



Chapter

[16]

Role of microbial diversity in ecosystem sustainability

Vishal Kumar Deshwal*

Department of Microbiology, BFIT Group of Institution, Sudhowala, Dehradun, India

Abstract

Microorganisms are ubiquitous i.e. they are present nearly everywhere in world. They are huge in number and play significant role in environment. Microorganisms have several vital roles in ecosystems: decomposition, oxygen production, evolution, and symbiotic relationships with plants etc. Microbial enzymatic activity is responsible in cyclic of essential nutrients. Microbial diversity can be characterized on the basis of morphology, physiology, genetic and geography etc. The microbial ecology is relationship between microorganisms and their biotic and abiotic environment. Microbes are huge in number and significant role in environment. Microorganisms have several vital roles in ecosystems such as decomposition of complex molecules, produce oxygen, symbiotic relationships with plants, recycling of nutrients and bioremediation. Plant growth promoting microorganisms enhances plant growth by production of plant growth hormones, enzyme production, siderophore production and HCN production etc. Microorganism uses processes such as Biodegradation, Biotransformation, and Co-metabolism for degradation of xenobiotic compounds. Few specific microorganisms are use in mining industry which process is known as bioleaching.

Keywords

Bioleaching, Microbial diversity, Microbial ecology, PGPR, Xenobiotics

Introduction

Microorganisms are microscopic living forms which may exist in unicellular form and multicellular forms. Diversity means variation so in simple word; microbial diversity is variation in microorganisms. This microbial diversity can be characterized on the basis of morphologically, physiologically, genetically and geographical etc. Anything which has variation, it comes under diversity. The diverse groups of communities of microorganisms are classified into Bacteria, Archaea and Eukaryote. In morphological diversity, microbes are classified on the basis of various forms such as unicellular, multi-cellular, rod shape, spherical, spiral, oval, flagellate, branched, unbranched etc.

Morphological diversity: These microscopic organisms have unique morphology and we can observe them with help of staining under microscope. In general, shape of Bacteria like a ball is called cocci, rod shaped bacteria are known as bacilli and some rod shaped bacteria are curved, spiral shaped bacteria is called as spirilla (singular spirillus) (van Teeseling *et al.*, 2017). Some bacteria are flagella which is responsible for motion and classified into Monotrichous- Single flagella at one end, Amphitrichous- single flagella at both ends, Lophotrichous- Tuft of flagella at one or both ends, Peritrichous- flagella surrounding the bacterial cell (Holt *et al.*, 1994). Further, Unicellular fungi forms oval type structure which broadly term as Yeast and other eukaryotic multi cellular forms are known as fungi which may bear spore beading structure like sporangia containing motile spore - zoospores or non-motile spore aplanospore which are asexual spores and other types of sexual spores such as Ascospore, zygospore etc. (Stajich *et al.*, 2009; Willey *et al.*, 2017).

Physiological diversity: Microbial physiology is defined as the study of how microbial cell structures, growth and metabolism function in living organisms. It is also conveyed as the study of microbial cell functions which includes the study of microbial growth and microbial metabolism. Microorganism is using various metabolic pathways for growth, repair and multiplication. There are two group of microorganisms based on oxygen metabolism- aerobic and anaerobic microbes (Willey *et al.*, 2017; Moat *et al.*, 2002). Aerobic microorganisms are use oxygen for metabolic activity and process is known as oxidation. Another group of anaerobic cannot perform activity under aerobic condition therefore they are called as anaerobic microbes and this process is known as fermentation. Other factors such as nutrients, pH, temperature etc. are also affected metabolic activity. In other words, we can say enzymes are responsible for metabolic activity, which are affected by environmental parameters. Various metabolic biochemical processes are come under this diversity (Willey *et al.*, 2017). Among micro-organisms fungi produce maximum exogenous enzymes in environment. An Autotrophic microbe can produce its own food using light, water, carbon dioxide, or other chemicals but other group which cannot manufacture its own food by carbon fixation and therefore derives its intake of nutrition from other sources of organic carbon, mainly plant or animal matter are known as "Heterotroph" (Willey *et al.*, 2017; Moat *et al.*, 2002).

Genetic diversity: Genetically diversity means variation in DNA sequence. A genome is an organism's complete set of DNA, including all of its genes. Each genome contains all of the information needed to build and maintain that organism. Microbial genomes are widely variable and reflect the enormous

diversity of bacteria, archaea and lower eukaryotes. The molecular-phylogenetic studies, researchers have compiled an increasingly robust map of evolutionary diversification showing that the main diversity of life is microbial, distributed among three primary relatedness groups or domains: Archaea, Bacteria, and Eucarya (Pace, 1997). One major difference between the genomes of microorganisms and higher eukaryotes, is the presence of circular, extra-chromosomal DNA called plasmids. Plasmids can be transferred via horizontal DNA transfer from one cell of the same generation to another, mediating the rapid evolution of many different organisms (Bohlin *et al.*, 2017; Bohlin and Pettersson, 2019). It means, each microorganism has its own specific genome. This genomic information can be used for identification and qualitative analysis of microorganism.

Geographical diversity: Microorganisms are distributed all over the world which includes plants, animals, and environment. Microbes show diversity in pH which is an important determinant of microbial community composition and diversity. Most microbes grow best around neutral pH values (6.5 - 7.0), but some thrive in very acid conditions and some can even tolerate a pH as low as 1.0. Such acid loving microbes are called acidophiles. Even though they can live in very acid environments, their internal pH is much closer to neutral values. But alkaliphiles are a class of extremophilic microbes capable of survival in alkaline (pH roughly 8.5–11) environments, growing optimally around a pH of 10 (Gomes and Steiner, 2004; Gupta *et al.*, 2013). Microorganism shows diversity on the basis of temperature and they are classified into 5 types.

