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REVIEW ARTICLE

ON THE STUDY OF SOIL MICROORGANISM DIVERSITY IN INDIAN CONTEXT

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ABSTRACT

Microorganisms are responsible for different soil ecosystem and biodiversity. Diversity of microorganisms of different area varies both in quality and quantity of microbs. Microorganisms available in biogeochemical cycles, mineralization, and solubilization of organic and inorganic matter in soil vary widely. Symbiotic and non-symbiotic bacteria make colony in plant root, rhizosphere and mycorhiza. Diversity and interaction of microorganisms in plant root and microbial activity in soil has been studied in detail in India and abroad. Present paper deals with such studies and reviews the available literature which may be useful for the researchers and planners equally.

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INTRODUCTION

A global concerns focus on environmental protection and natural resources management. Microbial diversity is responsible for variable reaction in different soil orders. Understanding of soil ecosystem function at the process level is necessary. Ecological approaches have primarily focused on the function of natural ecosystem where sustainability is viewed in terms of the maintenance and stability of ecosystem productivity has not been fully explored because of great microbial biodiversity in soil ecosystem.

Soil ecosystem

Around 1.5billion years ago; motile microorganisms migrated to different environments under the influence of different factors. Soil formation on the earth was started through biomediation but they were existence recently in history, about 300 years with Leeuwenhoek's invention of the microscope. The microbes execute most of the chemical transformation in the soil ecosystem. The thar desert of North Western India is distributed over 2.34 million km with about 91% area endemic to the Rajasthan.

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The low fertile sandy soil of this desert is poor in organic matter, having rapid water infiltration rates and rapid oxidation (Chowdhury, Michael, Anton, and Tripathi, 2007). Desert soil is an excellent ecosystem colonized by various groups of microorganisms with extremities of environment conditions soil microbial communities are among the most complex, diverse, and important assemblages in the biosphere (Zhou *et al*., 2003). Soil contains billions microorganisms, so many different types that accurate numbers remain unknown. The understanding of the composition of the microbial communities in soilis complex. In 1931, Waksman believed that a large body of information has accumulated that enables us to construct a clear picture of microscopic population of the soil and in 1932 Bergey's manual clarified that no organisms could be classified devoid of being cultured. Soil microorganisms are mostly small and inconspicuous and therefore rarely enjoy public attention in contrast to birds, flowers or other large and eye catching organisms and there is nothing similar for soil microfouna because these seem to be less facitating (Barrios, 2007).

Rhizosphere

Soil microorganisms are included in a wide variety of metabolic and physiological activities that influence the microhabitat. The plant root influcing soil volume where there is a high concentration of the carbon with zone of intense microbial metabolic activity occurring is called the rhizosphere. Higher population of bacteria including

Azotobactorchrococcum, *Beijerinekia* and *Actinomycetes* from the rhizosphere soil of Mycorrhizal plants (Bagayraj and Mengi, 1978). is observed because of root exudation (Barea *et al*., 1975) in rhizosphere affects rhizospheric microflora. In general mycorrhizal fungi through modifications to the plant root system, interact with beneficial soil organisms such as N2-fixing bacteria, Phosphate-solubilising Bacteria, Fungi and inhabiting nematodes. These interactions are important in the natural ecosystem for nutrient cycling (Gryndler, 2000). A large number of portion of soluble inorganic phosphate applied to agriculture soil as chemical fertilizer is rapidly immobilized soon after application and becomes unavailable to plants (Dadarwal *et al*., 1997). PSMs (Phosphate solubilizing microorganisms) include different group of microorganisms which not only assimilate phosphorus from insoluble forms of phosphates but they also cause a large portion of soluble phosphate to be released in quantities in excess of their requirements species of *Aspergillus* and *Penicilliumare* among fungal isolates identified to have phosphate solubilizing capabilities. Among bacterial genera with this capability are *Pseudomona*, *Azospirillum*, *Bacillus*, *Rhizobium*, *Burkholderia*, *Arthrobacter*, *Alcaligenes, Serratia*, *Enterobacter*, *Acinetobacter*, *Flavobacterium* and *Erwinia* (Rodriguez *et al*., 1996).

Gram positive and gram negative bacteria *Arthobactersp*. and *Pseudomonassp*. was greatest in the lowPhosphorus soil but the bacterial population of fertilized P and AM soil was generally not significantly different. They also found that G. mosseae had the lowest gram negative bacterial population while G. etunication soil had the highest population of both gram positive and gram-negative bacteria (Schreiner *et al*., 1997). Soil microorganisms isolated were identified on the basis of morphological and biochemical properties morphological method consisted of microscopic and microscopic method. The microscopic characterization method (Kawato and Sinobu, 1959). Isolated bacteria *Bacillus subtilis*, B. *Cerus*, B. *Polymyxa*. Agriculture soil Microorganisms isolated were *Escharichiacoli*, *Pseudomonas aeruginosa*, *Klebsiella pneumoniae, Enterobacter aerogenes, Shigella sp., Proteus Mirabilis, Bacillus anthracis, Bacillus Subtilis, Staphylocococcus aureus* and *Staphylococcus Epidermidis species, Fungi* suchas *Aspergillus niger, A. Flavus, Fusarium oxysporum, Trichoderma sp.* and *Rhizopus sp.* (Amir and Pineau, 1998). Microorganisms play an important role in biodegradation of soil agriculture waste and increasing the soil Fertility and improvement of crop production (Okoh *et al*., 1999).

