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MINI-REVIEW

Microbe-assisted phytoremediation of environmental pollutants and energy recycling in sustainable agriculture

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Abstract
The perception of phytoremediation is efficiently utilized as an eco-friendly practice of green plants combating and cleaning up the stressed environment without harming it. The industrial revolution was followed by the green revolution which fulfilled the food demands of the growing population caused an increase in yield per unit area in crop production, but it also increased the use of synthetic fertilizers in agriculture. Globally, the intensive use of inorganic fertilizers in agriculture has led to serious health problems and irreversible environmental damage. Biofertilizers improve the growth of the plant and can be applied as an alternative to chemical/synthetic fertilizers. Cyanobacteria, bacteria, and fungi are known as some of the principal microbe groups used to produce biofertilizers that form symbiotic associations with plants. Microorganisms perform a key role in phosphate solubilization and mobilization, nitrogen fixation, nutrient management, biotic elicitors and probiotics, and pollution management (biodegradation agents), specifically bacteria which also help in atmospheric nitrogen fixation and are thus available for the growth of the plant. Management or biodegradation of hazardous chemical residues and heavy metals produced by a huge number of large-scale industries should be given primary importance to be transformed by various bacterial strains, fungi, algae. Currently, modern omics technologies such as metagenomic, transcriptomic, and proteomic are being used to develop strategies for studying the ecology of microorganisms, as well as their use in environmental monitoring and bioremediation. This review briefly discusses some of the major groups of microorganisms that can perform different functions responsible for plant health, crop production, phytoremediation and also focus on the omics techniques reportedly used in environmental monitoring to tackle the pollution load.

Keywords Biofertilizer · Bacteria · Fungi · Pesticides · Microbial degradation · Phosphate solubilizer · Waste management

Introduction

Healthy, proficient, and sustainable crop production and agriculture need a continuous and sufficient supply of nutrients that can cope with the ever-growing demands of the population globally (Mahdi et al. 2010; El-Beltagi et al. et al. 2018, 2019a, b). Chemical or synthetic fertilizers improve plant nutrient requirements immediately, but indiscriminate use of them has produced many environmental hazards which include both ground and surface water pollution, soil quality deterioration, pollution in the air, and suppressing many other functions of the ecosystem as well (Puglia et al. 2021). Synthetic fertilizers are toxic chemicals and will accumulate in the human body. Poore and Nemecek (2018) affirm that air pollution is caused by the manufacturing of chemical fertilizers, and that water pollution results when the wastes from industries are dumped untreated into nearby water bodies. Eutrophication is the most devastating effect of chemical waste accumulation in water bodies. Therefore, soil pollution occurs when chemical fertilizers are added to the soil, resulting in a degradation of soil quality and health (Blattner 2020). In the same way, community wastes and sewage sludge offer an alternative, but their use can cause

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higher accumulations of heavy metals, which have adverse effects on crop growth (Iglesias et al. 2018). Therefore, an alternative strategy is needed to improve crop growth without harming plants as well as soil. As a result, the use of biofertilizers is an environmentally friendly way to reduce the use of synthetic fertilizers and can enhance crop production (Sofy et al. 2020a, b, 2021a, b, c). Hence, the role of microbes in promoting the growth of plants as biofertilizers regulates many processes like availability of nutrients, especially Mg, N, Fe, K, P. Organic material decomposition to improve crop growth is well understood (Lalitha 2017; Aly et al. 2012, 2013, 2017; Abu-Shahba et al. 2021). Biofertilizer, known as a component of specific microbial cells, stimulates the growth of plants while increasing the rate of nutrients through the phosphorous cycle, and nitrogen fixation (Mohamed and Gomaa 2012) (Fig. 1).

It is well understood that sustainable agriculture can be achieved using microbial inoculants (cost-effective input), which is the backbone of integrated nutrient management (Mohamed and Gomaa 2012). Biofertilizers are produced from potential microbe strains that help plants absorb nutrients by forming rhizospheric associations with plants in the soil. Biofertilizer or bioinoculant production is an easy and cost-effective method. An enormous advancement in the use and research of biofertilizers has been made in the past few decades (Kour et al. 2020). Soil can be considered a basic and good medium used for microbial growth. P solubilizing fungi and bacteria comprise 0.1–0.5% and 1–50%, respectively, of the whole microbial population in specific entities of the soil surface (Walpola and Yoon 2012). The biodegradation terminology is generally used in relation to pollution and waste management, ecology, and is specifically connected to bioremediation (Verma and Jaiswal 2016). The bioremediation process can be divided into three different phases. First, through attenuation naturally, without any amplification, human waste products could be vanished by innate microorganisms. Second, biostimulation functions in which both oxygen and nutrients in a system are applied in a way that improves their effectiveness and speeds up biodegradation as well (Mohamed et al. 2018a). Third, microorganisms during bioaugmentation can also be linked with related systems. These complementary organisms could be identified effectively as compared to flora observed natively degrading the targeted contaminants (Diez 2010).

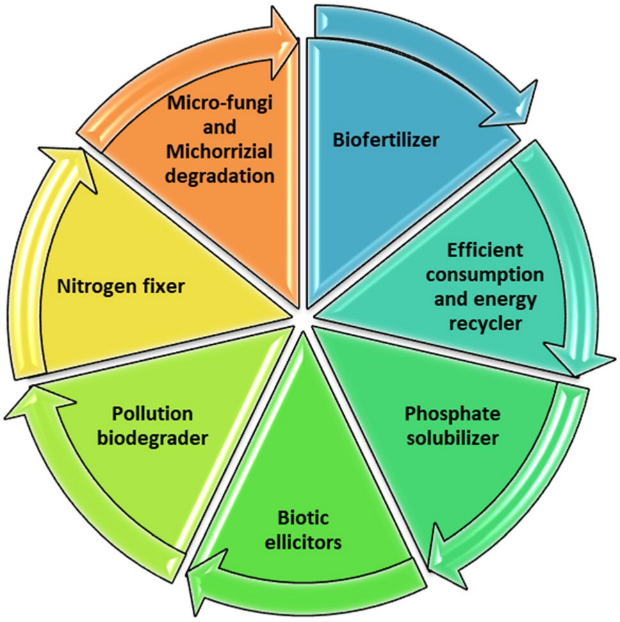

Fig. 1 Microbiomes of plant and soil with diverse parameters of plant growth promoting biofertilizers for soil fertility and PGP under the stressed and natural conditions

Microorganisms that are capable of effective use in pollutant degradation and of fast adaptation to a specific case in a short time period are required in remedial technology which is feasible (El-Mahdy et al. 2021). Being vital in finding solutions to various problems, microorganisms for the benefit of mankind have encountered the maintenance of a quality environment. Likewise, they are used to affect the health of humans and animals, ecological protection, genetic engineering, and industrial and municipal waste management positively. Responses that were not possible through physical or chemical engineering have been found to be cost-effective and feasible via microorganisms (El-Mahdy et al. 2021).

Microorganisms that are naturally associated with plants, such as probiotic bacteria, can enhance the growth of the host plant, as well as increase yield when applied in sufficient amounts (Sharma et al. 2012; Nadeem et al. 2015) (Fig. 1). Some probiotic bacteria that promote plant growth include *Acinetobacter, Alcaligenes, Arthrobacter*, and *Serratia*. Their beneficial effects on host plants are due to the production of phytohormones, antibiotics and lytic enzymes, as well as nitrogen fixation, mineral nutrient solubilization, and systemic resistance. They also help in improving the structure of soil by mixing its particles while secreting extracellular metabolites and breakdown of complex insoluble nutrients and organic materials into simple forms accessible to plants and induced disease and stress resistance (Maheshwari et al. 2012; Song et al. 2012; Prakash et al. 2016). This review aims to collect information about the use of microorganisms in bioleaching, biodegradation, bio composting, nitrogen fixation, phosphorous solubilization, soil fertility improvement, phytoremediation, biofertilizer and biodegradation process to remediate polluted environments and focus on the omics techniques reportedly used in environmental monitoring to combat the pollution load.

Environmental pollution

Agrochemicals are a category of various chemicals used and associated activities in agriculture. These chemicals or compounds include pesticides, chemical fertilizers, substances that promote growth, soil stimulants, feed additives, veterinary substances (Gupta 2019; Mohamed et al. 2012, 2018b). To increase agricultural production, balance and sustain land nutrients and the health of the soil, agrochemicals play an important role, protecting crops from infections and thus increasing crop yield. In the past, vast amounts of agrochemicals have been used to improve food production for the increasing world population (Meena et al. 2020b). In other terms, those agrochemicals played an important part in the success of the green revolution in most developed countries where the level of production was many times higher than before (Gupta 2019). The world population will be about 9.3 billion by 2050, up from today 7.2 billion (Meena et al. 2020a). This rise in the population would lead to a high increase in the demand for food and feed agrochemicals. For global food demand, therefore, a sustainable approach is needed. Agrochemicals are unavoidable in this sense. Therefore, farmers face a crucial challenge and agrochemicals therefore play a growing role (Meena et al. 2020a). The high quality and usability of chemicals and their benefits contribute significantly to their market development. Nonetheless, global food safety problems still demand agrochemicals on a steady basis. However, the environmental and human health toxicity of these agrochemicals is still a challenge (Meena et al. 2020a). Any agricultural activity that relies on agrarian chemicals or fertilizers is often evaluated by growing income at reduced costs based on their economic efficiencies and benefits. However, their possible environmental impacts are clearly less considered (Udeigwe et al. 2015). Using pesticides typically improves plant development by destroying pest, insects, and weeds to avoid or minimize plant illnesses. Moreover, the application of fertilizers will provide the land with many nutrients needed to grow crops and increase yields (Meena et al. 2020a).

Pesticides

Pesticides are regularly used in pest management in modern agriculture, but their overuse has threatened not only the environment but plants as well as these pesticides have the ability to pass through living tissues. A pesticide is a substance used for repelling, destroying, or avoiding pests. Pesticides are categorized generally as herbicides, fungicides, and insecticides depending on the target killed. Increased food demand due to population growth has forced people to use pesticides to boost crop production (Jayakumar et al. 2019). As a result, environmentally friendly pest control alternatives should be sought. The toxic and harmful effects of pesticides can be minimized using different microorganisms. Out of these microorganisms, bacterial strains not only reduce the toxic effect of pesticides but also promote growth as well. These bacterial strains include genera like *Bacillus, Gordonia, Azospirillum, Klebsiella, Serratia, Azotobacter, Paenibacillus, Enterbacter*, and *Pseduomonas* (Shaheen and Sundari 2013). Furthermore, apart from these, *Actinomycetes* have been reported to degrade and transform the ill effects of pesticides. Hydrolases and esterases are some of the key lytic enzymes produced by microorganisms while oxidases and transferases are found to be the major group of enzymes involved in the pesticide degradation process (Ortiz-Hernandez et al. 2013). As a result, using growth-promoting microorganisms is one of the most important ways to decontaminate soil with pesticides in a sustainable manner.

