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Bioremediation- a sustainable tool for diverse contaminants management: Current scenario and future aspects

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ABSTRACT

Bioremediation is well accepted technology for the removal of pollutants produced by the anthropogenic activities and rapid industrialization. Different innovative tools such as microbes could be employed for the bioremediation of toxicity in environment. The microbial based bioremediation is one of the most effective tools due to maximum output, cost-effectiveness, and non-toxic process. Microbes having capability to remediate, habors the different hot spots such as plant microbiomes (epiphytic, endophytic, and rhizospheric), and diverse extreme environments (psychrophilic, thermophilic, xerophilic, halophilic, acidophilic, and alkaliphilic). Microbes are known to degrade the different pollutants including azo dyes, heavy metals, agricultural wastes, pesticides, and polycyclic aromatic hydrocarbons. Thus, utilization of microbes and their consortia is highly accepted and recommended technology for decontamination of environment is a prime concern on account of being eco-friendly, non-hazardous, safe, and cost-effective. In the past two decades, there have been recent advances in bioremediation techniques with the ultimate goal to restore polluted environment for better survival of living beings and protecting the sanctity of nature. In the present review, the current scenario of microbial bioremediation of different pollutants is discussed along with factors affecting the bioremediation.

1. INTRODUCTION

Bioremediation is the process of cleaning environment by living microbes to maintain the overall ecological balance in nature. There are various fungi, bacteria, and other microorganism that are constantly at work to break complex organic compound into simpler ones by their enzymatic activity. Rise in agricultural practices and manufacturing industries have resulted huge pollutant release such as xenobiotics and heavy metals [1,2]. Increasing hazardous wastes have led to shortage of hygienic water as well as disturbance of soil and thus limiting crop production [3]. Therefore, the environment has turned into greatly polluted with the chemical pollutants that are deadly to environment and human fitness [4,5]. Bioremediation needed environmental condition which is constructive for the certain biochemical practice and relation among nutrients, contaminants, microorganisms, and electron acceptor or donors [6]. Bioremediation procedures depend on the utilization of metabolic prospective for neutralizing the noxious possessions of pollutants by either conversion to slighter lethal compounds complete mineralization of toxic compounds and immobilization of the pollutant [7].

Bioremediation has been applied in multiple areas such as waste water treatment and toxic chemicals remediation. As enhancing the process additives are added which may be disruptive to other organisms, hence, inhibiting the same environment *in situ*. It is restricted to those mix that are biodegradable (heavy metals such as cadmium and mercury are not readily absorbed or captured by organism) [8]. To a large extent research is necessary to build up and obtain bioremediation techniques. The product of biodegradation may be more constant or lethal compared to parent compound. The method of bioremediation has a chief advantage as it reduces cost compared with conventional techniques and is more eco-friendly with maximum output. The bioremediation is a permanent solution, that is, providing complete contaminant transformation to its molecular constituent rather than

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other remediation methods which involves the transfer of waste from one phase to another [9]. Different microbes the dominant microbes involved in bioremediation are *Aspergillus* [10], *Alcaligenes* [11], *Bacillus* [12], *Penicillium* [13], *Trichoderma* [14], and *Zobellella* [15]. In the present review, microbial bioremediation of different pollutants such as agricultural waste, heavy metals, xenobiotics, and polyaromatic hydrocarbons is discussed in detail.