Psychrophiles grow well from 0°C to 20°C and have an optimum growth temperature near to 15°C. They are readily isolated from Arctic and Antarctic. Another type of microbes are *psychrotrophs* or *facultative psychrophiles* which can grow at 0 to 7°C even though they have maximum growth ranges between 20 and 30°C. Other group, *Mesophiles* are microorganisms with growth optimum around 20 to 45°C. Further, *thermophiles* where microorganisms can grow at temperatures of 55°C or higher. These organisms flourish in many habitats including composts, self-heating hay stacks, hot water lines, and hot springs. In fifth group, a few thermophiles can grow at 90°C or above and some have maxima above 100°C and they are known as *hyperthermophiles* (Gupta *et al.*, 2014). Few Archaea such as *Pyrobaculum*, *Pyrodictium*, *Pyrococcus* and *Melanopyrus* and fungi such as *Ascomycete* and *Zygomycete* family can multiply at high temperature (Busk and Lange, 2013; Gupta *et al.*, 2014). *Thermotoga maritime* and *Aquifex pyrophilus* belong to bacterial group can exhibit the highest growth temperatures of 90 and 95°C respectively (Haki and Rakshit, 2003; Kumar *et al.*, 2011; Gupta *et al.*, 2014).

Microbial ecology and microbial niche

Microbial ecology is the science that specifically examines the relationship between microorganisms and their biotic and abiotic environment i.e. microbial ecology applies the general ecological principles to explain life functions of microorganisms *in situ*, i.e., directly in their natural environment rather than simulated under artificial laboratory conditions *ex situ* or *in vitro* (Panikov, 2010). The niche theory is based on the assumption that the species composition of an ecosystem is entirely determined by environmental conditions, a process known as habitat filtering (Dumbrell *et al.*, 2010). Simply, we can

say the ecological niche of a microorganism describes how it responds to the distribution of resources and competing species, as well as the ways in which it alters those same factors in turn. In essence, the niche is a complex description of the ways in which a microbial species uses its environment. The accurate ecological niche of a microbe is primarily determined by the specific metabolic properties of Microorganism (Horner-Devine *et al.*, 2007; Faust and Raes, 2012). Understanding of microbial ecology is difficult as microbial ecology is not permanent in site. The microbial ecology changes as change number and type of microorganisms under non-living habitats. Microbial ecologists have examined whether microbial communities are distinct in different environments, whether microbial diversity changes with habitat heterogeneity and distance, and whether microbial diversity shows explainable patterns of distribution comparable to such of microorganisms (Rosenzweig, 1995), the productivity-diversity relationship (Rosenzweig, 1995) or patterns of co-occurrence (Horner-Devine *et al.*, 2007). The microbial ecologists study the contributions of microorganisms to the carbon, nitrogen, and sulfur cycles in soil and in freshwater. The study of pollution effects on microorganisms also is important because of the impact these organisms have on the environment. Microbial ecologists are employing microorganisms in bioremediation to reduce pollution effects (Willey *et al.*, 2017).

Role of microorganisms in an ecosystem

Microorganisms are ubiquitous i.e. they are present nearly everywhere in world. They are huge in number and play significant role in environment. Microorganisms have several vital roles in ecosystems: decomposition, oxygen production, evolution, and symbiotic relationships with plants etc. Microbial enzymatic activity is responsible in cyclic of essential nutrients. In soil, microbial community is linked with ratio of nutrient i.e. carbon: nitrogen: phosphorous: sulphur ratio. At the same time, these ratios might be modulated by the different nature of available organic matter in each substratum and by the water nutrient concentrations.

Decomposition: Decomposers are present in dead animal or plant matter and they break down into more basic molecules. These micro-organisms produce diverse exogenous enzymes which convert complex form to simplest form which process is known as decomposition. In this decomposition process, various different products are released in environment such as carbon dioxide (CO₂), energy, water, plant nutrients and resynthesized organic carbon compounds. The successive decomposition of dead material or modified organic matter results in the formation of a more complex organic matter called humus (Juma, 1998; Bani *et al.*, 2018). So the process of decomposition provides nutrients that future plants and animals will be able to reuse, making soil more fertile.

Nutrients recycling: Microorganisms play important role in circulation of nutrients in ecosystem. Microorganism produces enzymes to degrade complex material into simplest form which can be utilized by other living forms. Further, microorganisms are responsible for running biogeochemical cycle.

Nitrogen fixation: Microorganisms have capability to fix atmospheric nitrogen. On the basis of such nitrogen fixing tendency nitrogen fixing microorganisms and classified into two group symbiotic

nitrogen fixer and free living (non-symbiotic) nitrogen fixer (Deshwal *et al.* 2013a). The symbiotic interactions between a legume and rhizobia result in a unique, nitrogen fixating plant organ, the nodule symbiotic nitrogen fixation throughout nodulation in legumes is well known, which help to reduce the application of inorganic N and can also play a major role as green manure in improving the soil fertility (Deshwal *et al.*, 2013b; Deshwal and Singh, 2014; Ney *et al.*, 2019). According to Postgate (1982), the atmosphere contains about 10^{15} tones of N_2 gas and nitrogen cycle involves the transformation of some 3×10^9 tonnes on global basis but lightning can fix atmospheric nitrogen i.e. transformation and 10% of world supply of nitrogen meets out by this process (Sprent and Sprent, 1990). The fertilizer industry also provides chemically fixed nitrogen globally. The consumption of fertilizer N increased from 8 to 17 Kg. ha⁻¹ of agriculture land in the 15-year period from 1973 to 1988 (FAO, 1990; Deshwal *et al.*, 2013; Mahmud *et al.*, 2020).

More than 100 years biological nitrogen fixation (BNF) has commanded the attention of scientists concerned with plant mineral nutrition and it has been exploited extensively in agricultural field (Dixon and Wheeler, 1986; Burris, 1994). Frages (1992) suggested that ecological principles and practices that are appropriate for the manipulation of rhizobia prove suitable model for other soil microorganism as well. Brockwell and Bottomley (1995) concluded that in particular efficient substitute for fertilization of crops and pastures occurs with the organic N. Recently, Ramírez-Puebla *et al.* (2019) mentioned that nearly 50% of the total nitrogen in crop fields is the contribution of BNF by diazotrophic bacteria of the total biosphere nitrogen.

