A Diverse Array of Microbial Taxa Affianced in Bioremediation to Counteract Environmental Pollution

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1 Introduction

Microbes are found in almost every place or environment on the earth because of their metabolic ability, which allows them to grow in various environmental conditions. Bioremediation employs microbes because of their nutritional versatility, and they have the ability to alter toxic pollutants for the production of biomass and energy gain (Abatenh et al., 2017). Humans have been using the resources of the earth for about more than two million years, which has led to the release of pollutants and wastes into the environment, and hence, the pileup of these pollutants is a serious threat to the ecosystem. These organic pollutants may also harm animals, plants, the health of humans, and aquatic ecosystems. The majority of these recalcitrant pollutants are carcinogenic and can accumulate in biological tissues by entering the food chain (Baghour, 2017). Some of these pollutants can even cause alteration in hormone homeostasis by blocking, interfering, or mimicking the hormone's function (Wielsøe et al., 2017). Similarly, pollutants like organochlorine pesticides (OCPs), polybromodiphenyl ethers (PBDEs), and polychlorobiphenyls (PCBs) are potential endocrine disruptors in wild animals (Vanden Berghe et al., 2013). There are multiple ways through which these pollutants are released into the environment such as oil spills during transportation, industrial and household effluent removal in the water bodies, pesticides used in agriculture, and so on.

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Oil spilling adversely affects the life of aquatic animals as when marine animals ingest it, oils travel to their liver and PAHs get activated by the enzymes, which makes the oil more reactive and toxic (Saadoun, 2015). Similarly, pesticides and heavy metals are contaminating both underground and surface water by runoff (Chekroun & Baghour, 2013). Hence, instead of collecting the effluents and pollutants, microbial bioremediation will be a well-organized procedure to convert the toxic elements into nontoxic ones. The biological agents used for the removal of pollutants are called bio-remediators.

The nutritional versatility of microbes can be used to aid in the biodegradation of contaminants. Bioremediation is the process by which some microbes convert, alter, and consume hazardous contaminants in order to produce energy and biomass production. The archaea, bacteria, fungi, and algae were found to be the prime bioremediators (Strong & Burgess, 2008).

Microbes require a variety of nutrients, including carbon, nitrogen, and phosphorus, to survive and continue their activity. Bio-optimization of the bacterial C:N:P ratio can be enhanced by providing an additional source of nutrients such as N and P. The addition of nutrients adjusts the critical nutritional balance for microbial growth and reproduction (Abatenh et al., 2017). This, in turn, impacts the rate and efficacy of biodegradation. Microorganisms combat pollutants when they have access to a variety of materials and substances that assist them in generating energy and nutrition to build additional cells (Nancharaiah et al., 2015). The efficiency of bioremediation is determined by a number of factors, including the chemical nature and concentration of contaminants, the physicochemical environmental attributes, and their availability to microorganisms (Abatenh et al., 2017).

The control mechanism and optimization of microbial remediation is one of the complicated systems that may require to own several dynamics, such as the presence of a microbiome capable of reducing or degrading the contaminants, availability of noxious waste to the microbial inhabitants, and the most important environmental factors such as nature of the soil, pH, nutrition, temperature, and the presence of gases like oxygen or other electron acceptors.

- Biological factors: Innumerable factors are involved in the degradation process of organic compounds, such as antagonism between microbial flora due to constrained carbon sources, antagonistic concords between microbes by bacteriophages and protozoa, pollutant concentration, and the amount of catalyst (number of microorganisms efficient in the breakdown process of the pollutants along with the quantity of enzymes synthesized by each microbial cell) (Kumar et al., 2011). The expression of specific enzymes by the organisms determines the degree of contaminant degradation. The key biological factors that affect the contamination are mutation, enzymatic activities, upright gene transfer, all type of interactions (succession, predation, and competition), size of population, and composition(Abatenh et al., 2017).
- Environmental factor: The metabolic features of the microbes and the physicochemical properties of the targeted pollutants determine the complex association that may occur during the bioremediation process. The environmental factors

such as pH, moisture, temperature, nature of the soil, nutrients, solubility in water, redox potential, and oxygen level mainly affect the growth and activity of bioremediants (microorganisms). This also takes into account the contaminant's physicochemical bioavailability, concentration, solubility, type, structure, and level of toxicity. These are the key factors that influence the kinetics of degradation studies (Sharma, 2020). In most aquatic and terrestrial environments, the optimal pH for biodegradation ranges from 6.5 to 8.5. Along with pH, moisture also plays an important role in the degradation of contaminants, as it influences the metabolic rate of contaminants and helps in their availability to microorganisms (Tahri et al., 2013).