2. MICROBIAL BIOREMEDIATION

The microbes involved in bioremediation are beneficial for sustainable environments. The addition of bioremediating microbes to contaminated site is as an alternative approach for the removal of pollutants. The microbes fall under the category of bacteria [Table 1] and fungi and they uses different mechanism for the bioremediating the pollutants [Figure 1]. The bioremediating microbes could be used as single inoculant as well as microbial consortium. Microbes are known to degrade several different pollutants such as agricultural waste, heavy metals, xenobiotics, dyes, and polyaromatic hydrocarbons [16]. Microbes involved in the bioremediation have been reported naturally reported and some of them are genetically engineered for making them more efficient. Traditional methods being used from ages to remove environmental toxic compounds have been unsuccessful, and thereby, revolutions in modern pollutant remediation technologies could enhance the bioremediation quality. The exponential growth of pollution led to the analysis of microbes and fabrication of genetically engineered microbes (GEMs) for reduction of contaminants through bioremediation technology [17]. In the current frame of reference, physicochemical approaches have been trained for the industrial and domestic wastes remediation but these approaches are harmful for the environment and costly. Engaging engineered microbiome can impart a secured and a financially stable approach then other techniques. Genetic engineering (GE) and biotechnology, GEMs are anticipated by modifying microbiome with a more persuasive protein to overexpress the desired character [18]. Genetically modifies microbes including algae, bacteria, and fungi have been applied to degrade various contaminants such as hexane, octane, oil spills, camphor, naphthalene, toluene, xylene, halobenzoates, and trichloroethylene. These modified strains of microbes are more persuasive than the authentic strains of microbes and have excessive degeneration capabilities with instant adaptation for several pollutants as substrates or metabolites. The future endeavors for the execution of GE to produce such strains for the well-being of the environment and public health is doubt less long and worthy [19]. Several reports have been reported recombinant microbes for bioremediating different environmental pollutants. In a report, recombinant bacterium *Caulobacter crescentus* was reported for the bioremediation of soluble heavy metal, that is, cadmium [20]. In a similar report, transgenic bacteria that can express polyphosphate kinase and metallothionein were reported for the bioremediation of mercury metal [21]. In a study, the expression of *ars*M was introduced in the *Sphingomonas desiccabilis* and *Bacillus idriensis*, for the methylation of arsnic [22].

A study by Misra *et al*. [69] reported the bioremediation of heavy metals by the genetically engineered extremophilic bacterium *Deinococcus radiodurans.* In another investigation, transgenic microbes *Pseudomonas fluorescens* were reported for the biodegradation of polycyclic aromatic hydrocarbons [70]. In a study, the textile dye Remazol Brilliant Blue R decolorization was achieved by the recombinant strain of *Aspergillus niger* in gene responsible for *Phanerochaete flavido-alba* laccase that was expressed [10]. The genetically modified bacterium *Pseudomonas putida* was reported for the biodegradation of organophosphates and pyrethroids. In this bacterium, the suicide plasmid with expression cassettes was constructed which contain *mpd* (organophosphate degrading gene) and *pytH* genes (pyrethroid-hydrolyzing carboxylesterase) [71]. In a study, the copper remediation was achieved by the genetically modified strain of *Saccharomyces cerevisiae* in which copper binding properties were increased by construction and integration of recombinant genes of humans, that is, MT_2 and GFP-$hMNT_2$ [72]. Another investigation has reported the biodegradation of oil and PAH compounds from the soil using recombinant bacterial strain *Pseudomonas putida*. This bacterial strain was cloned with catechol 2,3-dioxygenase (C23O) encoded gene (*nah*H) suing pUC18 vector [73]. Liu *et al*. [74] genetically modified the methanotroph *Methylomonas* sp. by inserting the herbicide bensulfuron-methyl hydrolase encoding gene *sul*E which resulted in the bioaugmentation of chemical pesticide contaminated soil.