Heavy metal

Due to increased anthropogenic activities, rapid industrialization and modern agricultural practices in recent years, heavy metal elements have been increasingly polluted and are one of abiotic stresses on plants, especially in developing countries (Akladious and Mohamed 2017; El-Beltagi et al. 2020). At any stage of the life cycle of plants, heavy metals play an important role. Unbalanced doses can, however, lead to both cytotoxic and genotoxic effects and therefore to plant genome instability. Soil that is polluted with heavy metals such as cadmium and lead, produces one of the plant's essential stress conditions. Several studies have shown that seed germination and seedlings are affected by heavy metal stress (Mohamed 2011). Inorganic and organic fertilizers, sewage sludge, water contaminated by irrigation, pesticides, and fungicides are the most important sources of heavy metals in agricultural soil. In the industrial and neighboring countries, heavy metals are extracted at high temperatures, such as smelling and casting, in particulate and steam forms into the atmosphere (Wuana and Okieimen 2011). In addition, heavy metal elements may be added to the soil from other industrial sources, such as plastic processing, textiles, microelectronics, wood storage, and paper processing. The internal effluents often lead to a higher level of heavy metals and other chemical elements in the rivers and lakes (Tchounwou et al. 2012). About 400 plant species are reported to remediate and cleanse sites having contamination. For instance, Zn and Cd affected contaminated soils can be effectively remediated by many *Brassica* sp. such as *B. napus, B. rapa* and *B. junica*. Plants and microbial activity are reduced in highly contaminated soil with metals, while low to moderately contaminated soil with heavy metals can be efficiently controlled by phytoremediation. Root length, regional temperature, soil, and contaminant nature are some of the criteria for plant species selection for phytoremediation (El-Mahdy et al. 2021). Plants with hyper-accumulator characteristics (low biomass) such as *Thlaspi* and *Arabidopsis* species or hypo-accumulator characteristics (high biomass) such as willow for phytoremediation of contaminants. Heavy metal accumulation varies with plant species and many researchers have reported that varying amounts of heavy metals are found in different plant species or even genotypes of species grown on the same soil. Grasses with high levels of biomass, effective stabilization of soil, rapid growth, and strong resistance, are the most widely used and evaluated plant species in the phytoremediation process as compared to shrubs and trees. Furthermore, grasses are also adaptable to sites of environmental stress and low nutrient concentrations. Moreover, leaching, erosion and runoff can be reduced due to the larger surface area of their fibrous roots and rigorous soil penetration. All these factors combine to make grass an effective tool for phytoremediation and soil stabilization (Table 1).

Phytoremediation strategies

The key concept of phytoremediation is to effectively clean up the environment from pollutants using green plants and microorganisms. This technology has great potential in the tropics, favoring plant growth and enhancing microbial activity due to climatic conditions (Liu et al. 2020). This method is applicable when metal contaminants have spread over far-flung places or the plant's root zone. In regions where pollution is low or moderate, phytoremediation is an economical, energy efficient and pleasing method.

Plants use different approaches to decontaminate wastewater, sludge, soils, and sediments, etc. which can be broadly termed as phytoremediation. Various phytoremediation technologies such as phytofiltration, volatilization, extraction, degradation, and stabilization, are used to eliminate organic and inorganic pollutants from contaminated places (each having a different mode of action) that greatly depends on the cleanup level, contaminant type, plant types and condition of the site (Jacob et al. 2018). Figure 2 represents the different assisted phytoremediation strategies. The absorption of pollutants removed from the field which are accumulated in different organs using plants in combination with crops to cleanse the soil of organic contaminants and heavy metals is termed phytoextraction. Taking up stowed contaminants from an aqueous medium using different plant organs (roots, excised shoots and seedlings) is known as phytofiltration. The halting or binding of pollutants with soil particles (thereby reducing their availability) using plants is known as phytostablization (Basu et al. 2020). The use of plants in taking contaminants and volatilizing them into the atmosphere is known as phytovolatilization. The degradation of organic contaminants using related microbes and plants is termed phytodegradation. The use of microbes in increasing organic contaminant degradation in the root zone of plants is known as rhizodegradation (Table 1).

Table 1 Plant adaptation strategies against heavy metal stress

Type of Phytoremediation	Mechanism	Heavy metals treated
Phytoextraction	Plants tend to accumulate heavy metals in harvestable parts	Cd, Co, Cr, Ni, Hg, Pb, Se, Zn
Phytostabilization	Immobilization of metal through absorption and accumulation by roots via vacuolar sequestration or cell wall binding, precipitation within the root zone (rhizosphere) by formation of complexes	Pb, Zn, Cu
Phytostimulation	Root exudates promote development of microorganisms (bacteria and fungi) within rhizosphere that are capable of degrading heavy metal contaminants into nontoxic products	Petroleum hydrocarbons, polyaromatic benzene, toluene, etc
Phytovolatilization	Plants take up contaminants, convert them into volatile forms, and release them into atmosphere via transpiration	Hg, Se, chlorinated solvents (carbon tetrachloride and trichloromethane)
Phytodecomposition	Both terrestrial and aquatic plants take up organic compounds and store or degrade them to less toxic or nontoxic by-products	TNT, DNT, nitrobenzene, nitrotoluene, chlorinated Solvents
Rhizofiltration	Plant roots absorb, concentrate, or degrade heavy metals from contaminated liquid effluents	Cd, Co, Cr, Ni, Pb, Hg, Se, Zn

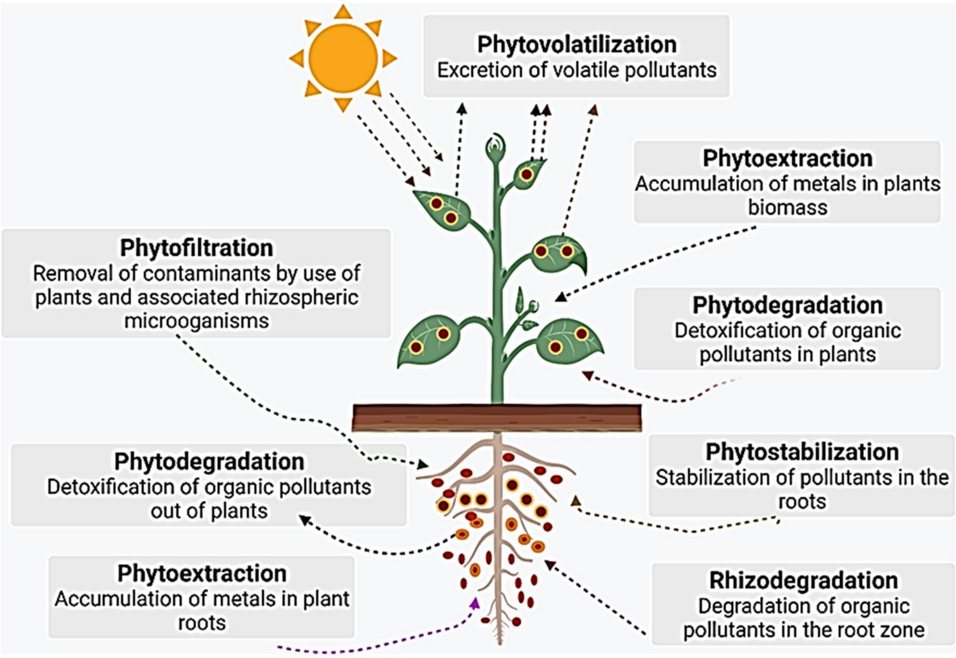

Fig. 2 Mechanism action of rhizosphere bacteria activates phytoremediation method in soil contaminated with metals enhance mobilization of metals

Role of microorganisms in sustainable agriculture

Due to their ability to produce plant growth-promoting substances/metabolites such as phytohormones, siderophores, and ammonia, microorganisms can increase soil nutrient availability through the solubilization of phosphate, nitrogen fixation, and organic compound mineralization.

Microbes as biofertilizers

Biofertilizers made from microorganisms are applied to the plant's surroundings, soil, or seed, which then live with the plant and increase plant growth because these microbes make available, supply, and uptake nutrients to the host plant. Biofertilizers are more beneficial for small and marginal farmers because they are easily available and accessible to them. Bacteria, cyanobacteria, and fungi are some of the important microbe groups used for the production of biofertilizers. These microorganisms form a symbiotic association with host plants. The nature and function of microbial fertilizer depend on the supply of N and P (Thomas and Singh 2019). Table 2 gives the major groups of biofertilizers (Singh et al. 2014).

Microbes as nitrogen fixer

The breathing air comprises about 80% of atmospheric N_2. Even though nitrogen is the most profuse and pervasive element in the air, it is still not available to plants, making it the most limiting nutrient to the growth of the plant. There are some groups of bacteria with the capability to fix atmospheric nitrogen, hence forming a different association with plants that are:

(1) Free living bacteria which fix atmospheric nitrogen in the soil.
(2) The host plant assimilates the ammonium produced by the nitrogen-fixing endophyte.
(3) Some bacteria live in the rhizosphere of plant roots without having endophytic symbioses.

These systems can fix nitrogen substantially, but there are some differences observed due to environmental conditions or plant–microbe associations. These microorganisms coexist with the host plants, allowing for efficient utilization of fixed nitrogen, thereby reducing denitrification, volatilization, and leaching (Hoffman et al. 2014).

Azospirillum

Azospirllum, besides rhizobia, is the most reviewed and used bacteria with notable advantages for a wide array of plant species (Fukami et al. 2016). Beij reported for the first time that the genus *Spirillum* was found and reclassified by Dr. Johanna Dobereiner and a group in Brazil during the 1970's due to the nitrogen fixing capability of nitrogen found in the atmosphere, such as *Azospirillum* (Tarrand et al. 1978). Later, *Azospirillum* discovered a diazotrophic, substituted nitrogenous fertilizer in crops including wheat (Cassan et al.