- Availability of nutrients: Although microorganisms can be found in contaminated soil, they are unlikely to be in sufficient numbers to allow for the bioremediation process. Nutritional elements are one of the critical elements of microbes for their growth and reproduction, which, in turn, impacts the rate and efficacy of biodegradation.
- Temperature: Temperature is one of the most critical physical elements that impact microbial viability and hydrocarbon composition. An increase and decrease in temperature may affect the biochemical reaction rates between microbes and pollutants. The temperature at which biological enzymes participate in the degradation pathway has an optimum value. They don't have the same metabolic turnover at all temperatures since each compound's degradation mechanism requires a different temperature. Temperature impacts the physiological features of the organism; hence, it can either speed up or slow down the bioremediation process (Kim et al., 2014).
- Concentration of oxygen: Varying microorganisms have different oxygen requirements. The amount of oxygen accessible in the system determines whether it is aerobic or anaerobic. Some species require oxygen, while others do not, and this requirement varies by organisms. The biodegradation rate depends on the oxygen requirement of organisms, because oxygen is a gaseous necessity for most living organisms. Biological degradation occurs in both aerobic and anaerobic conditions and by both anaerobic and aerobic organisms. The presence of oxygen can improve hydrocarbon metabolism in the majority of situations. Under aerobic conditions, hydrocarbons are easily degraded, whereas chlorate compounds can only be decomposed in anaerobic conditions (Kim et al., 2014).
- Metal ions: Metals are required by microorganisms in very small amounts, and their presence in larger amounts may hinder cell metabolism. To overcome the higher amount of metals, microbes either adopt or devolve metabolism. The presence of metal compounds also has an effect on the rate of degradation, either directly or indirectly. Metals and their toxic compounds can slow down the process of degradation (Kanamarlapudi et al., 2018).

This chapter will explain the role of different microbes employed in the bioremediation of these pollutants and their working mechanism.

2 Principle of Bioremediation

The inclusion of certain substances to boost autochthonous microbial assemblages (biostimulation) and/or the addition of specific microbial populations with effective biodegradation/detoxification ability (bioaugmentation) are two common microbial-based bioremediation techniques. Microbial species that may be useful for bioremediation of contaminated sediments can be isolated from the same location. Autochthonous microorganisms are expected to be more effective and environmentally friendly than the one which may require manipulation of the natural environment to improve their performance (e.g., adjusting oxygen and/or nutrient concentration, pH) (Sharma, 2020). Microbes (fungi, bacteria, and algae) in bioremediation converts the hazardous pollutants into microbial biomass, metabolites, CO_2, and H_2O. These microbes can be indigenous or can be added from outside to the contaminated sites for bioremediations. The microbes use these pollutants for their growth by degrading and transforming them using their metabolic reactions. Large number of microorganisms are required for the complete degradation of these pollutants. Hence, various potential microorganisms are brought from outside to the contaminated site for the proper degradation process, and this process is known as bioaugmentation (Tyagi & Kumar, 2021).

Bioremediation depends on favorable factors like pollutants' concentration and chemical nature, suitable environmental conditions, microbes' availability, electron acceptor and energy source, pH and moisture, and nutrients. Therefore, an appropriate environment is provided for the proper growth of microbes and the effective degradation of pollutants (I. Sharma, 2020).

2.1 Types of Bioremediations

Bioremediation is classified into ex situ remediation and in situ bioremediation and based on transportation, origin, and pollutant removal from the contaminated sites (Azubuike et al., 2016).