3. REMEDIATION OF DIVERSE POLLUTANTS

3.1. Remediation of Agricultural Waste

The by-products of crop production, crop harvesting, agro processing, and many more are the agricultural waste which includes both natural and non-natural substances. A major portion of the agricultural wastes is generated by the food harvesting and processing and sugar industries particularly in India [75]. Water management agricultural waste peels act as lignocellulosic materials with water biomass that consequences in the enhancement of adsorbents yield [76]. A combination of several crop residues and cattle manure is used in vermicomposting to obtain a value added product as a result [77]. In a report, thermophile *Geobacillus* sp. having amylolytic and cellulolytic activity was reported for degrading the mixture of market waste, rice straw, and cow dung [78]. Another study has reported, lignocellulolytic fungal strain and *Penicillium expansum* for the degradation of wheat straw and cattle/chicken mature efficiently [13]. Zhang *et al*. [79] reported *Phanerochaete chrysosporium* for compositing agricultural waste. In a report, efficient degradation of lignocellulosic and cellulosic waste was showed by *Pseudoxanthomonas* sp. [80]. Asgher *et al*. [81] reported agricultural waste degradation by the ligninolytic enzymes producing bacteria *Schizophyllum commune*. In a study, apple pomace, the main waste of the fruit industries, was reported to be degraded by the combination of yeast *Saccharomyces cerevisiae* and *Scheffersomyces stipites* [82]. In a similar report, the waste of Japanese bamboo was degraded and transformed into bioethanol by the white rot fungus, namely, *Phlebia* sp. [83]. The mushroom was reported as a remediating agent and its cultivation was reported for the removing the waste to fix the problem of food-to-waste-to-food system [84]. In another report, agricultural waste, that is, rice straw and corn cobs, was degraded by *Penicillium citrinum* after 6 days of inoculation [85]. The combination of fungal strains, namely, *Aspergillus niger* and *Phanerochaete chrysosporium* application on the rice was reported for the decomposition of the waste rice straw. The decomposition of rice straw by the fungal mixture was resulted in the production of biogas and eliminates the risk of toxicity for the crops [86].

3.2. Remediation of Polycyclic Aromatic Hydrocarbons Contaminated Soil

Polycyclic aromatic hydrocarbons having the two or more fused aromatic rings containing carbon and hydrogen are the micropollutants. This pollutant is carcinogenic in nature with very low or now degradation ability. They have been produced mainly through the incomplete combustion and organic matter pyrolysis.

Table 1: Bacteria responsible for bioremediation of different compounds.

Bacterial strains	Compounds	References
Achromobacter xylosoxidans	Colored distillery effluent	Chaturvedi *et al*. [23]
Acinetobacter brisouii	As and Cd	Bhakta *et al*. [24]
Acinetobacter junii	Reactive Red-120	Anwar *et al*. [25]
Acinetobacter seohaensis	Mercury	Pushkar *et al*. [26]
Alcaligens faecalis	Colored distillery effluent	Chaturvedi *et al*. [23]
Aneurinibacillus aneurinilyticus	As	Dey *et al*. [27]
Bacillus algicola	Crude oil	Lee *et al*. [28]
Bacillus anthracis	Colored distillery effluent	Chaturvedi *et al*. [23]
Bacillus atrophaeus	*n*-alkanes and PAH	Kiamarsi *et al*. [12]
Bacillus brevis	Hexachlorocyclohexane	Gupta *et al*. [29]
Bacillus cereus	Diesel oil	Maliji *et al*. [30]
Bacillus cibi	Oily sludge	Cerqueira *et al*. [31]
Bacillus circulans	Hexachlorocyclohexane	Gupta *et al*. [29]
Bacillus coagulans	Diesel oil and crude oil	Kehinde, Isaac [32]
Bacillus firmus	Vat dyes and Textile effluents	Adebajo *et al*. [33]
Bacillus licheniformis	PAH	Eskandary *et al*. [34]
Bacillus macerans	Vat dyes and Textile effluents	Adebajo *et al*. [33]
Bacillus mojavensis	PAH	Eskandary *et al*. [34]
Bacillus pumilus	Remazol navy blue dye	Das *et al*. [35]
Bacillus subtilis	Oil based paints	Phulpoto *et al*. [36]
Bacillus thuringiensis	Mercury	Dash *et al*. [37]
Brucella intermedius	Chromium	Chen *et al*. [38]
Burkholderia cocovenenans	Phenanthrene	Wong *et al*. [39]
Celeribacter persicus	PAH	Jami *et al*. [40]
Citrobacter koseri	Diesel oil and crude oil	Kehinde, Isaac [32]
Citrobacter sedlakii	Petroleum polluted soils	Ghoreishi *et al*. [41]
Comamonas aquatica	Copper and nickel	Ghosh *et al*. [42]
Corynebacterium variabile	Oil mixture, *n*-alkanes, and PAH	Zhang *et al*. [43]
Defluviimonas pyrenivorans	PAH	Zhang *et al*. [44]
Entrobacter cloacae	Lead	Kang *et al*. [45]
Entrobacter hormeachei	Petroleum polluted soils	Ghoreishi *et al*. [41]
Exiguobacterium aestuarii	As and Cd	Bhakta *et al*. [24]
Festuca arundinacea	PAH	Eskandary *et al*. [34]
Geobacter metallireducens	Acid Red 27	Liu *et al*. [46]
Isoptericola chiayiensis	Crude oil	Lee *et al*. [28]
Klebsiella oxytoca	Vat dyes and Textile effluents	Adebajo *et al*. [33]
Klebsiella pneumoniae	Mercury	Pushkar *et al*. [26]
Kocuria assamensis	Chlorpyrifos and malathion	Mehta *et al*. [47]
Listeria denitrificans	Textile azo dyes	Hassan *et al*. [48]
Lysinibacillus fusiformis	methyl red	Sari, Simarani [49]
Lysinibacillus sphaericus	Co, Cr, Cu, and Pb	Peña-Montenegro *et al*. [50]
Marinobacter aromaticivorans	PAH	Cui *et al*. [51]
Microbacterium hydrocarbonoxydans	Colored distillery effluent	Chaturvedi *et al*. [23]
Microbacterium oxydans	Uranium	Sánchez-Castro *et al*. [52]
Nocardia atlantica	Textile azo dyes	Hassan *et al*. [48]
Oceanimonas marisflavi	PAH	Lee *et al*. [53]

