish. The estimates of bacterial species vary widely, and about 107 distinct bacterial species could inhabit a 10 g soil sample [11]. To acquire just half of the Operational Taxonomic Units (OTUs) present in 1 g of soil, a sampling of approximately 16,284-44,000 would be required [12]. In each gram of soil sample, the total bacterial genome length will be equivalent to that of 1000 human

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The diversity of all other life-forms is declining due to human-induced global changes [14]. Plant/animal species richness has a positive effect on ecosystem productivity; the buffering effect against disturbances enhances the temporal mean of productivity. Globally, industrial activities contribute to major perturbations and significant alterations in the ecosystem functioning. Rapid acceleration of species extinctions, increased exchange of species, losses of populations of species and multiple changes to global nitrogen, carbon and hydrological cycles [15] are some of the notable manifestations. The diversity of plant/animals is regarded at different levels of resolution: (i) a-diversity distinguishes between diversity of species within a community of habitat, (ii) β-diversity refers to the rate and extent in changes of species, along a gradient of habitats and (iii) γ-diversity denotes to richness of species over a range of habitats [16]. For the microorganisms in soils, there are several microhabitats of rhizosphere, bulk soil, aggregates, decaying organic matter, macropores and micropores. When the mean quality of these habitats increases, the spatial variability and diversity of resources can increase. Habitat heterogeneity (‘patchiness’) and the phylogenetic diversity of bacteria are found to be positively correlated. The saturation of subsurface soils was found to have less diverse bacterial communities than unsaturated soils, probably due to increased patchiness of the unsaturated soils [17]. The increase in resources in large number of potential niches can allow both productivity and diversity to increase. Alternatively, the reduction in resource heterogeneity can decrease the microbial diversity. Loss of a few microbial species in any ecosystem due to pollution can lead to the loss of ecosystem functions. Maintaining biodiversity in the species-poor, polluted ecosystems is of greater significance to the remediation efforts.

High functional and genetic diversity, faster evolutionary rates and enormous dispersal capabilities of microorganisms make them as appropriate remediation agents. The polluted environments can be highly variable and also difficult to measure the environmental characteristics, at a resolution level that will be relevant to the microbial communities. The 'paradox of scale' can operate on several environmental factors which can affect the same microbial community differently, if the scale of inquiry is changed [18]. To understand and ultimately predict functions of complex systems of polluted environments, large date sets on chemical, physical, and microbiological properties of soils need to be generated by various methods. Both conceptual breakthroughs and technological developments are necessary for gaining better understanding of microbial diversity. As in the parable of blind men describing an elephant [19], each method, even if it gives a poorer view of microbial diversity, can help us to envision its wholeness. Besides employing them for degrading various pollutants, the microorganisms can also be applied as biosensors to detect pollutants. As a part of the International Genetic Engineering Machine Competition (IGEM), Gu et al. [20] built a self-powering electrochemical biosensor called ‘ElectrEcoBlu’. This biosensor is coupled with a microbial fuel cell to transduce a pollution input into an easily measurable electrical output signal. The recognition element of this engineered system is a pollutant responsive transcriptional activator (YxIR or DmR), which can bind BTEX and di-nitro-toluene. The reporter element consists of S-adenosylmethylene-dependent N-methyltransferase (PhzM) and flavin-dependent hydroxylase (PhzS), which convert the precursor compound Phenazine-1-Carboxamide (PCA) to pyocyanin-an electron-carrying redox mediator-in the biosynthetic pathway cloned from Pseudomonas aeruginosa into E. coli and a non-pathogenic Pseudomonas strain. Such integration of engineering techniques with scientific methodologies can provide new insights and serve as a reference framework for future developments in the synthetic biology, for detection before and after remediation.

References