2.1.1 In Situ Bioremediation

This process involves the pollutant treatment without disturbance or excavation in the actual contaminated area and is further divided into intrinsic in situ bioremediation and enhanced in situ bioremediation (Kumar et al., 2018; Tyagi & Kumar, 2021). Intrinsic bioremediation involves passive and unassisted remediation of contaminated sites without any human involvement. This technique contains both anaerobic and aerobic microbial actions for the treatment of recalcitrant and biodegradable pollutants (Azubuike et al., 2016). The enhanced in situ bioremediation involves polluted site enhancement by adding microbes, nutrients, and air to supplement microbial growth for the process of bioremediation. Some examples of enhanced in situ bioremediation are bio-stimulation, bio-sparging, bio-slurping, bioaugmentation, and bioventing (G. Singh, 2014). In situ bioremediation is mainly used for the treatment of areas contaminated with heavy metals, chlorinated solvents, hydrocarbons, and dyes (S. Kim et al., 2014).

2.1.2 Ex Situ Bioremediation

This method requires transportation and excavation of pollutants from the original site to another site for its treatment utilizing multiple techniques of bioremediations. This technique is then again divided into different categories like bioreactors, landfarming, biofilters, bio-piling, and composting that is based on treatment cost, degree and depth of pollutants, types of pollutants, and the geological and geographical features of polluted sites (Tyagi & Kumar, 2021).

3 Mechanism of Microorganism for Bioremediation

It is already stated above that the major groups of microorganisms employed in bioremediation are bacteria, algae, and fungi. There are two categories of bioremediation. The first is biosorption, and the second is bioaccumulation. Biosorption refers to the mechanism of passive adsorption that is reversible and fast (Wang et al., 2021). The metals on the cell surface are retained by physiochemical interactions like complexation, ion exchange, crystallization, adsorption, and precipitation (Khadiga et al., 2017). The biosorption of metals is affected by several factors like ionic strength, the concentration of biomass, size of particles, temperature, pH, etc. (Vilar et al., 2005). There can be both dead and living biomass for biosorption because it is cell metabolism independent. On the other hand, bioaccumulation contains both extra- and intracellular processes. Here limited role is played by the passive uptake. So, for bioaccumulation, only living biomass can occur (Chojnacka, 2010).

The cell wall of the microorganisms is comprised of multiple macromolecules like proteins and polysaccharides, along with several charged functional groups (imidazole, ester sulfate, carboxyl, sulfhydryl, phenol, hydroxyl, thioether, and amino groups) (Rosca et al., 2015; Akar & Tunali, 2006). The adsorption occurs in a solution when the positively charged metal present drifts towards the functional groups present in the solution. The cell wall composition gets influenced by the method of microbe cultivation. Therefore, this property can be used to increase the capacity of adsorption in microbes (Coelho et al., 2015) (Fig. 1).

Pollutants like heavy metals from wastewater can be removed by using bacteria through functional groups like aldehydes, ketones, and carboxyl groups existing in their cell wall (Kanamarlapudi et al., 2018). It will help in producing less sludge. Heavy metals can be removed by employing both gram-positive and gram-negative