Bacteria of family Rhizobiaceae are symbiotic and effectively convert atmospheric nitrogen which is utilized by the host. Rhizobiaceae family contains six genera namely *Rhizobium*, *Sinorhizobium*, *Mesorhizobium*, *Allorhizobium*, *Azorhizobium* and *Bradyrhizobium* (Deshwal and Chaubey, 2014). The Free-living diazotrophs correspond to a small fraction of the plant rhizospheres ecosystem, and they belong to alphaproteobacteria (Rhizobia, Bradyrhizobia, Rhodobacteria), betaproteobacteria (Burkholderia, Nitrospirina), gammaproteobacteria (*Pseudomonas*, *Xanthomonas*), firmicutes, and cyanobacteria (Morris and Schniter, 2018; Deshwal and Thapliyal, 2019), Actinomycetes and Frankia sp. (Deshwal and Tarik, 2018), Cyanobacteria (mainly *Nostoc* sp.), *Azospirillum* spp., *Azoarcus* spp. and *Herbaspirillum* (Burén and Rubio, 2017), *Clostridium pasteurianum*, *Klebsiella oxytoca* (Yates and Jones, 1974), *Azotobacter vinelandii* (Poole, 1997).

Carbon rotation in environment: Carbon is an essential element for life as we know it because of its ability to form multiple, stable bonds with other molecules. Without carbon, none of these molecules could exist and function in the ways that permit the chemistry of life to occur. Various carbon cycle steps are given below

Carbon in the Atmosphere: Carbon dioxide gas (CO_2) can released into the atmosphere through the activities of living things, such as the exhalations of animals, the actions of decomposer organisms, and the burning of wood and fossil fuels by humans. The CO_2 gas in atmosphere is the starting point of the carbon cycle (Lu and Conrad, 2005; Trumbore, 2006; Le Quere *et al.*, 2009).

Producers: Producers such as plants absorb carbon dioxide from the atmosphere under sunlight and use CO_2 to build sugars, lipids, proteins, and other essential building blocks of life.

Other producer organisms such as cyanobacteria are crucial to life on Earth because they can turn atmospheric carbon into living matter (Lu and Conrad, 2005; Trumbore, 2006).

Consumers: Herbivorous animals consume these plant form growth and metabolic activity. They use some of these carbon compounds from food to build their own bodies but much of the food they eat is broken down to release energy. Carnivorous consume primary consumers and uptake nutrients (Liang and Balsler, 2011)

Decomposers: Plants and animals that die without being eaten by other animals are broken down by other organisms, called “decomposers.” Decomposers include many bacteria and some fungi. Decomposers break down the chemical bonds in their food molecules. They create many chemical products, including in some cases CO₂ (Liang and Balsler, 2011).

Human Activities: Recently, humans have made some big changes to the Earth’s carbon cycle. By burning huge amounts of fossil fuels and cutting down roughly half of the Earth’s forests, humans have decreased the Earth’s ability to take carbon out of the atmosphere, while releasing large amounts of carbon into the atmosphere that had been stored in solid form as plant matter and fossil fuels (Le Quere *et al.*, 2009).

Release of phosphorus: Phosphorus is one of the important element for all forms of life. The phosphate (PO₄) makes up an important part of the structural framework that holds DNA and RNA together. Phosphates are also a critical component of ATP (adenosine triphosphate phosphate) which is a cellular energy carrier (Willey *et al.*, 2017). Few microbial strains has capability to solubilize non-solubilizing phosphorous in soil and as a results increase plant growth and productivity (Deshwal and Kumar, 2013a). In field study, Chabot *et al.* (1996) observed that phosphate solubilization by strains of *R. leguminosarum* bv. *phaseoli*, was the most important mechanism of maize and lettuce growth promotion. Antoun *et al.* (1998) also found that *Bradyrhizobium* sp (Lupinus) solubilized phosphate. Similarly, Dashi *et al.* (1998) observed that plant growth promoting rhizobacteria solubilized phosphate and accelerate nodulation, increase nitrogen fixation activity by field grown *Glycine max* L. Merr. under short season conditions.

Release sulphur into environment: Sulphur is an essential part of all living cells and Sulphur containing amino acids are always present in almost all kinds of proteins. The Plants can absorb directly the sulphur containing amino acids, e.g., cystine, homocysteine, cysteine and methionine. Besides S-containing amino acids, it is also an important part of growth factors like thiamine, biotin and lipoic acids (Willey *et al.*, 2017). However these amino acids fulfil only a small proportion or requirements for sulphur to the plants. To fulfil rest of the requirements of plants, sulphur passes through a cycle of transformation mediated by microorganisms. Sulphur compounds involved in the sulphur cycle are H₂S, S⁰, thiosulphate, sulphite (SO₃⁻) and sulphate (SO₄⁻). Most common forms of sulphur are H₂S, S⁰ and SO₄⁻. The greatest reservoir of sulphur in the biosphere is the sulphate in the oceans (Tourna *et al.*, 2014; Zhao *et al.*, 2017).

- **Source:** The major source of sulphur in marine environment is sulphate. While in the lithosphere, the sulphur is found as sulphate and iron sulphide (FeS). The metal sulphides (FeS) are readily oxidized to sulphates by both biological and chemical processes (Willey *et al.*, 2017).