Agriculture soil is a dynamic medium in which a large number of pathogenic and non- pathogenic bacterial and fungal flora lives in close association. Microbes in the soil are the key to carbon and nitrogen recycling. Microorganisms produce some useful compound that are beneficial to soil health, plant growth and play an important role in nutritional chains that are important part of the biological balance in the life in our planet (Paul and Clerk, 1966; Kummerer, 2004). Microbial activity in desert soil is highly dependent on characteristics such as temperature, moisture and the availability of organic carbon (Buyanovsky *et al*., 1982, Parker *et al*., 1984). Of these, moisture availability is the major constraint affecting microbial diversity, community structure and activity. Gram-positive spore formers and dominant and the population do not decline significantly even during summers (Rao *et al*., 1983).

Actinomycetes may constitute around 50% of the total microbial population in desert soils. However, Hethener reported only 1-2% representation of *Actinomycetes* in the sandy soil of Tassili N, Ajjer (Hethener, 1967). Dominant microflora desert soil is made up of *Coryneforms* i.e. *Archangium*, Cystobacter, Myxococcus, *Polyangium*, *Sorangium* and *Stigmatella*; Sub-dominant forms comprise *Acinetobacter*, *Bacillus*, *Micrococcus*, *Proteus* and *Pseudomonas*, *Cyanobacteria* also contribute significantly to the biota of hot arid regions in terms of primary productivity and nitrogen fixation (Bhatnagar *et al*., 2003). The dominant Cynobacterial forms of Thar Desert are *chroococcusminutes*, *Oscillatoria Pseudogeminata* and *Phormidiumtenue*, *Nostoc* sp. dominants amongst heterocystous forms. Fungal populations as viable propagate range from nil to 6.3x103 in Uzboi desert Takyr (Lobova *et al*., 1967; Cameron, 1969).

The Dominant genera include *Aspergillus*, *Curvularia*, *Fusarium*, *Mucor*, *Paecilomyces*, *Penicillium*, *Phoma* and *Stemphylium*, *XericMushrooms* such as *Coprinus*, Fomes, Terfezia and Termania have also been reported from desert (Trappe, 1981).The removal of zinc from soil polluted by effluents from textile industries was studies using two fungi Strands *Aspergillus Fumigatus* RH05 and *Aspergillus Flavus* RH07 (Goldstein *et al.,* 1997). Evidence of the involvement of microorganisms in solubilization of inorganic phosphates was reported as early as 1903 (Kucey *et al*., 1989, Khan *et al*., 2007). Phosphate solubilizing microorganisms (PSM) are ubiquitous and their numbers vary from soil to soil. Population of (PSM) and organic matter content of some selected arid soils of Rajasthan, India was reported by (Venkateswarul *et al.,* 1984). Phosphorous solubilization is carried out by a large number of *Saprophytic* bacteria and fungi acting on sparingly soluble soil phosphate, mainly by chelating-mediated mechanism (Bajpai and Rao, 1971, Moghimi *et al.,* 1978, Whitelaw 2000).

In general among the whole microbial population in soil phosphatsolubilizing fungi 0.1to0.5% of the total respective population (Chem *et al*., 2006). Phosphate solubilizing bacteria generally out number phosphat- solubilizing fungi by 2-150 flads (Banik and Dey 1982, Kucey,1983, Kucey *et al*. ,1989, Alam *et al*., 2002).The efficiency of different phosphatase and phytase secreating fungi isolated from arid soils of Rajasthan, India to hydrolyse different organic phosphatecompounds were reported (Tarafdar *et al.,* 2003. Aseri *et al*., 2009).

Mineralization of organic Phosphate

Mineralization of soil organic phosphate plays an imperative role in Phosphorus cycling of a farming system. Mineralization of organic to inorganic phosphate involves processes Catalyzed by phosphatases use organic phosphate as a substrate to convert it into inorganic form (Beech *et. al*. 2001). Some heterotropic microorganisms are also capable of solubilizing phosphates combined *with* calcium or magnesium (Atlas and Bartha 1998). These soluble forms can now be readily taken up by plants, algae, cynobacteria and autotrophic bacteria and assimilated into organic cellular components such as DNA, RNA, and ATP. Phosphatase enzyme is present in all organisms but only bacteria, fungi, and some algae are able to secrete the outside of their cell (Jones, 2002). Soil microorganisms such as Bacteria, yeast, Fungi, could produce pectinases (Yadav *et al*., 2009). Extracellular enzymes are produced by different varieties of microorganisms i.e. fungi, bacteria, yeast and Actinomycetes (Devi *et al.,* 2008). Bacteria are on the top of the list of alkaline protease produces. The genus Bacillus is the most common source of proteases (Gupta *et al*., 2002). Some example of potent alkaline protease producing Bacilli strain are B. *amyloliquifuciens*, B. *subtills* and B. *Lichiniformis*. Some other bacterial sp. which is also known for their protease production potential are *Staphylococcus*, *Flababacterium*, *Serratia*, *Alcaligenes*, *Vibrio*, *Brevibacterium*, *Pseudomonas*, and *Halobacterium*, (Gupta *et al*., 2005). Among Actinomycetes strain of *Nocardiopsis*, *Streptomyces* and *Nocardia* are potential ones. In fungi, Aspergili is the most predominant group for protease production and the strain of *Ophiostoma*, *Myxococcus*, *Penicillium*, *Rhizopus*, and *Neurospora*, etc are common produces of proteases (Gupta *et al*., 2005).

Conclusion

Microorganisms are playing important role in soil ecosystem and different industrial use. Soil provides wide habitat for different microbial activity is highly dependent on its characteristics. This is the major constraint affecting microbial diversity. On the basis of above account it can be concluded that in spite of much research done in this field, there are certain gaps in terms of ecosystems (including micro-ecosystems), species diversity and microbe-plant interactions. This field provides ample scope to investigate deeply in this area.

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