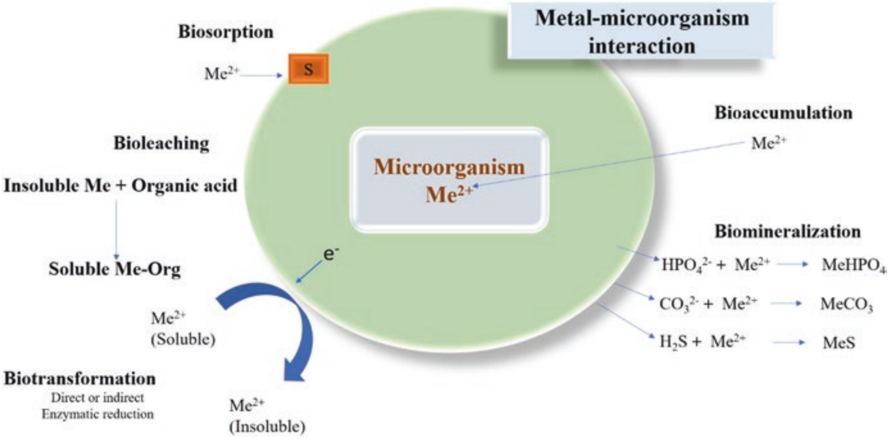

Fig. 1 Mechanism of microbes utilized in bioremediation

bacteria. Algae are also found helpful in bioremediation as brown, red, and green algae are employed as biosorbents (Bwapwa et al., 2017). Functional groups like xylans, alginic acids, uronic acid of sulfate groups, carboxyl groups, and galactans of bacteria can perform ion exchange and can produce toxic material, whereas algae usually do not produce toxic materials, so it's an advantage of using algae as biosorbents instead of other microbes like fungi and bacteria (Coelho et al., 2015). Fungi are one of the bioremediants used in the degradation of benzo(a)pyrene. However, limited information is available about it. It was discovered that, for the degradation of HMW PAHs like BaP, fungi use enzymes that are different from bacteria. A few studies have also shown that the fungal degradation process is also affected by selective pressure. Similarly, *P. chrysosporium* was found to have the ability of BaP degradation, but its ecological niche is given as a lignin degrader (Syed & Yadav, 2012).

4 Different Types of Pollutants

As stated above, microbes can degrade various pollutants like heavy metals, hydrocarbons, etc. Hydrocarbons (HCs) contain carbon and hydrogen in their structure, and they enter the environment from many sources (Table 1). With the flourishment of petrochemical industries, there is an increase in HC contamination, which has become a major environmental issue worldwide. Hydrocarbon groups of compounds can be neurotoxic and carcinogenic to various forms of life (Kothari et al., 2014). Besides this, heavy metals that are released from pesticides and fertilizers also contaminate the environment. Biological degradation of heavy metals is not possible as they can only be transformed from one organic or oxidation state to another. It was found that microbes can protect themselves from the toxicity of

Table 1 Source of different heavy metals. (Medfu Tarekegn et al., 2020)

Anthropogenic activities	Heavy metals
Electroplating, smelting	Zinc
Leather tanning, manufacturing, chromium salts, industrial coolants, mining	Chromium
Spent catalyst	Molybdenum
Fuel combustion, zinc melting, paint sludge, e-waste, incinerations, waste batteries	Cadmium
Smelting operations, electroplating, mining	Copper
Fuel burning, thermal power plants, smelting operations, natural/geogenic processes	Arsenic
Hospital waste, fluorescent lamps, thermal power plants, Chlor-alkali plants	Mercury
Bangle industry, ceramics, smelting operations, E-waste, paints, lead-acid batteries	Lead

metals by their multiple mechanisms like methylation, adsorption, reduction and oxidation, and uptake. In the bioremediation process of heavy metals, methylation plays an important part as methylated compounds are usually volatile (Abatenh et al., 2017). There are also several other types of pollutants and some are listed below for reference.

- *Polycyclic aromatic hydrocarbons (PAHs)*: These are hydrophobic organic components mainly found in soil, air, and sediments. It is mainly released from industries. It can accumulate in marine habitats and can sorb to organically rich soils (Tahri et al., 2013).
- *Pesticides*: These are mixtures of materials that are mainly made to prevent destruction from any pest in the agriculture field. Pesticides are divided into two categories. One is those that are degraded easily and are called nonpersistent, and the other is those that resist degradation and are called persistent (Tahri et al., 2013).
- *Polychlorinated biphenyls (PCBs)*: These are synthetic organic chemical mixtures. Polychlorinated biphenyls are used in various industries due to their high boiling points, chemical stability, non-flammability, and electrical insulating properties. They are toxic compounds that can cause cancer and endocrine disruption (Seeger et al., 2010).
- *Dyes*: They are extensively used in paper, textiles, printing, rubber product, pharmaceuticals, color photography, cosmetics, and various other industries (Rafii et al., 1997). The highest class of synthetic dye is the Azo dye, which is an aromatic compound. The dyes are not easily biodegradable due to their structures. Hence, wastewater treatment containing dyes generally involves chemical or physical methods like oxidation, adsorption, flocculation, filtration, etc. (Verma & Madamwar, 2003) (Table 2).