(Contd...)

Table 1: ***(Continued)***

Bacterial strains	Compounds	References
Paenibacillus dendritiformis	PAH	Bezza, Nkhalambayausi Chirwa [54]
Paenibacillus validus	Cd, Cu, Cr, Pb, Ni, and Zn	Rawat, Rai [55]
Planococcus rifietoensis	As and Cd	Bhakta *et al*. [24]
Plantibacter auratus	*n*-alkanes and PAH	Kiamarsi *et al*. [12]
Providencia vermicola	Radionuclide containing waste	Shukla *et al*. [56]
Providencia vermicola	Copper	Islam *et al*. [57]
Pseudoalteromonas agarivorans	Crude oil	Lee *et al*. [28]
Pseudomonas abietani phila	As and Cd	Bhakta *et al*. [24]
Pseudomonas alcaligenes	Lead	Kalita, Joshi [58]
Pseudomonas cepacia	Diesel oil and crude oil	Kehinde, Isaac [32]
Pseudomonas fluorescens	Fe^{2+}, Zn^{2+}, Pb^{2}+, Mn^{2+}, and Cu^{2+}	Paranthaman, Karthikeyan [59]
Pseudomonas migulae	Colored distillery effluent	Chaturvedi *et al*. [23]
Pseudomonas putida	Monocyclic aromatic hydrocarbons	Safiyanu *et al*. [60]
Pseudomonas resinovorans	*n*-alkanes, PAH	Kiamarsi *et al*. [12]
Pseudomonas stutzeri	Wastewater	Zhou *et al*. [61]
Rhizobium meliloti	PAH	Teng *et al*. [62]
Rhodococcus ruber	Methyl *tert*-butyl ether	Guisado *et al*. [63]
Rhodococcus soli	Crude oil	Lee *et al*. [28]
Serratia ficaria	Diesel oil and crude oil	Kehinde, Isaac [32]
Sphingobium naphtha	Aliphatic hydrocarbons	Chaudhary *et al*. [64]
Sphingomonas flava	Hexachlorocyclohexane	Böltner *et al*. [65]
Sphingomonas olei	Aliphatic hydrocarbons	Chaudhary, Kim [66]
Sphingomonas taejonensis	Hexachlorocyclohexane	Böltner *et al*. [65]
Staphylococcus aureus	Vat dyes and Textile effluents	Adebajo *et al*. [33]
Staphylococcus capitis	Hexavalent chromium	Zahoor, Rehman [67]
Staphylococcus epidermidis	Colored distillery effluent	Chaturvedi *et al*. [23]
Staphylococcus pasteuri	*n*-alkanes, PAH	Kiamarsi *et al*. [12]
Stenotrophomonas acidaminiphila	Hexavalent chromium	Li *et al*. [68]
Zobellella maritime	PAH	Lee *et al*. [15]