- **Assimilatory sulphate reduction:** In most habitats, sulphates are available to plants and microorganisms which is assimilated into sulphhydryl compounds (R-SH) that becomes a part of biomass of living organism. This reduction process in which sulphate becomes biomass is known as Assimilatory Sulphate reduction. Various microorganisms and green photosynthetic plants are involved in the process. Since animals can only uptake the reduced form of sulphur it is an important step to transfer the S into a food chain (Kumar *et al.*, 2018).
- **Release of H₂S:** H₂S is release to biosphere by both aerobic and anaerobic processes. They can be either release from decomposition of organic compounds (Desulphurylation) or by reduction of inorganic sulphate (Dissimilatory sulphate reduction) (Willey *et al.*, 2017; Kumar *et al.*, 2018).
- **Oxidation of hydrogen sulphide (H₂S) to elemental sulphur:** Hydrogen sulphide undergoes decomposition to produce elemental sulphur by the action of certain photosynthetic sulphur bacteria. (Kumar *et al.*, 2018; Fuentes-Lara *et al.*, 2019).
- **Oxidation of elemental sulphur to sulphates:** Elemental form of sulphur accumulated in soil by earlier described processes cannot be utilized as such by the plants. It is oxidized to sulphates by the action of chemolithotrophic bacteria of the family Thiobacteriaceae (*Thiobacillus thiooxidans*, *Thiobacillus ferrooxidans*, *Thiobacillus denitroficans*) (Willey *et al.*, 2017).

Micronutrient and macronutrient iron: Like other micronutrient and macronutrient iron is also necessary for living organism. Iron is the fourth most abundant element in the earth. Iron oxides, comprising minerals such as hematite, magnetite and limonite are most abundant of metal oxides in soil (Schwertmann and Taylor, 1989). Iron is required for large variety of metabolic process in virtually all organisms (Crichton *et al.*, 1987) except *Lactobacilli* (Archibald, 1983). In aerobic condition, iron is present in soil of neutral pH as insoluble ferric hydroxide polymers are not available biologically (Lindsay, 1979). Most microorganisms have efficient high affinity iron uptake system, to fulfil their requirements. In this process siderophore; low molecular weight iron (III) chelating agents are synthesized (Neilands, 1981). Siderophores chelate insoluble iron and solubilize iron and ferric siderophore complex are taken up by the cell through specific membrane receptors (Neilands, 1982).

Plant growth promotion: Plant Growth Promoting Microorganism are beneficial microbes which provides plant growth and increase soil fertility. These microorganisms release plant growth hormones, antimicrobial agent like HCN which indirectly kill pathogenic microbes, siderophore etc. Such microorganisms increase plant growth activity and productivity.

- **Plant growth hormones:** Plant growth-promoting rhizobacteria (PGPR) includes a wide variety of bacterial strains from different taxonomic groups that inhabit plant roots and their rhizosphere. Different PGPR strains can synthesize phytohormones such as auxin, ethylene, cytokinin, gibberellin, abscisic acid, jasmonic acid and salicylic acid (Tsukanova *et al.*, 2017). Plant growth promoting rhizobacteria produce plant growth hormones such as IAA which enhance the plant growth (Deshwal *et al.*, 2013a; Deshwal and Kumar, 2013b). IAA is well-known plant growth promoting hormones and 96% symbiotic nitrogen fixing rhizobia produced IAA (Arora *et al.*, 2001; Deshwal *et al.*, 2013). Lippman *et al.* (1995) observed that PGPR could directly

enhance plant growth by IAA production and increasing nutrient uptake. Noel *et al.* (1996) observed under gnotobiotics conditions, a direct growth promotion of the early seedling root, appears to involve the growth regulators such as IAA and cytokinin. Gibberellins are a group of hormones that perform various functions in the plant organism. They are the key regulators of reproductive organ formation and development and ripening of fruit and viable seeds (Plackett and Wilson, 2016). PGPR can influence the amount of endogenous gibberellin in plants, in a fashion similar to other hormones. For example, some PGPR strains can synthesize gibberellins (Bottini *et al.*, 2004; Deshwal *et al.*, 2013).

- **HCN production:** Few specific microorganisms produce one hydrogen cyanide (HCN) which has antimicrobial activity. This is one of the reasons, that plant growth promoting microorganisms. The HCN producing microorganisms control growth of different type of pathogens (Bagnasco *et al.*, 1998; Deshwal *et al.*, 2013). Previously, Nautiyal (1997) screened *Rhizobium* strains, among isolated 256 bacterial strains *Rhizobium* NBRI 19513 completely inhibited growth of *Fusarium oxysporum*, *Rhizoctonia bataticola* and *Pythium* sp. *in vitro*. Deshwal *et al.* (2003) observed that HCN producing *Bradyrhizobium* strains inhibited the growth of *M. phaseolina*.
- **Siderophore :** Siderophore effectively control the disease chlorosis: The mechanism by which plant avoid iron (chlorosis) are both more diverse and less investigated than the siderophore mediated iron up take system of microorganisms. Three strategies of iron assimilation have been identified in plant (Bienfait, 1989). Strategy I, found in non-gramineous monocots and all dicots, involves acidification of the rhizosphere, thus increasing iron solubility by approximately 10^3 per pH unit, the reduction of Fe^{3+} ion and Fe (III) chelates to Fe^{2+} ion and uptake of Fe (II) occurs. Strategy II, observed that in graminaceous monocots secretion of iron chelating agent (phytosiderophore) of mugineic acid family involves (Sugiura *et al.*, 1981) and where as in strategy III, was the uptake of microbial Fe (III) siderophores take place. Although extensive research has been directed to correct chlorosis by the applications of available iron compounds to the soil. Hence the, the siderophores production by rhizobial strains would prove considered as a potential way to improve nodulation and N_2 fixation in iron deficient conditions (Carson *et al.*, 1992; Deshwal *et al.*, 2013).