Table 2 Microorganisms involved in the bioremediation of dyes

Compounds	Microorganisms	References
Effluents of textiles and vat dyes	*Staphylococcus aureus*, *Bacillus macerans*, *Bacillus firmus*, and *Klebsiella oxytoca*	Adebajo et al. (2016)
Effluents of azo dyes	*Acinetobacter baumanii*, *Exiguobacterium indicum*, *Bacillus cereus*, *Exiguobacterium aurantiacums*	Kumar (2016)
Oil-based based paints	*Bacillus subtilis* strains NAP1, NAP2, and NAP4	Phulpoto et al. (2016)
Industrial dyes	*Penicillium ochrochloron*	Shedbalkar and Jadhav (2011)
RNB dye, sulfonated di-azo dye, Reactive Red HE8B, textile dye (Remazol Black B)	*Bacillus pumilus* HKG212, *Pseudomonas aeruginosa*, *Bacillus* spp. ETL-2012	Das et al. (2016); Patel and Gupte (2016)
Textile azo dyes	*Nocardia atlantica*, *Listeria denitrificans*, *Micrococcus luteus*	Hassan et al. (2013)

5 Group of Microorganisms Employed in Bioremediation

Bioremediation is mainly based on the catabolic action of the microbes (Hazen, 2018). And in this process, contaminant transformation doesn't provide any advantage to the cell. Hence, this process is called nonbeneficial biotransformation (Kumar et al., 2011; Wasilkowski et al., 2012). Multiple studies have proved that several microorganisms can naturally absorb the ions of toxic heavy metals (Wasilkowski et al., 2012). Typically, eukaryotes are different from prokaryotes based on their cellular structure. The interaction between heavy metals and microorganisms partially depends on whether the organism is eukaryotic or prokaryotic. It is because prokaryotes are less sensitive to heavy metals than eukaryotes (Perpetuo et al., 2011). In eukaryotes, metals can interact via ether by intracellular chelation or by active metal extrusion, and transformation process to convert into less hazardous chemical forms. Microbes convert toxic pollutants enzymatically into harmless products to increase the efficiency of bioremediation (Sharma, 2012). It was also seen that bacteria have developed resistance to heavy metals (Table 3) and render them harmless (Mejáre & Bülow, 2001). Various microbes (anaerobes, aerobes, and fungi) are involved in this enzymatic degradation.

As multiple pollutants can be present at the site of contamination, various groups of microbes are required for efficient bioremediation. Some microbes are capable of degrading petroleum hydrocarbons and utilize them as a source of energy and carbon. As microbes can only remain alive in a limited range of chemical contaminants, the organism used in the remediation process needs to be selected carefully (Table 4). It is the potential of microbes to introduce oxygen into the hydrocarbon for the metabolic pathway of the cell that affects the degradation process. Some bacteria exhibit a chemotactic response through which they search for contaminants and move toward them.

Table 3 Microorganisms employed in bioremediation of heavy metals

Compounds	Microorganisms	References
Cd, Cr, Pb	*Rhodopseudomonas palustris*, *Aerococcus* sp.	Sinha and Biswas (2014); Sinha and Paul (2014)
Cr, Ni, Cu, U	*Aeromonas* sp., *Pseudomonas aeruginosa*	Sinha et al. (2011)
Cadmium	*Bacillus safensis* (JX126862) strains (PB-5 and RSA-4)	Priyalaxmi et al. (2014)
Cadmium	*Cladosporium* sp., *A. fumigatus*, *Microsporum* sp., *Terichoderma* sp., *Paecilomyces* sp., *Aspergillus versicolor*	Mohammadian Fazli et al. (2015)
Lead, copper, cobalt, and chromium	*Lysinibacillus sphaericus*	Peña-Montenegro et al. (2015, p. 5)
Cu^{2+}, Mn^{2+}, Pb^{2+}, Zn^{2+}, and Fe^{2+}	*Pseudomonas aeruginosa* and *Pseudomonas fluorescens*	Paranthaman and Karthikeyan (2015)
Heavy metals	*Cunninghamella elegans*	Tigini et al. (2010)
Nickel, mercury, lead, and heavy metals	*Saccharomyces cerevisiae*	Chen and Wang (2007); Tálos et al. (2021)

5.1 *Bioremediation by Bacteria*

Several studies have been done on degradation through bacteria. It was also seen that bacteria feed on hydrocarbons (Yakimov et al., 2007). Bioremediation of hydrocarbons by bacteria can occur in anaerobic or aerobic conditions (Grishchenkov et al., 2000). The most common genera of bacteria participating in bioremediation processes include *Alcaligens*, *Acinetobacter*, *Arthrobacter*, *Achromobacter*, *Burkholderia*, *Alteromonas*, *Enterobacter*, *Flavobacterium*, *Pseudomonas*, *Bacillus*, etc. (Ghattas et al., 2017), and some of the examples are listed in Table 5 (Hassanshahian et al., 2012). Likewise, genera, for instance, *Alcanivorax*, *Thallassolituus*, *Oleispira*, *Cycloclasticus*, and *Marinobacter*, along with obligate hydrocarbonoclastic bacteria (OHCB), are well acknowledged for their ability to remediate or degrade hydrocarbons.