Polycyclic aromatic hydrocarbons could be generated from the natural (volcanic eruptions and forest fire) and anthropogenic (residential wood burning, vehicle emission, petroleum catalytic cracking, and fossil fuels combustion in industries) sources. This pollutant has several hundred PAHs combination such as anthracene (three rings) benzo(a)anthracene (four rings), benzo(a)pyrene (five rings), benzo(r,s,t)pentaphene (six rings), chrysene (four rings), and several others. The micropollutant PAH removal could be achieved with the help of microbial remediation [87,88]. In a report, *Paracoccus* sp. was reported for the remediation of PAH-contaminated soil [89]. The phytoremediation of PAH in an aged contaminated soil was reported by the combination of alfalfa and *Rhizobium meliloti* [62]. In a similar report, the synergism of plant alfalfa and *Bacillus* sp. was reported for the phytoremediation of PAH [90].

In another report, degradation of PAH was achieved by microbial consortium containing different species of *Stenotrophomonas* bacterium isolated from oil contaminated soil [91]. Similarly, another study have showed the PAH removal from heavy crude oil contaminated soil by microbial consortium of bacterial and fungal species, namely, *Aspergillus nomius, A. flavus, Trichoderma asperellum, Klebsiella* sp., *Pseudomonas aeruginosa,* and *Stenotrophomonas maltophilia* [92]. Another investigation has reported PAH biodegradation along with oil sludge removal from the soil by the bacterium *Paenibacillus dendritiformis* [54]. In a report, PAH degradation was showed by the fungal strain *Scopulariopsis brevicaulis* which was isolated from an aged PAH-contaminated soil [93]. Bacterium, *Pseudomonas* sp. sorted out from the soil contaminated with motor oil, was reported for the production of biosurfactants and degradation of PAH [94]. The synergistic effect of two bacteria and a plant, namely, *Bacillus licheniformis* and *B. mojavensis* and *Festuca arundinacea* was reported for elimination of PAH by phytoremediation [34]. In an investigation, PAH biodegradation was reported by various species of genera *Pseudomonas*, *Parvibaculum, Pseudoxanthomonas,* and *Lewinella* [95]. In a report, *Bacillus* sp. was reported for the bioremediation of the PAH-contaminated soil [96]. *Sphingomonas* sp. MJ-PV has been reported to exhibited capability of biodegradation and presences of *mlrA* (microcystin-degrading gene). This novel bacterium having capability of degrading polycyclic aromatic hydrocarbons (naphthalene, pyrene, and phenanthrene) has been sorted out from agricultural soil [97]. The isolated bacteria have been identified as *Sphingomonas formosensis* CC-Nfb-2^{T} have capability of possesses serine palmitoyl transferase gene (*spt*), which is responsible for PAH. The labor division quality of consortia