Degradation of xenobiotic compounds

Xenobiotics are released into the environment by human activities, and they often cause problems such as environmental pollution, since most such compounds cannot be readily degraded, and have harmful effects on human beings and the natural ecosystem. However, some microorganisms that degrade man-made xenobiotics have been isolated. Most of these aerobic xenobiotics-degrading bacterial strains use xenobiotics as their sole source of carbon and energy, and thus they are excellent models for studying the adaptation and evolution of bacteria in the environment. Although plants have the inherent ability to detoxify some xenobiotic pollutants, they generally lack the catabolic pathway for complete degradation/mineralization of these compounds compared to microorganisms (Eapen *et al.*,

2007). Three major processes such as *Biodegradation*, *Biotransformation*, and *Co-metabolism* are responsible for degradation of xenobiotic compounds. Microorganisms perform most of the biodegradation of both natural products and industrial chemicals. Collectively, microorganisms play a key role in the biogeochemical cycles of the Earth. The substances transformed (conversion into another form) or degraded by microorganisms are used as a source of energy, carbon, nitrogen, or other nutrient, or as final electron acceptor of a respiratory process (Fetzner, 2000).

The “*biodegradation*” involves the breakdown of organic compounds, usually by microorganisms, into biomass and less complex compounds, and ultimately to water, carbon dioxide, and the oxides or mineral salts of other elements present. Further, “*Biotransformation*” is the metabolic modification of the molecular structure of a compound, resulting in the loss or alteration of some characteristic properties of the original compound. “*Biotransformation*” may effect the solubility, mobility in the environment, or toxicity of the organic compound. A microbial population growing on one compound may fortuitously transform a contaminating chemical that cannot be used as carbon and energy source, a process referred to as 'co-metabolism'. The phenomenon has also been called 'co-oxidation' and 'gratuitous' or 'fortuitous' metabolism. Usually, the primary substrate induces production of (an) enzyme (s) that fortuitously alter (s) the molecular structure of another compound (Fetzner, 2000; Willey *et al.*, 2017). Aerobic degradative bacteria of xenobiotics are *Pseudomonas*, *Gordonia*, *Bacillus*, *Moraxella*, *Micrococcus*, *Escherichia*, *Sphingobium*, *Pandora*, *Rhodococcus*, and anaerobic xenobiotics degradative bacteria are *Pelatomaculum*, *Desulphovibrio*, *Methanospirillum*, *Methanosaeta*, *Desulfotomaculum*, *Syntrophobacter*, *Syntrophus* (Varsha *et al.*, 2011).

Microbial leaching

In general, bioleaching is a process described as “the dissolution of metals from their mineral sources by certain naturally occur microorganisms” or the use of microorganisms to transform elements so that the elements can be extracted from a material when water is filtered through it (Brierley, 1978; Lundgren and Malouf, 1983). Microbial extraction of metals has been in application for ore leaching for centuries, though the mechanism remained unknown. Specifically copper was recovered by man as early as 1000 BC from metal laden waters which passed through copper ore deposits. Specific Bacteria capable of oxidising Sulphur compounds to sulphuric acid (Devasia *et al.*, 1993). This was followed by the isolation of the iron and sulphur oxidising bacteria, *Thiobacillus ferrooxidans* (now called *Acidithiobacillus ferrooxidans*) to lay the foundation for subsequent research into the role of microorganisms in leaching. A consortium of microorganisms namely *Acidithiobacillus ferrooxidans*, *Acidithiobacillus thiooxidans*, *Leptospirillum ferrooxidans*, *Sulpholobus* spp. and thermophilic bacteria including *Sulpholobus thermosulphidoxidans* and *Sulpholobus brierleyi* are known to be involved in bioleaching. Anaerobes would also be found in leaching areas (Devasia *et al.*, 1993; Botero *et al.*, 2007; Pollmann *et al.*, 2016).

Bioleaching of copper: Biological copper leaching is practiced in many countries including Australia, Canada, Chile, Mexico, Peru, Russia and the United States of America. Copper recovery from

bioleaching accounts for about 25% of the world copper production. Following the initial isolation of *Acidithiobacillus ferrooxidans* from coalmine water in 1947, studies quickly disclosed its presence in copper-leaching operations. *Acidithiobacillus ferrooxidans* is also found in the Malanjhand Copper Mines (Devasia *et al.*, 1993; Cornejo *et al.*, 2008).

Bioleaching of uranium: Uranium leaching proceeds by the indirect mechanism as *Acidithiobacillus ferrooxidans* does not directly interact with uranium minerals. The role of *Acidithiobacillus ferrooxidans* in uranium leaching is the best example of the indirect mechanism (Devasia *et al.*, 1993; Tsuruta, 2007).

Bioliberation of gold: Iron- and sulphur-oxidising acidophilic bacteria are able to oxidise certain sulphidic ores containing encapsulated particles of elemental gold, resulting in improved accessibility of gold to complexation by leaching agents such as cyanide. Bio-oxidation of gold ores is a less costly less polluting alternative to other oxidative pre-treatments such as roasting and pressure oxidation (Devasia *et al.*, 1993; Natarajan, 1998).

Conclusion

Microbial diversity is variation in microbes on the basis of physical, biological, genetically or geographical. This diversity play an important role in various diverse ecology where variation in pH, temperature, aerobic or anaerobic, nutrients, xenobiotic compounds and toxic environment. Microbes survive unfavourable condition and convert complex, toxic material into simple and non-toxic material. Further, diverse plant growth promoting microbes increase soil fertility, plant growth and productivity of essential crops. Such diverse microorganisms are use in agriculture, food and dairy, pharmaceutical, hospital, cosmetic, mining, environment cleaning, waste management etc. Without microbial diversity, the world cannot survive.