Table 2 The important groups of microbial fertilizers

Group of biofertilizers	Subgroup	Examples
Nitrogen fixing	Free-living	*Beijerinkia, Azotobacter, Derxia, Anabaena, Aulosira, Stigonema, Cylindrospermum, Clostridium, Tolypothrix, Stigonema, Nostoc, Rhodospirillum, Klebsiella, Rhodopseudomonas, Bacillus polymvxa, Chromatium and Desulfovibrio*
	Symbiotic	Frankia, Symbiotic (*Azorhizobium*, *Rhizobium*, *Allorhizobium*, *Sinorhizobium*, *Mesorhizobium*, *Bradyrhizobium*), *Trichodesmium*, and *Anabeana azollae*
	Associative	*Azospirillum* spp. *(A. brasilense, A. lipoferum, A. amazonense, A. halopraeferens, and A. irakense), Acetobacter diazotrophicus, Herbaspirillum* sp., *Azoarcus* sp., *Bacillus*, *Klebsiella*, *Alcaligenes*, *Pseudomonas*, and *Alcaligenes*
Phosphorus (microphos)	Phosphate solubilizers	*Bacillus subtilis, B. megaterium var. phosphaticum, B. polymyxa, B. circulans, Penicillium* sp., *Pseudomonas straita, Trichoderma, Rhizobium, Aspergillus awamori, Rhizoctonia solani*, *Achromobacter*, *Burkholderia*, *Aereobacter*, *Erwinia*, *Microccocus*, *Flavobacterium*, and *Agrobacterium*
	Phosphate mobilizing	Arbuscular mycorrhiza *(Glomus* sp., *Gigaspora* sp., *Acaulospora* sp., *Scutellospora* sp., *and Sclerocystis* sp.*)*, ectomycorrhiza *(Laccaria* spp., *Pisolithus* spp., *Boletus* spp., *Amanita* spp.*)*, ericoid mycorrhizae *(Pezizella ericae), and* orchid mycorrhiza *(Rhizoctonia solani)*
Micronutrients	Potassium solubilizing	*Bacillus edaphicus, B. mucilaginosus, and Paenibacillus Glucanolyticus*
	Silicate and zinc solubilizing	*Bacillus subtilis, Thiobacillus thioxidans, and Saccharomyces* sp.
Growth promoting	Plant growth promoting rhizobacteria	*Agrobacterium, Achromobacter, Alcaligenes, Arthrobacter, Actinoplanes, Azotobacter, Bacillus, Pseudomonas fluorescens, Rhizobium, Bradyrhizobium, Erwinia, Enterobacter, Amorphosporangium, Cellulomonas, Flavobacterium, Streptomyces, and Xanthomonas*

2015), rice (Marks et al. 2015) and many others (Fukami et al. 2016). Among the 20 species mentioned so far, *A. lipoferum* and *A. brasilense* are the most important of all for different genetic and physiological studies (Fibach-Paldi et al. 2012). *Azospirillum* has a great potential to colonize a great number of perennial and annual plants which can fix atmospheric nitrogen. It is also not limited to a specific host; hence it is considered as a general potent root colonizer. *Azospirillum* is reported to improve growth and production in many crops, especially carrots, tomatoes, peppers, and eggplants (Bashan et al. 2013).

Atmospheric nitrogen is converted to ammonium at low nitrogen levels under micro-aerobic conditions by *Azospirillum* using a nitrogenous complex. Two components of these enzymes, i.e. denitrogenase protein (MoFe protein, *Nif* DK) and denitrogenase reductase (Fe protein, *Nif* H) are used in this mechanism. The denitrogenate protein contains an iron-molybdenum co-factor which is the N_2 reduction site while an electron transfer from the electron donor to the nitrogenase protein occurs by the denitrogenase reductase protein (Burris and Roberts 1993). A genetic study revealed that *A. brasilense*, one of the species of *Azospirillum*, helps with nitrogen fixation. Both the nitrogenous components are linked by *A. brasilense Nif* HDK genes which are similar to those of *Klebsiella pneumoniae Nif* HDK genes (Perroud et al. 1985). Moreover, processing and electron transport involve *Nif* and fix (additional genes) and are isolated from *A. brasilense* which are helpful in the nitrogenase enzyme complex, nitrogen fixation regulation and FeMo cofactor biosynthesis (Frazzon and Schrank 1998).

Azospirillum is known to be a commercially utilized and studied bacterial plant growth promoter nowadays. It not only has the capability of atmospheric nitrogen fixation but is also effectively found in many pathways of plant growth promotion, specifically in phytohormone biosynthesis. By activation of defense mechanisms in plants, they also play a role in plant protection against biotic and abiotic stresses, for example, induced systematic resistance and tolerance (Fukami et al. 2018) as shown in Fig. 3.

Azotobacter

Azotobacter is a Gram-negative aerobic soil dwelling, free-living spherical-shaped bacteria forming thick-walled cysts belonging to the family Azotobacteriaceae that comprises of species like *Azotobacter paspali*, *A. nigricans, A. vinelandii, A. chroococcum, A. beijerinckii* and *A. armeniacus* (Salhia 2013). *Azotobacter* sp. is usually known as an aerobic nitrogen fixer and is free living (Sivasakthi et al. 2017). The genus *Azotobacter* was discovered by a Dutch botanist, Beijerinck, in 1901. Among the 6 species of *Azotobacter*, the first aerobic free-living nitrogen was reported as *A. chroococcum*. These bacteria utilize atmospheric nitrogen gas for their cell protein synthesis. This cell protein is then mineralized in soil after the death of *Azotobacter* cells thereby

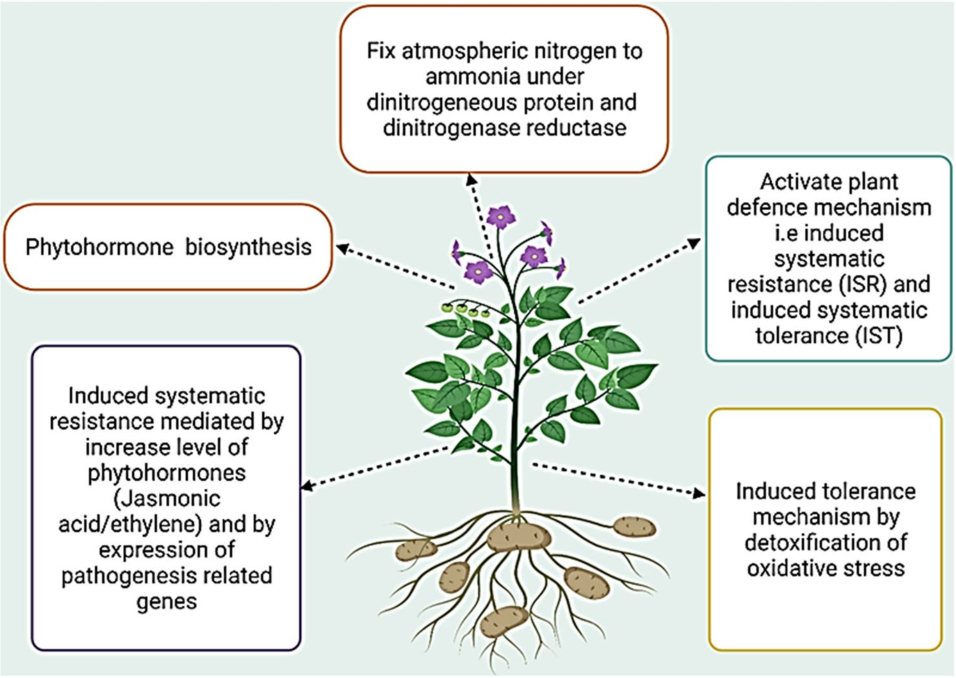

Fig. 3 Mechanisms of tolerance of biotic and abiotic stresses induced by *Azospirillum* in plants (Fukami et al. 2018)

contributing towards the nitrogen availability of the crop plants. They pose advantageous impacts on the crop growth and yield through the biosynthesis of biologically active substances, instigation of rhizospheric microbes, production of phytopathogenic inhibitors, alteration of nutrient uptake and eventually magnifying the biological nitrogen fixation (Lenart 2012). *Azotobacter* has the capability of nitrogen fixation (15–20 kg ha^{-1}) and acts as a bio-inoculant that enhances 10–12% of crop productivity (Jaga and Singh 2010). *Azotobacter* is one of the alternative methods instead of chemical fertilizers and pesticides. Treatment with *Azotobacter* caused increment in root and shoot dry matter content, plant height, root length, and disease control (Arora et al. 2018).

Blue green algae (BGA) and *Azolla*

Free-living cyanobacteria, also known as blue green algae, fix atmospheric nitrogen through photosynthesis. Initially found in rice fields, they are now found in a wide range of ecosystems, including the oceans, forests, and wetlands. Cyanobacteria require a humid climate with adequate water, temperature, light, and nutrient availability. The dominant nitrogen fixers include *Anabaena, Aulosira, Culothrix* and *Nostoc* (Sahu et al. 2012). Cyanobacteria can increase soil fertility, thereby increasing crop yield. *Anabaena* and *Nostoc*, which live in soils, rocks and form symbiotic relationships with plants in liquid medium can fix about 20–25 kg ha^{-1} of nitrogen (Kour et al. 2020). They have evolved multiple specialized cell types, including nitrogen-fixing heterocysts, spore-like akinetes, and the cells of motile hormogonia filaments. Vegetative cells, under favorable conditions, are common photosynthetic cells. Heterocysts are thick-walled cells that are specialized structures for atmospheric nitrogen fixation into ammonia, nitrates, and nitrites as they contain vital nitrogenous enzymes while spores forming cells under stress conditions are known as akinetes. Cyanobacteria contain vitamins, phytohormones, and amino acids which are growth-promoting substances. They also improve water-holding capability, decrease saline stress, suppress weed growth and improve the availability of phosphorus in the soil. Moreover, they are also potent biodegrading organisms proficient at elevating different types of pollutants (Vijayakumar and Manoharan 2012).

Anabaena-azollae symbiosis

Anabaena azollae, a potential biofertilizer is a symbiotic cyanobacterium, used for rice production and forms a relationship with ferns (Parween et al. 2017). *Azolla* can fix atmospheric N_2 in a symbiotic relationship with *Anabaena azollae*, which is a cyanobacterium. It can fix 40–60 kg ha^{-1} of atmospheric nitrogen in rice and is considered as an alternative to synthetic nitrogenous fertilizers (Kour et al. 2020). The colonies of *Anabaena azollae* are related to the shoot apex of *Azolla* which contains generative filaments (without heterocysts). The nitrogenase activities are increased by cyanobacterial filaments which are present in the cavity of older leaves that terminate to grow (Adams et al. 2012). Chloroplast present in the mesophyll cells of *Azolla* can also reduce photosynthetic carbon by an important enzyme called RuBisCO (Rae et al. 2013).

Acetobacter

Acetobacter, anaerobic nitrogen fixation agent, is a key inoculant for sugarcane, forming colonies with their roots and a symbiotic relationship with coffee (Wani et al. 2016). The genus was divided into two groups, the *Acetobacter aceti* group and the *Acetobacter pasteurianus* group phylogenetically (Yamada 2016). The species of the genus were characterized by the oxidation of acetate and lactate, acetic acid production from ethanol, no production of 2,5-diketo-D-gluconic acid from D-glucose, and UQ-9 as the major (Malimas et al. 2017). *Acetobacter diazotrophicus* was first reported as an acetic acid bacterium capable of nitrogen fixation (Gillis et al. 1989). *Acetobacter nitrogenifigens* was the second species to possess a nitrogen-fixing ability and considered to be a plant growth-promoting bacterium as well (Pedraza 2016). The two nitrogen-fixing species are quite distant phylogenetically; the former was classified in the *A. pasteurianus* group, and the latter was in the *A. aceti* group. Because of the high nitrogen content, symbioses with rhizobia and actinorhizal are important organisms for biofertilizers. About 70% (150 kg ha^{-1}) of the nitrogen requirement of sugarcane is fixed by *Acetobacter* (Boddey et al. 1995).

A. aceti is economically important because it is used in the production of vinegar by converting the ethanol in wine into acetic acid. The acetic acid created by *A. aceti* is also used in the manufacturing of acetate rayon, plastics production, rubber production, and photographic chemicals. *A. aceti* is considered an acidophile, which means it can survive in acidic environments, due to having an acidified cytoplasm which makes nearly all proteins in the genome to evolve acid stability. *A. aceti* has become important in helping to understand the process by which proteins can attain acid stability (Wani et al. 2016).