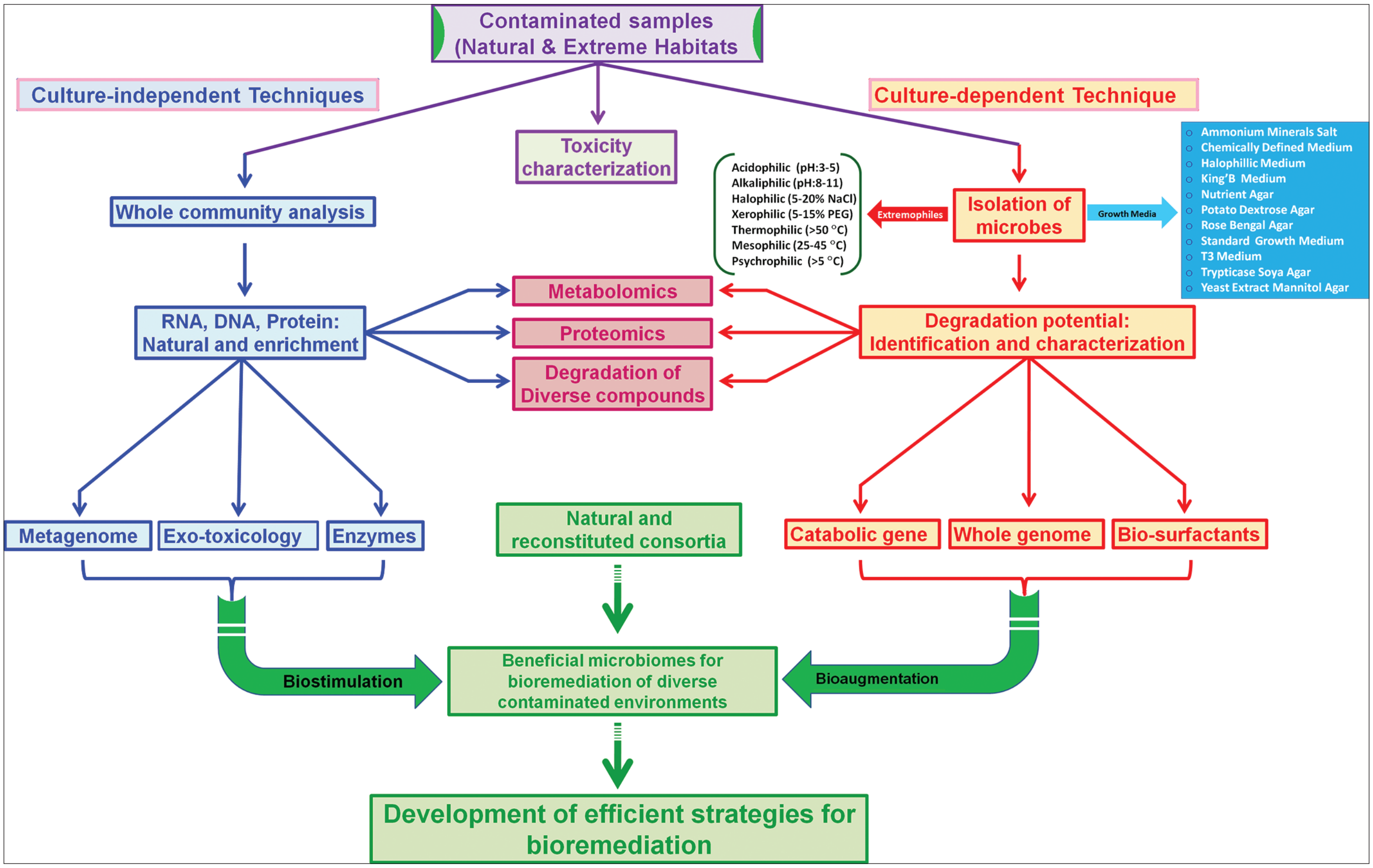

Figure 1: A Schematic representation showing different approaches for bioremediation. Adapted with permission from Kour *et al*. [7].

promotes the degradation of persistent pollutants more effectively in a fastest way [29] as single bacterial strains are unable to reduce the organic pollutants like PAHs [98-100]. Similarly, five culturable bacterial consortium degrades pyrene at three fold rate than single bacterial strain [101].

3.3. Remediation of Dyes

Vibrant ad colorful dyes came about 180,000 years back and since then, the dyes have been used and become an important part of the industries. Until of the late 19th, the dyes were obtained from the natural raw materials such as vegetables extract, branches, berries, leaves roots of the plants, and plants blossoms [102]. The major limitation of the dyes obtained from the natural raw materials was limited colors range due to which synthetic colorants were introduced in the world. In 1856, the world's first commercial synthetic dyes were introduced which was pale purple dye and it was developed unexpectedly through W.H. Perkin [103]. The synthetic dyes are have broad range of color spectra and they are everlasting even on the exposure of water, sunlight, chemicals, and perspiration. In short period of time, synthetic dyes have attracted the mankind attention and have substituted the natural dyes. Among the various types of synthetic dyes, azo dyes are widely used (50%). Azo dyes contain single to countless azo groups (–N=N–) and named according to the chemical configuration. Azo dyes are largely used in the numerous trades including textile manufacturing, cosmetics, foodstuffs, and paper printing [104]. The dyes used in the various industries have been estimated that about 10–15% of the dyes do not bind and found freely into the environment which generates a high caliber of liquid waste effluent [105].