References

- Antoun, H., Beauchamp, C.J., Goussard, N., Chabot, R. and Lalande, R. (1998). Potential of *Rhizobium* and *Bradyrhizobium* species as plant growth promoting rhizobacteria on non-legumes, effect on radishes *Raphanus sativus* L. *Plant and Soil*, 204: 57-67
- Archibald, F. (1983). *Lactobacillus plantarum*, an organism not require iron. *FEMS Microbiology Letters*, 19: 29.
- Arora, N.K., Kang, S.C. and Maheshwari, D.K. (2001). Isolation of siderophore producing strains of *Rhizobium meliloti* and their biocontrol potential against *Macrophomina phaseolina* that causes charcoal rot of groundnut. *Current Science*, 81: 673-677.
- Bagnasco, P., De La Fuente, L., Gualtieri, G., Noya, F. and Arias, A. (1998). Fluorescent *Pseudomonas* spp as biocontrol agents against forage legume root pathogenic fungi. *Soil Biology and Biochemistry*, 30: 1317-1322.
- Bani, A., Pioli, S., Ventura, M., Panzacchi, P., Borruso, L., Tognetti, R., Tonon, G., Brusetti, L. (2018). The role of microbial community in the decomposition of leaf litter and deadwood. *Applied Soil Ecology*, <https://doi.org/10.1016/j.apsoil.2018.02.017>
- Bienfait, H.F. (1989). Prevention of stress in iron metabolism of plant. *Acta Botanica Neerlandica*, 38: 105-129.
- Bohlin, J. and Pettersson, J.H.O. (2019). Evolution of Genomic Base Composition: From Single Cell Microbes to Multicellular Animals. *Computational and Structural Biotechnology Journal*, 17: 362-370.

- Bohlin, J., Eldholm, V., Pettersson, J.H., Brynildsrud, O. and Snipen, L. (2017). The nucleotide composition of microbial genomes indicates differential patterns of selection on core and accessory genomes. *BMC Genomics*, 18(1): 151.
- Botero, A.E.C., Torem, M.L. and de Mesquita, L.M.S. (2007). Fundamental studies of *Rhodococcus opacus* as a biocollector of calcite and magnesite. *Mineral Engineering*, 20: 1026-1032.
- Bottini, R., Cassan, F. and Piccoli, P. (2004). Gibberellin production by bacteria and its involvement in plant growth promotion and yield increase. *Applied Microbiology and Biotechnology*, 65: 497-503.
- Brierley, C.L. (1978). CRC. *Critical Reviews in Microbiology*, 6(3): 207-61 <https://doi.org/10.3109/10408417809090623>
- Brockwell, J. and Bottomley, P.J. (1995). Recent advances in inoculant technology and prospects for the future. *Soil Biology and Biochemistry*, 27: 683-697.
- Burén, S. and Rubio, L.M. (2017). State of the art in eukaryotic nitrogenase engineering. *FEMS Microbiology Letters*, S: 365-370.
- Burris, R.H. (1994). In, Nitrogen fixation with non-legumes, Ed. Hegazi, N.A., Fayez, M. and Monib, M.; The American University in Cairo, Egypt, pp 1-11.
- Busk, P.K. and Lange, L. (2013). Cellulolytic potential of thermophilic species from four fungal orders. *AMB Express*, 3: 47-56.
- Carson, K.C., Holliday, S., Glenn, A.R. and Dilwarth, M.J. (1992). Siderophore and organism acid production in root nodule bacteria. *Archives of Microbiology*, 157: 264-271.
- Chabot, R., Antoun, H. and Cescas, M.C. (1996). Growth promotion of maize and lettuce by phosphate solubilizing *Rhizobium leguminosarum* bv *phaseoli*. *Plant and Soil*, 184: 311-321.
- Cornejo, P., Meier, S., Borie, G., Rillig, M.C. and Borie, F. (2008). Glomalin-related soil protein in a Mediterranean ecosystem affected by a copper smelter and its contribution to Cu and Zn sequestration. *Science of the Total Environment*, 406: 154-160.
- Crichton, R.R., Ponee-Ortiz, Y., Koch, M.H.J., Parfait, R. and Stuhmann, H.B. (1978). Isolation and characterization of phytoferritin from pea *Pisum sativum* and lentil *Lens esculenta*. *Biochemistry Journal*, 171: 349-386.
- Dashi, N., Zhang, F., Hynes, R. and Smith, D.L. (1998). Plant growth promoting rhizobacteria accelerate nodulation and increase nitrogen fixation activity by field grown *Glycine max* L Merr under short season conditions. *Plant and Soil*, 200: 205-213.
- Deshwal, V.K. and Chaubey, A. (2014). Isolation and Characterization of *Rhizobium leguminosarum* from Root nodule of *Pisum sativum* L. *Journal of Academic and Industrial Research*, 2(8): 464-467.
- Deshwal, V.K. and Kumar, P. (2013a). Plant growth promoting activity of Pseudomonads in Rice crop. *Journal of Academic and Industrial Research*, 2(11): 152-157.
- Deshwal, V.K. and Kumar, P. (2013b). Effect of Heavy metals on Growth and PGPR activity of Pseudomonads. *Journal of Academic and Industrial Research*, 2 (5): 286-290.
- Deshwal, V.K. and Singh, S.B. (2014). Impact of co-inoculation of *Pseudomonas* and *Rhizobium* strains on seed germination and plant growth activity in Maize plant. *European Journal of Molecular Biology and Biochemistry*, 1(1): 39-42.
- Deshwal, V.K. and Tarik, M. (2018). Isolation and characterization of antibiotic producing actinomycetes against certain pathogens. *Journal of Plant Development Sciences*, 10(9): 529-532.
- Deshwal, V.K. and Thapliyal, N. (2019). Plant growth promoting *pseudomonas* strains effectively enhance plant growth of *Oryza sativa*. *Journal of Plant Development Sciences*, 11(8): 471-474.
- Deshwal, V.K., Pandey, P., Kang, S.C. and Maheshwari, D.K. (2003). Rhizobia as a biological control agent against soil borne plant pathogenic fungi. *Indian Journal of Experimental Biology*, 41: 1160-1164.
- Deshwal, V.K., Singh, S.B., Kumar, P. and Chubey, A. (2013). Rhizobia Unique Plant Growth Promoting Rhizobacteria: A Review. *Indian Journal of Experimental Biology*, 2(2): 74-86.
- Devasia, P., Natarajan, K.A., Sathyanarayana, D.N. and Rao, G.R. (1993). Surface Chemistry of Thiobacillus Ferrooxidans Relevant to Adhesion on Mineral Surfaces. *Applied Environment Microbiology*, 59(12): 4051-4055.
- Dixon, R.O.D. and Wheeler, C.T. (1986). Nitrogen fixation in plants. Blackie, Glasgow, United Kingdom.
- Dumbrell, A.J., Nelson, M., Helgason, T., Dytham, C. and Fitter, A.H. (2010). Relative roles of niche and neutral processes in structuring a soil microbial community. *The ISME Journal*, 4: 337-345.
- Eapen, S., Singh, S. and D'souza, S.F. (2007). Advances in development of transgenic plants for remediation of xenobiotic