5.2 *Bioremediation by Fungi*

Fungi have been recognized for their potential to synthesize enzymes (e.g., catalases, laccases, peroxidases, etc.) that breakdown organic pollutants and/or immobilize inorganic contaminants. Fungi can survive in freshwater as well as in marine habitats with complex soil matrix (Deshmukh et al., 2016). Fungi can remain alive in various climatic conditions, including harsh ones, and aid in the ecosystem balance (Anastasi et al., 2013). Some studies also reported that they could survive in

Table 4 Interaction of hydrocarbons and microorganisms

Pollutants	Microorganisms	References
Anthracene, striatum Pyrene, dibenzothiophene lignin peroxidase, 9-methylanthracene	*Gleophyllum striatum*	Yadav et al. (2011)
Monocyclic hydrocarbons like xylene and benzene	*Pseudomonas putida*	Bahadure et al. (2013); Idris et al. (2015)
Toluene, benzene, phenol compounds, monocyclic aromatic hydrocarbons, xylene, and ethyl benzene	*Penicillium chrysogenum*	Abdulsalam (2012); Pereira et al. (2014)
Benzopyrene, phenanthrene	*Candida viswanathii*	Hesham et al. (2012)
Aromatic hydrocarbons	*Ralstonia* sp., *Pseudomonas* sp., *Acinetobacter* sp., and *Microbacterium* sp.	Simarro et al. (2013)
Naphthalene	Diatoms and green algae, cyanobacteria, and *Bacillus licheniformis*	Sivakumar et al. (2012)
Methylnaphthalenes, PAHs, and dibenzofurans	*Coprinellus radians*	Aranda et al. (2010)
Hydrocarbons	*F. solani*, *A. fumigatus*, *A. niger*, and *P. funiculosum*	Jawhari (2014)
Triphenylmethane and biphenyl	*Phanerochaete chrysosporium*	Wolski et al. (2013)
Toluene, diesel, and petrol polycyclic aromatic hydrocarbons	*Acinetobacter*, *Flavobacterium*, *P. putida*, *P. mendocina*, *P. alcaligenes*, *P. veronii*, and *Achromobacter*	Idris et al. (2015)
Phenol	*Pseudomonas aeruginosa*, *Bacillus subtilis*, *Alcaligenes odorans*, *Corynebacterium propinquum*	Singh (2013)

wastewater treatment plants (Badia-Fabregat et al., 2015). They are potential candidates for bioremediation as they can survive in various habitats and secrete multiple enzymes. Fungi are capable of breaking polymeric compounds with their extracellular multienzyme complexes. With the aid of their hyphal system, they can penetrate the substrate and colonize. It can transfer and redistribute the nutrients to their mycelium (Tahri et al., 2013). In aerobic environments, fungi metabolic pathways implicated in hydrocarbon breakdown may begin with oxidation mediated by alkane-oxygenase enzymes and cytochrome P450 monooxygenases. *Aspergillus*, *Drechslera*, *Curvularia*, *Fusarium*, *Mucor*, *Lasiodiplodia*, *Rhizopus*, *Trichoderma*, and *Penicillium* are a few genera of fungi that have mostly been found to be capable of degrading aromatic hydrocarbons. A few examples of fungi able to degrade pollutants are listed in Table 6.