Microbes as phosphate solubilizer and mobilizer

Global food scarcity is one of the most serious challenges of the twenty-first century, putting pressure on the agricultural sector to increase food demand in the future. To cope with the situation, scientists put a great deal of effort into centralizing the soil plants interactions. It needs a better understanding of the agro-ecosystem and synergy to utilize agricultural land in an ideal way. Presently, due to the green revolution, food availability is not a problem to deal with, rather the timely distribution to far lands are an issue. The green revolution proved to be one of the most acknowledged human achievements that transformed developing countries (food deficient) into developed ones (food surplus). Macro and micronutrient deficiencies have been tackled through the green revolution, such as the use of chemical fertilizers, superphosphates are commonly recommended to overcome phosphorus deficiencies.

These fertilizers are often in limited supply in host countries; therefore, their import is a major outlay for poor farmers in developing countries. After the green revolution, increased agricultural production entailed the addition of phosphate to increase soil phosphate status but also improved crop production. The multiple applications of chemical fertilizers are not only expensive but also an environmental risk (Battaglia et al. 2018) which adversely affects the microbial population in the rhizosphere and bioenergy production (Kumar et al. 2019). There is also a risk of xenobiotic contamination in manure used to fertilize agricultural soils (Meena et al. 2020a; Molaei et al. 2017). P is generally known to be involved in plant growth and development (promoting the development of roots, rapid maturity of the plant, and the production of seeds), biotic stresses, and the efficiency of water use (Magalhaes et al. 2017). Its preliminary controls vital physiological processes controlling plant growth and development which are mainly dependent on energy utilization by two phosphate molecules such as adenosine diphosphate and triphosphate (ADP and ATP) (Krishnaraj and Dahale 2014). P constitutes 0.05% of soil content where only a small quantity is available to plant biologically a fraction of 0.2% of the total dry mass of the plant (Alori et al. 2017). P exceeds (10 mM) in the bioavailable form which is distributed to all plant tissues through special transporters and transducers. The reduced quantity of P in the soil solution apparently makes the element a vital factor for plant growth, given that P is relatively substantial for crop production (Bhat et al. 2017). Additionally, the activity of P as deposition and fixation, pH dependent may lead to P availability being reduced, and thus low efficiency of fertilizers containing P. Likely, due to precipitation and adsorption of P in lime soils, this severely hampered the efficiency of available P (Sanders et al. 2012). Therefore, a significant challenge faced by modern agriculture and technology requires advanced solutions to improve the bioavailability of P.

Microbes as phosphate solubilizer

The way of meeting global food demand is a challenge, the use of conventional phosphorus (P) fertilizers potentially causes water and soil pollution through waterway eutrophication, depletion of soil fertility, and accumulation of toxic elements such as excess amounts of selenium (Se), arsenic (As) in the soil. Phosphorus is a vital nutrient for the growth and development of plants, it is available in soil in a huge quantity but in most plants it is unavailable (Oteino et al. 2015) that may lead to the problem of the application of phosphate fertilizer in agroforestry exercises. Soil phosphorus depletion is a major limiting factor in the yield of agroforestry globally (Turner et al. 2018; Nikolic et al. 2011). Seed inoculation with phosphate solubilize microorganisms (PSM) is an environmentally friendly budding strategy to improve crop production. Numerous microorganisms are capable of mineralizing insoluble phosphate and releasing plant available soluble P, resulting in high crop yields. Despite their importance in soil fertility, PSM has yet to replace chemical fertilizer on a commercial scale due to a lack of understanding of the mode of action and proper application in sustainable agriculture (Alori et al. 2017).

There are various microorganisms that secrete enzymes and organic acids (nuclease, phytase, and phosphatase) for insoluble P degradation in soil (Bashan et al. 2013). However, they are less efficient in their natural state (Collavino et al. 2010). However, it is important to inoculate P solubilizing microorganisms with high efficiency in an artificial way to increase the quantity of available P (Prodhan et al. 2019). Therefore, improved P absorption and use by crops is of great importance both ecologically and economically (Abbas et al. 2018). As a result, inoculation with highly efficient mutant strains is critical (Prodhan et al. 2019) to crop P absorption, which represents both ecological and economic perspectives (Abbas et al. 2018). Numerous soil microorganisms have been reported which can reverse the process of phosphate fixation by solubilizing inorganic soil phosphate compounds (Zhu et al. 2012). Soil borne bacteria (*Pseudomonas, Enterobacter*, and *Bacillus*) and fungi (*Penicillium* and *Aspergillus*) capable of plant growth promotion have been proven effective as phosphate solubilizers (Babalola and Glick 2012).

Microbes as phosphate mobilizer

Leguminous plants (nitrogen fixing plants) require more P than non-leguminous plants (those that need mineral N fertilizer) as the nodule's formation involves a high P level. An inadequate concentration of P is a prerequisite for biological nitrogen fixation (BNF) and deficiency results in reduced BNF potential. P fertilization will not only give rise to enhance number and mass of nodules, but a better BNF potential too. Phosphate solubilizers are soil microbes that play a vital role in P transformation with a combination of other abiotic factors like soil type and environment. These microorganisms affect the soil pH of the rhizosphere, eventually producing chelating agents that lead to the solubilization of phosphates (Zhu et al. 2012). Soil borne bacteria, fungi, and *Actinomycetes* species are predominately considered as phosphate solubilizing microorganisms (Babalola and Glick 2012). Agricultural lands are a huge sink of organic and inorganic P available either in unavailable or in immobilized form. PSM is responsible for the mobilization of unavailable P to plants by direct or indirect means. The net P in degraded and productive reserves remains constant (Fonte et al. 2014), but the level in later reserves has increased to 40%. The reason enumerated in the study is the availability of P that is inorganically high in degraded soil and is adsorbed by the soil. Generally, P in inorganic form is known to be highly reactive with metallic ions (calcium, aluminum, and iron) present in such strata which help P adsorption by 75–90%. The external application of P fertilizers may not solve the problem as a very low amount will be available for plants due to high adsorption (Zhu et al. 2012). Microbial inoculants called P-mobilizing microbes help in recovering obstacles by mobilization of available P, even in insoluble ground form (Yadav et al. 2014; Owen et al. 2015).

Microbes as nutrient manager

Remotion of the top layers of the soil profile which are rich in nutrients and organic matter can cause depletion of nutrients, water holding capacity, soil structure, and loss of fertility (Montgomery 2007). Agricultural crop production mainly depends on better soil structure and the availability of nutrients in such types of soil to support the growth of plants. Globally, synthetic fertilizers with excessive use have polluted soil and air with a residual effect on water as well. Thus, some essential efforts could be required as an alternative and environmentally friendly solution to hazardous and costly chemical fertilizers. This encouraging approach to soil structure improvement and bioavailability of nutrients can be enhanced by microbes like bacteria or fungi, either soil borne or applied as biofertilizers. These organic amendments or bacterial and fungal inoculants can be taken as a significant option incorporated as nutrient management in crop integration strategy in degraded types of soils (Medina et al. 2010). Introducing all these inoculants can translocate, achieve, mobilize and mineralize phosphorous (P), potassium (K) and iron (Fe) resources, and also helps with atmospheric nitrogen fixation and surging organic matter (Leifheit et al. 2014; Ahemad and Kibret 2014).

In the early ages, agricultural specialists were used to practicing the application of organic fertilizers and earthworms for soil fertility improvement (Rashid et al. 2014a, b; Shah et al. 2013). These practices have proved to be useful in the agroecosystem while managing and improving nutrients in the soil (Lubbers et al. 2013). However, the cost of maintaining a healthy microbial population may have a direct impact on crop price indices, whereas these microorganisms, bacteria, and fungi may be found in some earth constituents such as soil and water. These are known to be the cheapest microbial beings enhancing soil aggregates and soil pores formation, improving soil fertility (Miller and Jastrow 2000), as polysaccharides with outer cellular layers are considered beneficial and responsible for aeration and porosity in the soil forming aggregates (Gupta and Germida 2015).

Microorganisms as probiotics and their potential to enhance crop productivity

Probiotics are defined as live microorganisms that when administered in adequate amounts, confer a health benefit on the host. Health benefits have mainly been demonstrated for specific probiotic strains of the following genera: *Lactobacillus, Bifidobacterium, Saccharomyces, Enterococcus, Streptococcus, Pediococcus, Leuconostoc, Bacillus,* and *Escherichia coli* (Hill et al. 2014). Even though microbial cells found in nature can be used to formulate and use commercially effective probiotics, they must first be identified and studied for disease-causing potential, isolation, and probiotic perspective to gain approval for use (Soccol et al. 2010). Numerous studies have also been reported on probiotics in humans, where plant probiotics, on the other hand, have attained great attention these days. Plant probiotics, as cultured microbials, have plant growing potential with features such as phosphate solubilization, nitrogen fixation, siderophore production, and boosting plant immunity against various diseases (Nadeem et al. 2015; Sharma et al. 2012). While secreting extracellular metabolites, combined soil particles, and breaking down of insoluble nutrients and compound organic materials into simpler forms enhance the structure of the soil and make them all available for the growth of plants and encourage resistance to diseases and stress (Song et al. 2012; Maheshwari et al. 2012; Abd El-Rahman et al. 2012; Abd El- Rahman and Mohamed 2014).

Probiotics have been extensively researched for human and animal health (Thomas et al. 2015; Nakatsuji et al. 2017). On the other hand, it has been reported that beneficial microbes of plants may also contribute to improving the quality of sustainable production in the agricultural sector (Timmusk et al. 2017). The increased population with challenges of demands and needs on a daily basis is a great issue to be faced by the agricultural division. Production and yield of crops have been disturbed by climate change effects, varied temperature, and rainfall patterns, and also urbanization, which has affected agricultural sectors and water quality either for irrigation or drinking purposes (Olesen and Bindi 2002). However, new investment techniques, policies and studies should be carried out to mark a strong relationship between crops and probiotics on an influential track in the environment (Mauchline and Malone 2017). Plant probiotics reported *as Phyllobacterium*, performed as root colonial, are a source of vitamin C enhancer and plant growth promoter in strawberries (Flores et al. 2015), where these in the form of *Pseudomonas* play a significant role through biotic control action (Hu et al. 2017).

Role of microorganisms in biodegradation and energy recycling

The global environment faces huge stress on natural resources due to population pressure, the industrial revolution, and rapid urbanization. Pollution is caused by large quantities of waste produced by the intuitive activities of modern advancement (Raj et al. 2018). Large-scale industries consume a huge amount of raw materials, leading to radioactive waste and chemical contaminants piling up to a large extent, making the environment and biosphere unhealthy. Materials and energy losses arose due to the increase in the production of waste (Jhariya et al. 2018). Hence, significant management of these waste materials should be given prime importance (Sharma and Shah 2005).