- pollutants. *Biotechnology Advances*, 25(5): 442-451.
- FAO (1990). Fertilizer year book FAO Rome, Italy. pp. 79.
- Faust, K. and Raes, J. (2012). Microbial interactions: from networks to models. *Natural Reviews in Microbiology*, 10: 538-550.
- Fetzner, S. (2000) Biodegradation of xenobiotics In: *Biotechnology: Fundamentals in Biotechnology*, vol X Eolss Publishers, Oxford, UK, pp. 215-246.
- Frages, J. (1992). An industrial view of *Azospirillum* inoculant, formulation and application technology. *Symbiosis*, 13: 15-26.
- Fuentes-Lara, L.O., Medrano-Macias, J., Pérez-Labrada, F. and Rivas-Martínez, E.N. (2019). From elemental sulfur to hydrogen sulfide in agricultural soils and plants. *Molecules*, 24: 2282.
- Gomes, J. and Steiner, W. (2004). The Biocatalytic Potential of Extremophiles and Extremozymes. *Food Technology and Biotechnology*, 42: 223-235.
- Gupta, G.N., Srivastava, S., Khare, S.K. and Prakash, V. (2014). Extremophiles: An Overview of Microorganism from Extreme Environment. *International Journal of Agriculture and Environment Biotechnology*, 7(2): 371-380.
- Haki, D.J. and Rakshit, S.K. (2003). Developments in industrially important thermostable enzymes: a review. *Bioresource Technology*, 89: 17-34.
- Holt, J.G., Krieg, N.R., Sneath, P.H.A., Staley, J.T. and Williams, S.T. (1994). In, *Bergey's manual of Determinative Bacteriology*. Williams and Wilkins Press, Baltimore, USA.
- Horner-Devine, M.C., Silver, J.M., Leibold, M.A., Bohannan, B.J.M., Colwell, R.K., Fuhrman, J.A., Green, J.L., Kuske, C.R., Martiny, J.B.H., Muyzer, G., Ovreas, L., Reysenbach, A.L. and Smith, V.H. (2007). A comparison of taxon co-occurrence patterns for macro- and microorganisms. *Ecology*, 88: 1345-1353.
- Juma, N.G. (1998). The pedosphere and its dynamics: a systems approach to soil science. Edmonton, Canada, Quality Color Press Inc, pp. 315.
- Kumar, L., Awasthi, G. and Singh, B. (2011). Extremophiles: A novel source of industrially important enzymes. *Biotechnology*, 10: 121-135.
- Kumar, U., Panneerselvam, P., Gupta, V.V.S.R., Manjunath, M., Priyadarshinee, P., Sahoo, A., Dash, S.R., Kaviraj, M. and Annapurna, K. (2018). Diversity of Sulfur-Oxidizing and Sulfur-Reducing Microbes in Diverse Ecosystems, T. K. Adhya et al. (eds.), *Advances in Soil Microbiology: Recent Trends and Future Prospects*, Microorganisms for Sustainability 3, https://doi.org/10.1007/978-981-10-6178-3_4
- Le Quéré, C., Raupach, M.R., Canadell, J.G., Marland, G., Bopp, L., Ciais, P., Conway, T.J., Doney, S.C., Feely, R.A., Foster, P., Friedlingstein, P., Gurney, K., Houghton, R.A., House, J.I., Huntingford, C., Levy, P.E., Lomas, M.R., Majkut, J., Metzler, N. and Woodward, F.I. (2009). Trends in the sources and sinks of carbon dioxide. *Nature Geosciences*, 2: 831-836.
- Liang, C. and Balsler, T.C. (2011). Microbial production of recalcitrant organic matter in global soils: implications for productivity and climate policy. *Nature Reviews in Microbiology*, 9: 75.
- Lindsay, W.L. (1979). *Chemical equilibria in soil* Wiley, New York
- Lippman, B., Leinhos, V. and Bergmann, H. (1995). Influence of auxin producing rhizobacteria on root morphology and accumulation in maize *Zea mays* L caused by inoculation with Indole-3-acetic acid IAA producing *Pseudomonas* and *Actinobacter* strains or IAA applied exogenously. *Angewandte Botanik*, 68: 31-36.
- Lu, Y. and Conrad, R. (2005). *In situ* stable isotope probing of methanogenic archaea in the rice rhizosphere. *Science*, 309: 1088-1090.
- Lundgren, D.G. and Malouf, E.E. (1983). Microbial Extraction and Concentration of Metals. *Advances in Biotechnology Processes*, 1: 223-249.
- Mahmud, K., Makaju, S., Ibrahim, R. and Missaoui, A. (2020). Current Progress in Nitrogen Fixing Plants and Microbiome Research. *Plants*, 9: 97.
- Moat, A.G., Foster, J.W. and Spector, M.P. (2002). *Microbial physiology*, 4th edition, Wiley-Blackwell.
- Morris, J.J. and Schniter, E.J. (2018). Black Queen markets: Commensalism, dependency, and the evolution of cooperative specialization in human society. *Journal of Bioeconomy*, 20: 69-105.
- Natarajan, K.A. (1998). An integrated biotechnological approach to gold processing - an Indian experience. *Mineral Processing and Extraction*, 19: 235-251.