Table 5 Heavy metal degradation by bacteria

Microorganisms	Metals	References
Bacillus circulans MN1	Cr	Chaturvedi (2011)
Bacillus cereeus		Nayak et al. (2018)
Sporosarcina saromensis (M52)		Zhao et al. (2016)
Acinetobacter sp.		Bhattacharya et al. (2014)
Immobilized *B. subtilis* (B bead)		Benazir et al. (2010)
Pseudomonas aeruginosa (P)		
Streptomyces sp.	Pb	Kumar et al. (2011)
Staphylococcus sp.		
Bacillus firmus		Salehizadeh and Shojaosadati (2003)
Methylobacterium organophilum		Bharagava and Mishra (2018)
Cellulosimicrobium sp. (KX710177)		
Desulfovibrio desulfuricans	Cu, Ni	Kumar et al. (2011)
Bacillus firmus		Kim et al., (2015)
Flavobacterium sp.		Kumar et al. (2011)
Desulfovibrio desulfuricans (KCTC5768)		Congeevaram et al. (2007)
Vibriofluvialis	Co	Jafari et al. (2015)
Vibrio parahaemolyticus (PG02)	Hg	
Pseudomonas aeruginosa		
Klebsiellap neumoniae		
Enterobacter cloacae		Al-Garni et al. (2010)
Pseudomonas sp.	Zn	Kumaran et al. (2011)
Bacillus firmus		Salehizadeh and Shojaosadati (2003)

5.3 Bioremediation by Algae

Microalgae from the genera *Scenedesmus platydiscus*, *Chlorella vulgaris*, and *S. capricornutum* have been shown to be effective in the breakdown of polycyclic aromatic hydrocarbons like naphthalene, phenanthrene, and pyrene, along with the immobilization of metals. Algae are capable of utilizing mixed hydrocarbon substrate and crude oil. It can degrade aromatic hydrocarbons, iso-alkanes, and n-alkanes. Researchers also stated about diatoms, brown alga, red alga, green algae, and cyanobacteria that could oxidize naphthalene. A few more examples are listed in Table 7. The synthesis of exopolysaccharides, which can facilitate the absorption of contaminants on the cell surface and/or their complexation into less accessible forms, is crucial to microalgae's ability to remove hazardous chemicals, thus lowering their bioavailability and toxicity. Depending on the microalgal species, the contaminant bound to the membrane or cell wall (exopolysaccharides) can remain adherent or be absorbed and chelated by phytochelatin molecules.

Table 6 Degradation of different pollutants by fungi

Microorganisms	Compounds	References
Saccharomyces cerevisiae (Y)	Chromium	Benazir et al. (2010)
Aspergillus sp.		Congeevaram et al. (2007)
Candidapara psilosis	Mercury	
Aspergillus niger	Nickel	Taştan et al. (2010)
Aspergillus sp.		
Aspergillus versicolor		
Phoma eupyrena, *Myceliophthora thermophila*, *D. purpureofuscus*, *Doratomyces nanus*	Polychlorinated biphenyls	Mouhamadou et al. (2013)
T. viride, *A. foetidus*, *Aspergillus niger*	Decolorization of textile dyes	Jebapriya and Gnanadoss (2013)
Exophiala xenobiotica	Gasoline	Isola et al. (2013)
Rhizopus sp., *A. niger*, *Mucor* sp., *Penicillium* sp.	Crude oil	Damisa et al. (2013)
R. stolonifera and *Gongronella* sp.	Folpet and metalaxyl	Martins et al. (2013)
Aspergillus terreus	Chloropyriphos	Silambarasan and Abraham (2012, p. 1)
Pythyme, *Acrimonium*, *Curvularia*, *Aspergillus*	Heavy metals	Akhtar et al. (2013)
Pleurotus eryngii	Naphthalene	Hadibarata et al. (2013a)
Armillaria sp.	Anthracene	Hadibarata et al., (2013b, p. 022)

Table 7 Degradation of different pollutants by algae

Microorganisms	Pollutants	References
Portieria hornemannii	2,4,6-trinitrotoluene	Cruz-Uribe et al. (2007)
Acrosiphonia coalita		
Macrocystis integrifolia	Phenol	Navarro et al. (2008)
Lessonia nigrescens		
Ulva lactuca	Polybrominated diphenyl ethers	Qiu et al. (2017)
Ulva lactuca	Polycyclic aromatic hydrocarbons	NET et al. (2014)
Cladophora sp.	Malachite green	Khataee et al. (2011)
Cystophora sp., *Ulva* sp.	Dichlorodiphenyltrichloroethane	Sudharshan et al. (2013)
Ulva lactuca	Chloramphenicol	Leston et al. (2013)