One of the effective measures for a sustainable and healthy environment is to introduce an effective system for waste management using beneficial microbes. Among the most common methods are the incineration method, sanitary landfills, recycling and avoidance and reduction (Mondal and Palit 2019). Whether the sustainable environment should be free from pollutants or pollutants must be clean. Recently, waste management and biodegradation of contaminants have been made possible due to the use of microorganisms. Biodegradation, biotransformation, bioremediation, and composting are some of the biotechnological tools to reduce a large number of contaminants efficiently (Banerjee et al. 2018). Green algae (*Cladophora* sp.) have been reported to have a high range for removing toxic metals, making them potential and alternative agents for waste management. The smooth running of wastewater treatment methods involves a potent role in microbial ecology (Maghraby and Hassan 2018). Therefore, microorganisms are cost-effective, environmentally safe, and eco-friendly and can also be used in different biotechnological systems for the treatment of waste (Mondal and Palit 2019). The process exploits contemporary methods and tools using a wide range of microbes in an organized way without distressing the ecosystem. Biodegradation, biotransformation, and composting are some of the common and effective techniques used in the waste management process, while *Scenedesmus platydiscus, Staphylococcus* sp., *Bacillus* sp., *Streptococcus* sp., *Corynebacterium* sp., *Chlorella vulgaris*, and *S. quadricaud*are some of the beneficial microorganisms used in the process of waste management (Mondal and Palit 2019). Biodegradation of solid wastes can be achieved by different types of microorganisms which include fungi, mesophilic bacteria, protozoa and actinomycetes that colonize the heaps of these wastes (Gajalakshmi and Abbasi 2008).

Different types of bacteria can degrade hydrocarbons that are taken from the aquatic environment. These include *Corynebacterium* sp., *Streptococcus* sp., *Enterobacter*, *Staphylococcus* sp., *Shigella* sp., *Acinetobacter* sp., *Alcaligenes* sp., *Klebsiella* sp., *Escherichia* sp., and *Bacillus* sp. Which have the powerful capability to degrade hydrocarbon. Many bacteria can remove and remediate the pesticide atrazine from the soil (Wang et al. 2013). Zhang et al. (2012) isolated *Rhodobacter sphaeroides* W16 and *Acinetobacter lwoffii* DNS32 from the soil in cold areas subjected to long-term atrazine application in China. Both bacteria can produce reactive oxygen species (ROS), but subsequently, ROS is scavenged in response to the oxidative stress caused by atrazine. This may be the reason for the lower oxidative damage in atrazine-degrading bacteria cells upon atrazine exposure. Furthermore, dichlorodiphenyltrichloroethane from contaminated soil is degraded by *Bacillus* sp., *Staphylococcus* sp. and *Stenotrophomonas* sp. (Kanade et al. 2012). Moreover, biodegradation of toxic materials in contaminated soil can be made possible by endophytic and rhizospheric bacteria associated mostly with plants (Divya and Deepak 2011). These rhizoshperic bacteria, especially *Pseudomonas* sp., can also help with the recycling of nutrients and fixation of nitrogen (Meena et al. 2015). Besides nutrient recycling, *Pseudomonas* along with *Bacillus* sp. can also efficiently degrade xenobiotic compounds as well (Janssen et al. 2005). Among the waste materials, plastic is considered the most vulnerable material in almost all types of ecosystems. This is due to its non-degradable properties which can result in severe environmental hazards. The accumulation of plastic materials can significantly hamper both aquatic as well as terrestrial habitats (Mondal and Palit 2019). Microbial degraders and their metabolic enzymes are among the environmental agents that participate in the degradation process, which results in the conversion of the carbon in the polymer chains into smaller biomolecules or into carbon dioxide and water (Mir et al. 2017). Biodegradation by various microbes, such as heterotrophic bacteria and fungi, is reported for both biodegradable and non-biodegradable polymers (Muhamad et al. 2015). Table 3 describes some of the various plastic materials which can be degraded by different types of bacterial strains.

Role of microorganisms in pollution biodegradation

Biodegradation refers to the decay of organic substances as performed by a wide range of living organisms, primarily fungi, yeast, and bacteria, but also possibly other organisms in the microbiological sense. In a very large variety of compounds such as hydrocarbons like oil, polyaromatic hydrocarbons, radionuclides, metals, and polychlorinated biphenyls endeavor to harness the naturally occurring, and surprising catabolic diversity to accumulate, transform, and degrade in bioremediation and biotransformation techniques (Ogilvie and Hirsch 2012).

Over a long period, highly poisonous organic compounds such as pesticides, fuels, dyes, polycyclic aromatic hydrocarbons (PAHs), and polychlorinated biphenyls (PCBs) have been produced and left behind in the environment as an indirect or direct use in the last few decades. Metals and radionuclides are some different synthetic chemicals released by native vegetation that are highly resistant in comparison to

Table 3 Bacteria used in plastic degradation

Plastic	Bacteria	Reference
Polyurethane	*Corynebacterium* sp., *Pseudomonas* sp., *Arthrobacter globiformis, Bacillus* sp.	Howard et al. (2012)
Low-density polyethylene (LDPE)	*Rhodococcus ruber C208, Brevibacillus borstelensis 707, Rhodococcus ruber C208, Staphylococcus epidermidis, Bacillus cereus C1*	Chatterjee et al. (2010)
High-density polyethylene (HDPE)	*Bacillus* sp., *Micrococcus* sp., *Vibrio* sp., *Arthrobacter* sp., *Pseudomonas* sp.	Balasubramanian et al. (2010)
Degradable polyethylene	*Rhodococcus rhodochrous ATCC 29672* *Nocardia steroids GK 911, Bacillus mycoides*	Seneviratne et al. (2006)
Polyethylene bags	*Pseudomonas aeruginosa, Pseudomonas putida, Bacillus subtilis*	Nwachukwu et al. (2010)
Polyethylene carry bags	*Serratia marcescens, Bacillus cereus, Pseudomonas aeruginosa, Streptococcus aureus, Micrococcus lylae*	Aswale and Ade (2009)
Degradable plastic	*Pseudomonas* sp., *Micrococcus luteus, Bacillus subtilis, Streptococcus lactis, Proteus vulgaris*	Priyanka and Archana (2011)
Polycaprolactone	*Pseudomonas sp., Rhodococcus sp.*	Urbanek et al. (2017)
Microplastic	*Proteobacteria, Bacteroides*	De Tender et al. (2015)

organic matter that degrades when introduced into the environment (Diez 2010). Microbial fungi can be well defined in terms of the organism's alliance consisting of essential eukaryotic organisms, which tend to range from unicellular yeasts to significant molds of mycelium. Fungi are important for microbiota degradation because they break down organic matter into dissolved form and aid in the decay of carbon in the biosphere. Fungi, as compared to other microorganisms, can be observed in all those places with low pH and moisture, which can benefit them from decomposing organic substances. These are fitted out with complexes of multi enzymes, and thus, are more efficient at breaking down compounds, specifically polymeric herbals. They have the capability to penetrate and colonize easily due to the hyphal structures they possess, and therefore, can move and sort out supplements within their mycelium (Matavuly and Molitoris 2009). On the other hand, mycorrhiza is recognized as a beneficial association between a fungus and the roots of vascular plants. Mycorrhiza remediation is termed as the use of mycorrhiza in bioremediation. Fungi also play a vital role in recalcitrant polymers recycling like lignin and reducing harmful wastes/pollutants from the environment either by application of filamentous or unicellular fungi.

Some biodegradable pollutants

Hydrocarbons

Hydrocarbons are a naturally occurring compound that contains both hydrogen and carbon elements. Aromatic hydrocarbons, linear hydrocarbon branched hydrocarbons, and cyclic hydrocarbons are the three types (Saadoun 2015). The simplest aromatic compound is benzene (C_6H_6) in its structure and aliphatic hydrocarbons are further classified into alkanes, alkenes, and alkynes (Das and Chandran 2011). PAHs have been identified as a class of dynamic hydrophobic contaminants that can be observed in soil sediments and air. The primary source of PAH pollution is waste products of industry (Adeniji et al. 2019), whereas studies have been carried out for more than twenty years, just because of its environmental persistency, prevalence, and toxicity (Okere and Semple 2012). Absorption of PAHs into soil rich in organics, sediments, and accumulation in aquatic beings, especially in fish, can also be transferred through the consumption of seafood from one organism to another. PAH biodegradation can be counted as significant to the reduction of chemical contaminants and cycling carbon (Adeniji et al. 2019). *Bacillus* is found as the largest bacteria degrading hydrocarbons, where the bacterial strains fit into the *Pseudomonas* genus, and support biodegradation of aromatic hydrocarbons obtained from Gram-negative soil. Different genera, *Aeromonas, Bacillus, Mycobacterium, Rhodococcus* and *Corynebacterium* have been reported to have biodegrading pathways (Chen et al. 2015).

Polychlorinated biphenyls (PCBs)

Polychlorinated biphenyls (PCBs) as a combination of synthetic organic compounds, because of their chemical balance, non-combusting, electrical insulating properties and raised boiling point, have been used in industrial, mechanical, and commercial applications (Anezaki et al. 2015). They can also be used as dyes, plastics, heat transfer equipment, and copy paper with no carbon. However, these could be toxic as they cause malignant growth and function as disrupters of the endocrine (Nie et al. 2012; Seeger et al. 2010). Both aerobic and anaerobic bacteria have the capability of PCB transformation. Lower PCBs are oxidized by aerobic microbes, while higher PCBs are reductively dehalogenated by anaerobic microbes (Seeger et al. 2001). Plant growth promoting rhizobacteria (PGPR) are soil borne microbes which can be either found in the colonial form in adventitious plants or roots promoting advanced development in plants (Saharan and Nehra 2011). Rhizoremediation is the process of exposing plants collectively to specific microorganisms while constructing pollutant extraction structures (Jing et al. 2007).

Pesticides

Pesticides are known as a combination of various substances proposed for mitigating, repelling and destroying pests. There are two kinds of pesticides, persistent which has the capability to resist degradation, and non-persistent which can be degraded rapidly (Bolognesi and Merlo 2011). The degradation of pesticides results in the discharge of the initial compounds from coal oxygen (CO_2) and air (H_2O). Through pesticide degradation, microorganisms use energy. However, degradation effectiveness relies on different parameters such as heat, pH of land, humidity levels, the biodegradation of pesticides via microbes has an important effect on the health of agrarian crops. In addition, microbes also have other important benefits, such as variety, wide dispersal, and adjustment of different cellular processes (Cui et al. 2012). The degradation of imidacloprid and metribuzin is also engaged in the degradation of *Burkholderia cepacia* type CH-9 (Madhuban et al. 2011). *Acinetobacter calcoaceticus* degraded bifenthrin (Tingting et al. 2012), i.e., a synthesized pesticide. The capabilities for cypermethrin (CMP) degrading are noted as photosynthetic bacterium (GJ-22) (Yin et al. 2012). Another research shows very elevated biodegradable permethrin capacities and cypermethrin pesticides in *Pseudomonas putida* and *P. mendocina* (Mendoza et al. 2011). A bacterial consortium of six bacterial strains, namely *Stenotrophomonas maltophilia, Proteus vulgaris,* *Vibrio metschnikovii, Serratia ficaria, Serratia* spp., and *Yersinia enterocolitica* has the capacity to degrade tetrachlorvinphos (Akbar and Sultan 2016). With the prospective implementation of the degradation of chlorpyrifos (CP) pesticide, various types of *Streptomyces* were recognized (Briceño et al. 2012). As lindane was known to be degraded by *Fusarium verticilloides* and later used the degraded products as a carbon source (Pinto et al. 2012). The biodegradation behavior against aldicarb, atrazine, and alachlor has been shown in another unacclimatized blended community (Nyakundi et al. 2011) of bacteria and white-red funguses. Methomyl and diazinon (pesticides) were degraded by red fungi extracted from contaminated plants (Sagar and Singh 2011). Endosulfan (pesticide) can be removed from environment by applying strains of microbes (*Aspergillus*) (Javaid et al. 2016). Various fungal strains also possess DDD pesticide degradation ability (Ortega et al. 2011). Odukkathil and Vasudevan (2013) stated that degradation of various types of pesticides can be achieved by *Phanerochaete chrysosporium*.