- Nautiyal, C.S. (1997). Rhizosphere competence of *Pseudomonas* sp NBRI9926 and *Rhizobium* sp NBRI9513 involved in the suppression of chick pea *Cicer arietinum* L pathogenic fungi, *FEMS Microbiology and Ecology*, 23: 145-158.
- Neilands, J.B. (1981). Microbial iron compounds. *Annual Reviews in Biochemistry*, 50: 715-731.
- Neilands, J.B. (1982). Microbial envelope protein related to iron. *Annual Reviews in Biochemistry*, 36: 285-309.
- Ney, L., Franklin, D., Mahmud, K., Cabrera, M., Hancock, D., Habteselassie, M., Newcomer Q. and Fatzinger, B. (2019). Rebuilding Soil Ecosystems for Improved Productivity in Biosolarized Soils. *International Journal of Agronomy*, 5827585: 1-10.
- Noel, T.C., Sheng, C., Yost, C.K., Pharis, R.P. and Hynes, M.F. (1996). *Rhizobium leguminosarum* as a plant growth promoting rhizobacterium: direct growth promotion of canola and lettuce. *Canadian Journal Microbiology*, 42: 279-283.
- Pace, N.R. (1997). A molecular view of microbial diversity and the biosphere. *Science*, 276: 734-740.
- Panikov, N.S. (2010). Microbial ecology. In: Wang LK *et al.* (eds) Handbook of Environmental Engineering, Volume 10: Environmental Biotechnology. Springer Science-Business Media, LLC: New York, NY.
- Plackett, A.R.G. and Wilson, Z.A. (2016). Gibberellins and plant reproduction *Annual Plant Reviews*, 49: 323-358.
- Pollmann, K., Kutschke, S., Matys, S., Kostudis, S., Hopfem S. and Raff, J. (2016). Novel Biotechnological Approaches for the Recovery of Metals from Primary and Secondary Resources. *Minerals*, 6: 54, <https://doi.org/10.3390/min6020054>
- Poole, R.K. and Hill, S. (1997). Respiratory protection of nitrogenase activity in *Azotobacter vinelandii*-Roles of the terminal oxidases. *Bioscience Reports*, 17: 303-317.
- Postgate, J.R., Partidge, C.D.P., Robson, R.L., Simpson, F.B. and Yates, M.G. (1982). A method for screening hydrogenase negative mutants of *Azotobacter chroocum*. *The Journal of General Microbiology*, 128: 905-908.
- Ramírez-Puebla, S.T., Ormeño-Orrillo, E., Rogel, M.A., López-Guerrero, M.G., López-López, A., Martínez-Romero, J., Negrete-Yankelevich, S. and Martínez-Romero, E. (2019). La diversidad de rizobios nativos de México a la luz de la genómica. *Revista Mexicana de Biodiversidad*, 90: 902681.
- Rosenzweig, M.L. (1995). Species Diversity in Space and Time. Cambridge University Press, Cambridge.
- Schwertmann, U. and Taylor, R.M. (1989). In Minerals in soil environments (eds Dixon, JB and Weed, SB Soil Sci Soc Am, WI).
- Sprent, J.I. and Sprent, P. (1990) Nitrogen fixing organisms. Pure and applied aspects. Chapman and Hall, London, United Kingdom.
- Stajich, J.E., Berbee, M.L., Blackwell, M., Hibbett, D.S., James, T.Y., Spatafora, J.W. and Taylor, J.W. (2009). The Fungi, *Current Biology*, 19(18): R840-5.
- Sugiura, Y., Tannaka, H., Mino, Y., Ishida, T., Ota, N., Inoue, M., Non, K., Yoshioka, H. and Takemoto, T. (1981). Structure properties transport mechanism of iron III complex of mugineic acid, a phytosiderophore. *Journal of the American Chemical Society*, 103: 6979-6982.
- Tourna, M., Maclean, P., Condron, L., O'Callaghan, M. and Wakelin, S.A. (2014). Links between sulphur oxidation and sulphur-oxidising bacteria abundance and diversity in soil microcosms based on functional gene analysis, *FEMS Microbiology Ecology*, 88: 538-549.
- Trumbore, S. (2006). Carbon respired by terrestrial ecosystems - recent progress and challenges. *Global Change and Biology*, 12: 141-153.
- Tsukanova, K.A., Chebotar, V., Meyer, J.J.M. and Bibikova, T.N. (2017). Effect of plant growth-promoting Rhizobacteria on plant hormone homeostasis *South African Journal of Botany*, 113: 91-102.
- Tsuruta, T. (2007). Removal and recovery of uranium using microorganisms isolated from North American uranium deposits. *Am J Environ Sci*, 3, 60-66.
- van Teeseling, M.C., de Pedro, M.A. and Cava, F. (2017). Determinants of Bacterial Morphology: From Fundamentals to Possibilities for Antimicrobial Targeting. *Frontiers in Microbiology*, 8: 1264.
- Varsha, Y.M., Naga Deepthi, C.H. and Chenna, S. (2011). An emphasis on xenobiotic degradation in environmental cleanup. *J Bioremediation and Biodegradation*, 11: 1-10.
- Willey, J., Sherwood, L. and Woolverton, C.J. (2017). Prescott's microbiology, 10th edition, McGraw hill publication, New York, United States.

Yates, M. and Jones, C. (1975). Respiration and Nitrogen Fixation in *Azotobacter*. In *Advances in Microbial Physiology*; Elsevier BV: Amsterdam. *The Netherlands*, 11: 97-135.

Zhao, C., Gupta, V.V., Degryse, F. and McLaughlin, M.J. (2017). Abundance and diversity of sulphuroxidising bacteria and their role in oxidising elemental sulphur in cropping soils. *Biology Fertilization Soils*, 53: 159.

Cite this chapter as: Deshwal, V.K. (2021). Role of microbial diversity in ecosystem sustainability. In: *Biological Diversity: Current Status and Conservation Policies*, Volume 1, Eds. Kumar, V., Kumar, S., Kamboj, N., Payum, T., Kumar, P. and Kumari, S. pp. 242-255, <https://doi.org/10.26832/aesa2021-bdcp-016>