6 Genetically Engineered Microorganisms (GEMS) in Bioremediation

Molecular biology is rendering tools to enhance the ability of the microorganisms employed in the remediation process. It is accelerating evolution of new activities and making new pathways by collecting the catabolic segments of various microorganisms (Ramos et al., 1994). Genetically modified microorganisms have been shown to have the ability to degrade pollutants in groundwater, soil, and activated sludge (Abatenh et al., 2017). Multiple genes subjected to the degradation of various environmental pollutants like chloro-benzene acids, toluene, toxic wastes, and other halogenated pesticides have been identified. For every single toxic compound, one separate plasmid is required. One plasmid can't degrade all groups of toxic compounds. The plasmids are divided into four groups: (a) hexane-, octane-, and decane-degrading plasmids are called OCT; (b) toluene- and xylene-degrading plasmids are called XYL; (c) camphor-decomposing plasmids are called CAM; and (d) naphthalene-degrading plasmids are called NAH (Ramos et al., 1994). One study has shown the potential to modify the gene of a bacterial strain to degrade different groups of hydrocarbons. They made a multiplasmid having pseudomonas strain in it (Markandey, 2004). It is capable of oxidizing polyaromatic, terpenic, aromatic, and aliphatic hydrocarbons. The utilization of genetically modified microbes in heavy metal removal has increased many interests. For instance, for simultaneous expression of the metallothionein and mercury transport system for the removal of Hg^{2+} from heavy metal wastewater, *Rhodopseudomonas palustris* was developed (Deng & Jia, 2011). Similarly for chromium removal, *Alcaligenes eutrophus* AE104 (pEBZ141) was developed (Srivastava et al., 2010). A few more examples of genetically modified organisms are listed in Table 8. Using genetically modified organisms is a very useful and effective approach for removal of toxins that indigenous bacteria cannot breakdown. GMOs play a crucial role in industrial-waste remediation, reducing the toxicity of some hazardous substances, and assisting in the removal of pollution caused by hydrocarbons. For the successful production of GMOs in a short amount of time, a variety of molecular methods such as horizontal DNA transfer in bacteria, molecular cloning, electroporation, protoplast transformation, homologous recombination transformation, conjugation, and

Table 8 Genetically modified organisms involved in bioremediation

Genetically engineered bacteria	Heavy metals	References
Ralstonia eutropha CH34	Cd^{2+}	Azad et al. (2014)
Achromobacter sp. AO22	Hg	
Sphingomonas desiccabilis and *Bacillus idriensis* strains	As	
Escherichia coli and *Moraxella* sp.	Cd and Hg	
P. fluorescens 4F39	Ni	
Mesorhizobium huakuii B3	Cd^{2+}	
Deinococcus radiodurans strains	Hg	
Pseudomonas fluorescens OS8	Cd, Hg, Zn, Pb	
Staphylococcus aureus RN4220 and *P. putida* 06909	Cd	
Pseudomonas K-62	Hg	
Acidithiobacillus ferrooxidans strain	Hg	
E. coli SE5000	Ni	
P. putida strain	Cr	

transformation of competent cells are available. The bioremediation methods incorporating GMOs have more benefits when it compared to the conventional means, because it can be easily applied to the contaminant place.

7 Conclusion

Microbial processes are necessary for global carbon cycle maintenance, and these processes are one of the key parts of bioremediation. It’s an attractive and fruitful technique to eliminate pollutants from the environment as a continuous accumulation of these pollutants will destroy the environment and different habitats due to their toxicity. The degradation speed can be determined against the addition of biological agents like nutrients and appropriate conditions. It has been seen that this process is less effective in the natural environment, which gives minimum results. Therefore, this problem can be minimized if an appropriate atmosphere can be provided at the contaminated sites. Genetic engineering is also playing a great role in improving the ability of microbes employed in bioremediation. Microbial bioremediation has a promising future due to its eco-friendly nature and sustainability. It has more advantages than disadvantages as very less toxicity is generated in this procedure. The number of sites is increasing day by day that is utilizing this technique worldwide. Different species are still getting explored from multiple sites for the development of this process.

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