Dyes

Dyes can be widely used in cosmetics, rubber products, fabric, drugs, paper, printing, and various other products (Venkataraman 2012). The largest and most substantial class of manufactured dyes are aromatic compounds (–N=N–) known as azo dyes, consumed in manufacturing applications (Venkataraman 2012). Such dyes are unproductively biodegradable due to the structures and wastewater treatment which contain them including physical and chemical techniques. For example, oxidation, adsorption, filtration, coagulation–flocculation, and electrochemical methods. The biological process for dye removal from the effluent is partially dependent on the use of fungi and bacteria that decolorize synthetic dyes produced by various chemical methods (Lade et al. 2015; Placido et al. 2016). Senthilkumar et al. (2014) studied *Phanerocheate chrysosporium*, which produces extracellular enzymes such as, lignin peroxidase, manganese peroxidase and laccase mediated decolorization of various dyes. Singh and Singh (2010) examined another fungus named *Trichoderma harzianum* which has been employed for cleaning the effluent from the textile industry. A fixed amount of Congo red and Bromophenol blue dyes were completely degraded by fungal mycelium using a semi-solid PDA medium. This study showed that the medium containing Congo red, Direct green, Bromophenol blue, Acid red and Basic blue inhibited the growth of *Trichoderma harzianum* in comparison to the control treatment (growth in the medium without dye). Out of these dyes, Bromophenol blue was found to show the maximum growth inhibitory effect (43%). For bioremediation, diverse fungal cultures were used due to their characteristic features such as fast growth, a large amount of biomass and wide hyphal spectra which made the fungus more effective as compared to bacteria (Anastasi et al. 2013).

The main advantage of working with bacteria is that they are easy to culture and can grow more quickly as compared to other microbes. The dye degradation ability of bacteria can easily be enhanced by molecular genetic manipulation. Bacteria can catabolize chlorinated and aromatic hydrocarbon based organic pollutants, which can be decomposed using them as an energy source (carbon source) (Yang et al. 2014) and have the ability to oxidize sulfur-based textile dyes to sulphuric acid (Nguyen et al. 2016). Many studies have shown favorable results in identifying bacteria which can degrade different azo-based dyes at a faster rate. Different bacterial groups under traditional aerobic, anaerobic and under extreme oxygen deficient conditions cause an azo dye reduction for decolorization. The chemical reaction during the reduction of the azo dyes starts with the breaking of azo bonds (—N=N—) under an aerobic environment by the azoreductase enzyme which results in a colorless solution of aromatic amines (Mendes et al. 2015). Wang et al. (2014) reported that metabolites formed as a result of dye reduction can further be catabolized either by aerobic or anaerobic processes. Several bacteria have been reported to possess the ability to degrade azo dyes into colorless amines (Sudha et al. 2014). Ali et al. (2011) studied the behavior of aerobic bacteria that were able to propagate in the presence of azo compounds. The intermediate sulfonated amines formed in this process may be aerobically degraded.

Radionuclide

A radionuclide is considered as an atom having an unstable nucleus, and with abundant accessible energy in communication with radiation molecules formed recently, through transformation on the inner side or inside the nucleus. The formation of alpha and beta particles can result when radioactive decay passes through a radionuclide and results in gamma ray emission (Petrucci et al. 2002). Heavy metal bioremediation can be accomplished through biotransformation, in which, unlike organic pollutants, heavy metals can be reduced or gradually transformed into a structure. Biosorption (physiochemical sorption of metals to the surface of the cell), intracellular accretion, bioleaching (mobilization of heavy metals through methylation responses or organic acid excretion), conversion of enzyme catalysis or bio-mineralization etc. are the systems where microorganisms perform action on heavy metals, as shown in Fig. 4 (Lioyd and Lovley 2001).

Heavy metal

Heavy or toxic metals such as Cd, As, Hg, Pb, or Se, are nonessential elements, whereas Zn, Mo, Cu, Mn, Co, and Ni are essential elements which are essential for plant growth, development, and metabolism. Increased concentrations of the latter elements up to supra optimal values can lead to poisoning (Mohamed et al. 2016a, b; Latif and Mohamed 2016; Akladious and Mohamed 2017; El-Beltagi et al. 2020; Sofy et al. 2020a; Moustafa-Farag et al. 2020). Many microorganisms, especially various strains of bacteria, especially *Bacillus* sp., *Alcaligenes faecalis, Pseudomonas aeruginosa* etc., have the ability to remove different kinds of heavy metals like Cu, As, Cd and Zn from polluted sites (Ashoka et al. 2017) (Fig. 5). Rubber is one of the other waste materials which can be effectively recycled by sulphur oxidizing and reducing bacteria like *Thiobacillus ferroxidans* and *Pyrococcus furiosus*, hence considered as an efficient measure to manage rubber wasters (Keri et al. 2008). Table 4 illustrates that various pollutants can also be bio-transformed using beneficial microbes to mitigate the harmful effects of pollutants on the environment.

The application of omics tools in bioremediation

Phytoremediation has been one of the cost-effective remediation techniques in use for years now. The purpose of plants to attenuate the xenobiotics makes them a more feasible method than physical and chemical processes. The transgenic plants result in either degradation of the xenobiotics or increased resistance of the plant to the pollutant (Callaghan 2013; Chandran et al. 2020). The industrial effluents are estimated to be 5% saline and hypersaline. Microbial diversity is less as compared to non-extreme environments. Thus, degradation of the pollutant has become a significant problem in such regions. The halophilic microorganisms are proposed to be a favorable applicant for the remediation of hypersaline environments. The genomic sequence analysis discloses the genes that might be involved in degradation. Further, proteomic analysis of the microbe in the presence of different concentrations of hydrocarbons affirms the genes involved in the degradation (Wei et al. 2017). Application of techniques like RT-qPCR quantifies the expression of various hydrocarbon-degrading genes and thus provides an insight into the shift in the microbial communities (Yergeau et al. 2012).

Microorganisms utilize organic compounds as a sole carbon source and to manage their biomass and assemble suitable enzymes and cofactors for their oxidation/reduction. Hence, the organic compounds should be nontoxic or less damaging to microbial growth. The microorganisms participating in the metabolic degradation of organic compounds are heterotrophic. Molecular methods like cloning, fingerprinting, amplified ribosomal intergenic spacer analysis (ARISA), restriction fragment length polymorphism (RFLP) are used to study microbial diversity (Fig. 6). These techniques yield information on how environmental factors change the microbial community structure. More advanced techniques like Illumina and 454 sequencing are also being used to study the microbial diversity of polluted areas. Different approaches are used to remediate contaminated soils (Yergeau et al. 2014). The present scenario includes the implementation of various omics tools (Table 5) to study the microbial diversity of the contaminated soil with that of uncontaminated soil, thus providing better insight for the development of new remediation techniques or improving the already existing methods. The uptake of heavy metals like mercury can lead to biomagnification. The heavy metals

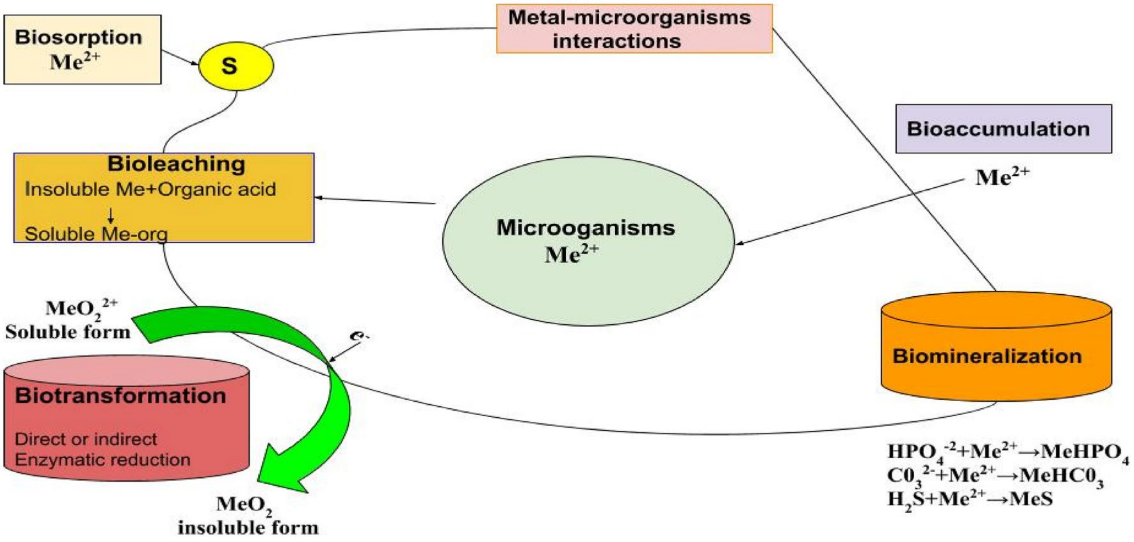

Fig. 4 Mechanism for microbial process used in technologies for bioremediation adapted from Lloyd and Lovley (2001)

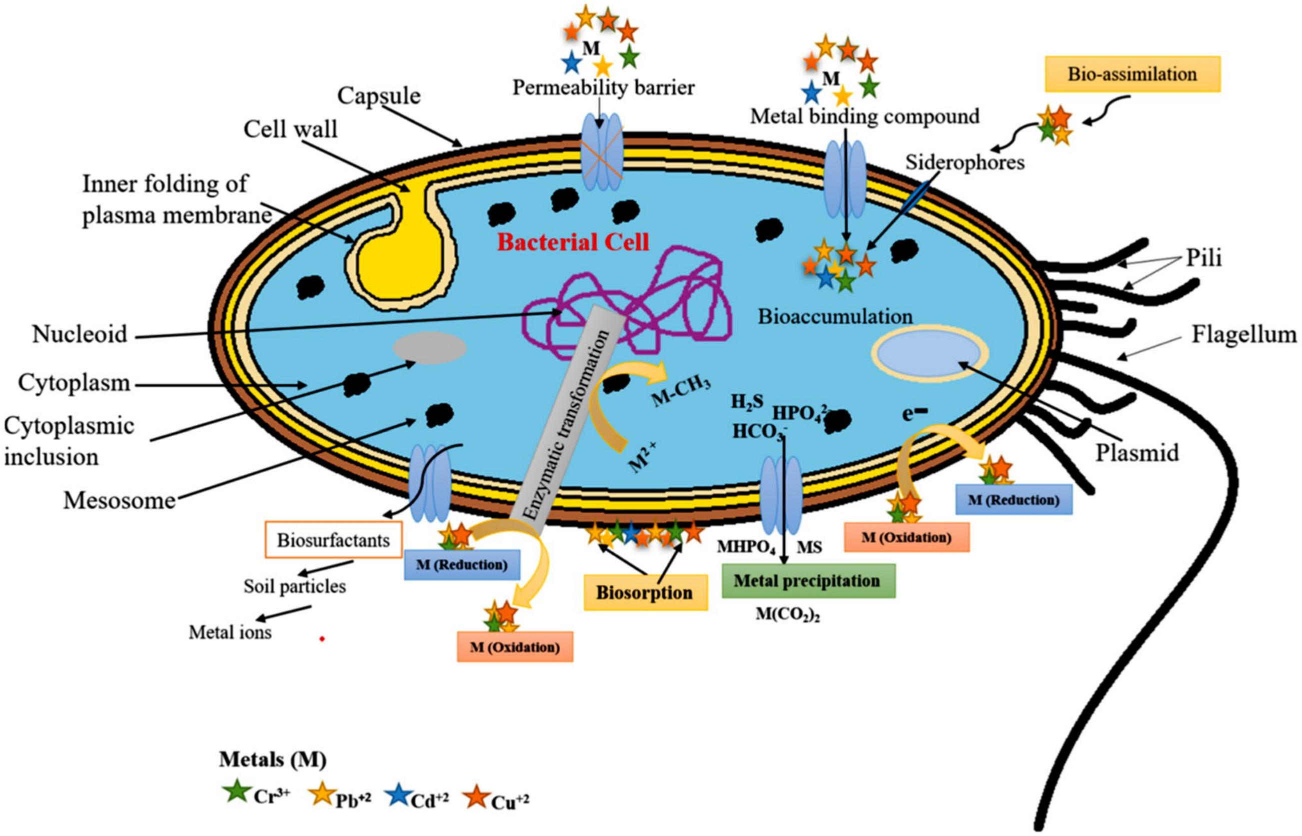

Fig. 5 Microbes interaction with metals and their biochemical process during metal detoxification at the contaminated site (Sharma et al. 2021)

Table 4 Relationship between plant and microbes for tolerance and phytoremediation of heavy metals

Heavy metals	Plant species	Microbes	References
Zn	*Brassica juncea*	*Bacillus mucilaginosus* HKK-1	Rathore et al. (2019)
Cu	*Cajanus cajan*	*Proteus vulgaris* KNP3	Rai et al. (2020)
Ni	*Cicer arietinum*	*Pseudomonas* sp.	Ahemad (2019)
Ni	*Ricinus communis*	*Pseudomonas* sp. M6	Rai et al. (2020)
Cr	*Eichhornia crassipes*	*Pycnoclavella. diminuta*	Rai et al. (2020)
Cu, Cd, Zn	*Eucalyptus grandis, Ailanthus altissima*	*Glomus mosseae*	Abbaslou and Bakhtiari (2017)
As	*Trifolium repens* L.	*Glomus versiforme*	Wang et al. (2018)
Ni	*Helianthus annuus*	*Claroideoglomus claroideum* (BEG210)	Ma et al. (2019)
Cu, Pb, Cd, Zn, Ni, Cr	*Helianthus annuus* L.	*Funneliformis caledonium, Funneliformis mosseae*	Zhan et al. (2018)
Fe, Cu, Cd, Pb, Zn	*Glomus mosseae*	*Vetiveria zizanioides*	Kafil et al. (2019)
Pb, Cr, Cd, Ni	*Glomus aggregatum, Funneliformis mosseae, Rhizophagus intraradices, Rhizophagus fasciculatus*	*Zea mays* L.	Singh et al. (2019)
Cd	*Funneliformis mosseae*	*Lycopersicon esculentum* L.	Li et al. (2020)
Cu	*Rhizophagus irregularis*	*Phragmites australis*	Wu et al. (2020)
As	*Aspergillus flavus* MTCC 25041	*Oryza sativa*	Mohd et al. (2017)
Pb, Cu	*Serendipita indica*	*Ocimum basilicum*	Sabra et al. (2018)
Cd, Pb	*Fusarium sp.* CBRF44	*Brassica napus*	Shi et al. (2017)
Cd, Pb, Zn	*Mucor sp.* CBRF59, *Fusarium sp.* CBRF14	*Brassica napus*	Deng et al. (2014)

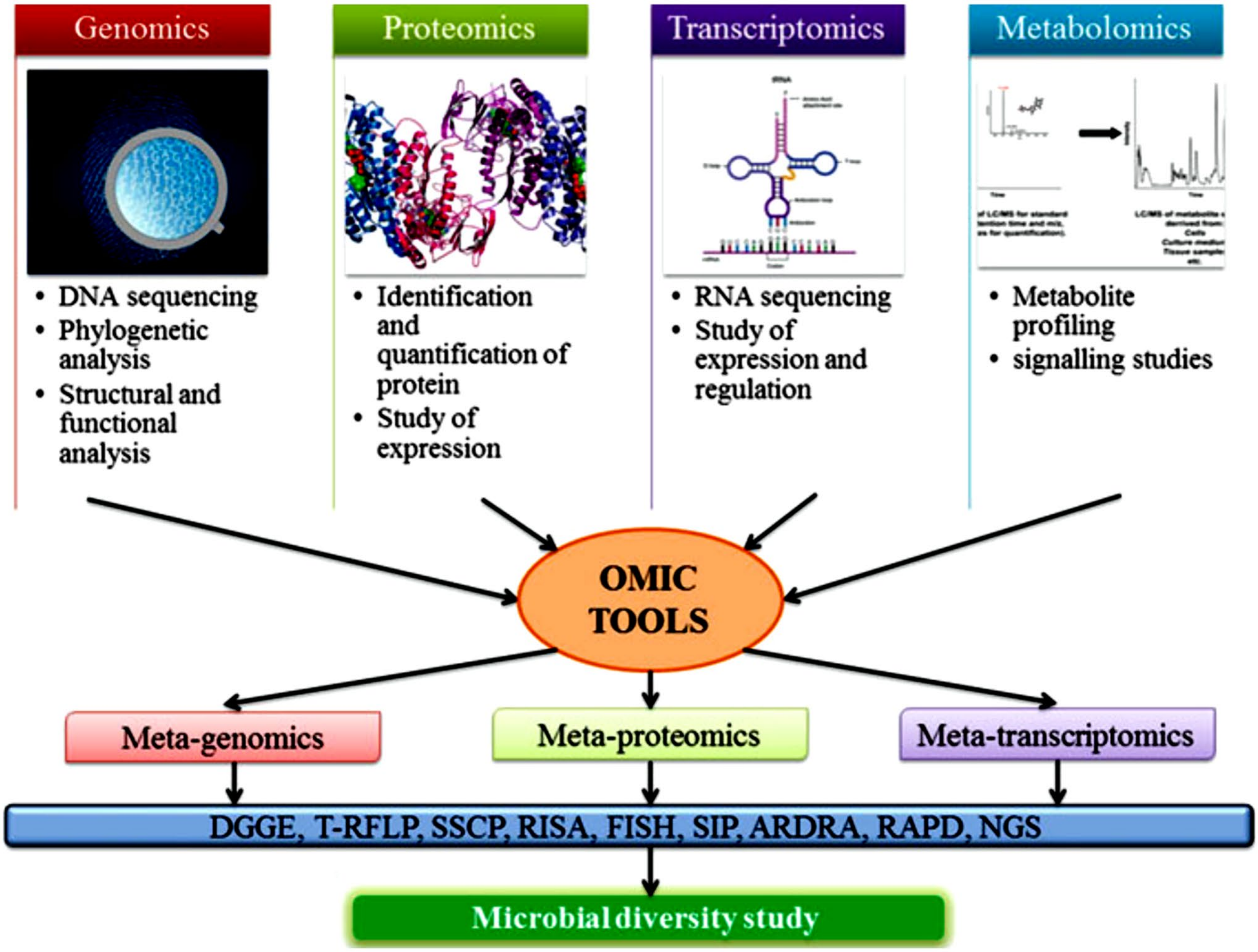

Fig. 6 Application of omics tools in soil bioremediation

interrupt the energy metabolism of the plants. Transcriptomics helps in the early detection at molecular levels. The changes in the genes in the presence of a low and high concentration of metals can also be studied (Beauvais-Flück et al. 2017). The tools of genomics like DGGE (denaturing gradient gel electrophoresis) of 16S rRNA enhance the study of several communities of microbes in non-polluted and polluted soils and, therefore, help in the isolation of heavy metal-resistant bacterial strains (Utturkar et al. 2013).

Molecular approaches like genomics, proteomics, transcriptomics, metabolomics, fluxomics, etc. give more vision about the microbial communities inhabiting a particular environmental niche (Gupta et al. 2020). These methods have accelerated the study of microbial community structure, which was earlier dependent on culture technologies (Gutleben et al. 2018). It possesses the potential to evaluate the genetic diversity of environmentally pertinent microorganisms and analyze novel functional genes related to the catabolism of pollutants (Meena et al. 2019). Omics technology is a molecular biological approach that facilitates the analysis of biomolecules like DNA, RNA, proteins, and metabolites from individual organisms and the whole community at the same time (Gutierrez et al. 2018). To study gene regulation in the anthropogenic environment, mRNA expression (transcriptomics), and whole community expression (metatranscriptomics) can be studied (Roume et al. 2015).

Genomics and 16S rRNA for bioremediation

The identification of microbial communities using modern genomic tools has enabled the detection of distinctive microorganisms that were not approachable by culture-based techniques. Gene amplification (using PCR) and sequencing techniques have proven exceptionally useful in evaluating the microbial community (Gołebiewski and Tretyn 2020). 16S rRNA gene sequence analysis can be used for a complete assessment of microbial diversity by selectively amplifying and sequencing the hypervariable regions of the 16S

Table 5 Application of advanced omic approaches in soil bioremediation

	Contaminants	Omic tools	Applications	References
Biotransformation	Mercury	Transcriptomics	Analyzing metabolic pathway and tolerance response	Beauvais-Flück et al. (2017)
	Uranium, nickel, cobalt, cadmium	Genomics	To determine the genomic sequence of *Caulobacter* sp. strain OR37	Utturkar et al. (2013)
	Cadmium and zinc	NSG	Pyrosequencing revealed the interaction between *Arabidopsis halleri* and the microbial community	Muehe et al. (2015)
	Cadmium	Proteomics, transcriptomics	Study the response of the plant to cadmium, viz., high through put techniques	Villiers et al. (2012)
Biodegradation	Hydrocarbon, pesticides, herbicides	Metagenomics	Degradation of herbicides and pesticides by identifying a novel gene	Jayaraman et al. (2019)
	Fertilizers	Metagenomics	Analysis of organically fertilized zoo soil using metagenomics	Meneghine et al. (2017)
	Hydrocarbons	Proteomics	Assessment of microbial function and diversity in petroleum-associated environments	Pal et al. (2019)
			Biodegradation and structural analysis of aniline degrading bacteria	Hou et al. (2018)
		Genomics	Subtraction of cDNA revealed presence of zinc finger motifs in the high accumulators of organic pollutants	Inui et al. (2015)
			Genomic analysis and enrichment of root endophytic bacteria from *Populus deltoides*	Utturkar et al. (2016)
			Analysis of pyrene degradation by bacterial consortia	Wanapaisan et al. (2018)
		Functional Metaproteome	Analysis of microbial community structure using rhizoremediation	Kotoky et al. (2018)
		Next-generation sequencing	Microbial distribution analysis in PAH-contaminated landfill soil	Koshlaf et al. (2019)
			Bacterial diversity analysis in heavy oil well reservoir	Krolicka et al. (2017)
		Transcriptomics	Analysis of alkane degradation by *Pseudomonas extremaustralis*	Tribelli et al. (2018)
			Analysis of drainage effect on paddy soil microbiome	Abdallah et al. (2019)
	Herbicide	Metabolomics	Study of alachlor biodegradation by *Paecilomyces*	Szewczyk et al. (2015)

rRNA gene. It is a highly efficient and cost-effective technology easily accessible by various bioinformatics tools and has become a frequently used technique for profiling intricate microbial communities (Han et al. 2020). 16S rRNA was used to elucidate the composition of microbial communities and the multifariousness of the dioxygenase genes in the soil of a coal tar mixing plant to study the genetics of PAH degradation (Sakshi and Haritash 2020). Kou et al. (2018) reported 16S rRNA gene amplicon sequencing to study the abundance and diversity of the microbial community in soil polluted with heavy metals like lead, zinc, and copper in Shanghai. 16S rRNA gene sequencing along with membrane fatty acid profile was used to identify soil bacterium *Pseudomonas* species capable of degrading polyurethane from a site containing an abundance of fragile plastic waste (Cárdenas Espinosa et al. 2020).

Metagenomics

A major share of the microorganisms in the environment is non-culturable under laboratory conditions (Rashid and Stingl 2015). Metagenomics can be used to explore such non-culturable microbes thriving in different environments (Bilal et al. 2018). Metagenomic sequences reveal DNA sequences of uncultured microbes thriving in the environment which can be used for new biotechnology applications. The metagenomic information will enable researchers to integrate pure culture studies with genomics (Hodkinson and Grice 2015). It uses the pool of environmental genomes of microorganisms which increases the probability of discovering unique genes and diverse pathways with new enzymes containing highly specific catalytic properties (Awasthi et al. 2020).

The metagenomic approach was used to characterize genes and metabolic pathways associated with the degradation of phenol and other aromatic compounds in sludge from a petroleum refinery wastewater treatment system (Silva et al. 2013). Gaytán et al. (2020) combined physical and chemical analysis with metagenomics to explicate probable metabolic pathways associated with polyurethane degrading to alleviate plastics and xenobiotics pollution. The persistent impact of petroleum pollutants on the taxonomic and metabolic structure of microbial mats was studied using metagenome and enriched mRNA metatranscriptome sequencing (Aubé et al. 2020).

Transcriptomics

The subdivision of genes transcribed in an organism is known as transcriptome. It is a potent network amid the proteome, genome, and cellular phenotype. It is also called gene expression profiling because it provides an understanding of the up or down-regulation of genes under various environments in microbial communities. Comparative transcriptomics revealed highly upregulated degradation pathways and putative transporters for phenol to improve phenol tolerance and utilization by lipid accumulating *Rhodococcus opacus* PD630 (Yoneda et al. 2016). Transcriptome analysis of activated sludge microbiomes decoded the role of the nitrifying organisms in heavy oil degradation (Sato et al. 2019). Transcriptome analyses of crude oil degrading *Pseudomonas aeruginosa* strains revealed the significance of differentially expressed genes implicated in crude oil degradation (Das et al. 2020).

Proteomics

A proteome is the set of proteins formed inside a cell, tissue, organ, or organism. The branch of science that explores and study of proteomes is called proteomics. Proteomic analysis helps in decoding molecular mechanisms, metabolic pathways, post-translational modifications, etc. inside the cell. It has enabled the tracking and analysis of universal expression of proteins in microorganisms residing in contaminated areas due to human-induced activities (Kim et al. 2004). Meta-proteomics or community proteomics is the analysis of complete protein profiles from microbial communities inhabiting a specific environment (Hart et al. 2018). It is also defined as a functional genomics approach because it helps in exploring the protein expression pattern of one organism and helps in generating a protein map of all expressed proteins by one organism thriving in a selected environment (Meena et al. 2019).

The metabolism of an organism is dependent on environmental factors. Changing external stimuli triggers changes in protein expression and assessing such changes can be effective in bioremediation approaches (Mattarozzi et al. 2017). Several studies report the characterization and quantification of proteins expressed by microorganisms present in diverse ecosystems like soil, marine, and freshwater environments, sediment, soil, activated sludge, acid mine drainage biofilms, human or animal microbiome and plant associated microorganisms (Wang et al. 2016).

Metaproteomics has also been reportedly used to distinguish metabolic activities of microbes important for the bioremediation of contaminated environments. The expression of catabolic enzymes, such as catechol 2,3-dioxygenases, 1,2-cis-dihydrodiol dehydrogenase, and 2-hydroxymuconic semialdehyde was reported in Sphingomonadales and uncultured bacteria assisting in the bioremediation of compost (Bastida et al. 2016). A culture-dependent community proteomic study reported that the soil microbial community becomes convoluted in hydrocarbon-contaminated soil compared to untreated soil (Bastida et al. 2014).

Metabolomics

A metabolome is the total metabolites in an organism and the study of the metabolite profile of a cell within a given condition is called metabolomics (Beale et al. 2017). A cell produces a range of primary and secondary metabolites when subjected to external stress which has enabled us to understand and analyze the effect of environmental conditions on the metabolome of organisms (Malla et al. 2018). Metabolome-based approaches have facilitated to establish models that can predict microbial activities under bioremediation strategies.

Metabolomics analyzes the metabolites produced by the cell in response to changing environmental conditions which in turn provides information about the regulatory events in a cell (Krumsiek et al. 2015). These metabolites can be used as bioindicators to screen the biological effects of contaminated waste for a better perception of the environment. Proteogenomic and metabolomic approaches were used to identify the pathways and enzymes used by marine bacteria *Mycobacterium* sp. DBP42 and *Halomonas* sp. ATBC28 to degrade plasticizers like dibutyl phthalate (DBP), bis (2-ethyl hexyl) phthalate (DEHP), and acetyl tributyl citrate (ATBC) (Wright et al. 2020).

Fluxomics

Fluxomics is a quantitative approach that studies the rates of metabolic reactions, changes in metabolic rates inside a biological individual. Fluxome is the complete set of metabolic fluxes in a cell which provides information about several cellular processes, thus it is a distinctive phenotypic characteristic of cells. Flux analysis offers vital information about the phenotype since it assesses the metabolome in its functional communications with the genome and environment (Dettmer et al. 2007).

Metabolic flux analysis was used to investigate the constitutive metabolic network for the co-utilization of sugar and aromatic carbons in *Pseudomonas putida* (Kukurugya et al. 2019). Flux distributions using 13C-MFA (Metabolic flux analysis) was used to identify the effect of phenol on the carbon metabolism in wild-type *Escherichia coli* cultured under varying phenol concentrations (Kitamura et al. 2019).

Challenges and future perspectives of phytoremediation in environmental waste management

Phytoremediation is an efficient green technology and a demanding field of study has gained wide recognition during the past few decades. Plants treated with heavy metals were grown using hydroponic techniques under laboratory conditions in many experiments, but researchers admitted that solution culture is very different from soil even though promising results were obtained under in vitro conditions. The biggest problem with soil conditions is the binding of metal particles with soil in insoluble form, reducing their availability. There are several limitations to large-scale field application of organic pollutants, even though they are successfully used in many demonstration projects. To overcome such issues, genetically modified plants specifically produced for the phytoremediation process are used nowadays. Besides, research in the field of phytoremediation is naturally interdisciplinary, which really requires complete basic knowledge of ecology, soil chemistry, microbiology and plant biology, and environmental engineering as well. More studies need to be conducted to understand the interactions among principal factors in the rhizosphere, including plant roots, soil microbes, and metals. Advancement in technology of chromatographic and spectroscopic techniques needs to be enhanced to understand the future of plant tissues containing metal ions, where the plant tolerance and hyper-accumulation involved can also be improved in return. Due to low solubility, metal absorption by roots is restricted, which needs advanced environmentally friendly and cost-effective research on chemicals carrying chelating properties which will also improve metal bioavailability. For such purposes, some plant species could also be identified which have the capability of rotation for maintaining effective extraction rates.

Conclusion

Research scientists have focused on environmental sustainability which can be considered as a highlighted issue these days. Plants use different approaches to decontaminate wastewater, sludge, soils and sediments, which can be broadly termed as phytoremediation. Pesticides, fungicides, and heavy metal-based chemical fertilizers are some of the agrochemicals which are nowadays used in agriculture systems around the world and are considered as one of the major contenders for causing pollution of the world's surface water. Microbial activities involve environmental restoration and carbon cycling on a global scale via biodegradation. Microbial probiotics have the potential to enhance plant growth and promote biocontrol. *Azospirillum* consumes nitrogenous complexes and converts atmospheric nitrogen to ammonium in aerobic conditions at low nitrogen levels. Microbes solubilizing phosphorous make the insoluble P form into an available form which improves the quality, yield, and growth of crops. The increase in P bioavailability in soil is caused by the most proficient P solubilizers, *Pseudomonas, Bacillus, Aspergillus, Rhizobium*, and *Penicillium*. The usage of beneficial microorganisms is an effective way to be introduced to biodegradation of environmental contaminants, waste management, and sustainable ecology. Fungi are important for microbiota degradation because they break down organic matter into dissolved form and aid in the decay of carbon in the biosphere. Therefore, ecological biotechnology favors solving and tackling all these issues using beneficial microbes or technological bioremediation. To carry out and maintain these activities, it is important to promote the application of natively available beneficial microbes and work towards the improvement of their biodegradation capabilities for the sake of a sustainable future and the environment. Modern omics approaches like genomics, proteomics, transcriptomics, metabolomics, and fluxomics have eliminated the boundaries to study the mechanisms involved in various bioremediation pathways. It has enabled the incorporation of new strategies for efficient bioremediation processes. Omics approaches have the potency to anticipate microbial metabolism in polluted environments.

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