Dyes have become a major pollutant because of toxic and mutagenic nature. The removal is one current need as dye presence in the environment is affecting marine and land animals; plants vegetation and humans. The dye removal through the process of bioremediation is one of the most effective and environmental friendly techniques. Bioremediation of dyes through the microbes is largely known and huge amount of research has been conducted so far. Various groups of microbes have been reported for the bioremediation of dyes including bacteria, fungi (yeast), and algae [Table 2] [106-146]. In a report, the microbial mixture of fungal and bacterial strains, namely, *Penicillium* sp. and *Exiguobacterium* sp. was reported for decolorizing the Reactive Dark Blue K-R dye by 60% [147]. In a another report, azo dye acid red 27 was decolorized by the *Shewanella oneidensis* under the anoxic and anaerobic conditions [148]. Kolekar and Kodam [149] reported *Alishewanella* sp. for the decolorization of reactive blue 36 within 6 h of incubation. *Geobacter metallireducens* was reported for the degradation of acid red 27 by 66.3–93.7% in 40 h [46].

Dye reactive red-120 was degraded by the bacterial strain *Acinetobacter junii*. This strain was degrading the dye in the presence of 150 g L^{-1} of NaCl [25]. In another report, five different azo dyes, namely, Red HE7B, Red Black-B, Dark Navy Blue H2GP, Light Navy Blue HEG, and Reactive Violet-5 were decolorized by the *Trichoderma koningii* which was isolated from the plant rhizosphere growing in effluent contaminated soil [14]. Macro fungi, *Pleurotus ostreatus,* was reported for the decolorization of the two dyes, that is, nylon blue and cotton yellow by 78.10% and 90.81%, respectively, within 15 days at 28 ºC temperature and pH 3.0 [140]. *Chlorella vulgaris* was reported for decolorization of indigo blue dye [150]. In a report, the salt tolerant

Table 2: Fungal strains remediating different strains.

Fungal strains	Compounds	References
Absidia glauca	Polychlorinated dibenzo-p-dioxins	Delsarte *et al*. [106]
Acremonium sclerotigenum	*n*-Alkanes	Barnes *et al*. [107]
Anthracophyllum discolor	Pentachlorophenol	Rubilar *et al*. [108]
Aspergillus awamori	Cr, Cd, Pb, and Ni	Rawat, Rai [55]
Aspergillus flavus	Cr, Cd, Pb, and Ni	Rawat, Rai [55]
Aspergillus fumigatus	Cadmium	Talukdar *et al*. [109]
Aspergillus niger	Remazol Brilliant Blue R	Benghazi *et al*. [10]
Aspergillus niveus	Chromium	Chaudhary *et al*. [110]
Aspergillus penicillioides	Pb and Cd	Paria, Chakraborty [111]
Aspergillus sclerotiorum	Pyrene and benzo[a]pyrene	Passarini *et al*. [112]
Aspergillus sydowii	Triphenyl phosphate	Feng *et al*. [113]
Aspergillus terreus	Chlorpyrifos	Silambarasan, Abraham [114]
Aspergillus tubingensis	Tannery wastewaters	Prigione *et al*. [115]
Aspergillus ustus	Petroleum hydrocarbons	Benguenab, Chibani [116]
Bionectria ochroleuca	Polychlorinated dibenzo-p-dioxins	Delsarte *et al*. [106]
Byssochlamys spectabilis	PAH	Rosales *et al*. [117]
Cerrena unicolor	Textile mill effluents	Verma *et al*. [118]
Chaetomium aureum	Lead	Chakroun *et al*. [119]
Cladophialophora bantiana	Hydrocarbons	Badali *et al*. [120]
Cordyceps cicadae	Acetochlor	Erguven [121]
Coriolopsis byrsina	Textile mill effluents	Verma *et al*. [118]
Cunninghamella echinulata	Petroleum Hydrocarbons	Chibuike, Obiora [16]
Cyberlindnera samutprakarnensis	Acid Red B	Song *et al*. [122]
Doratomyces nanus	Polychlorinated biphenyls	Mouhamadou *et al*. [123]
Doratomyces purpureofuscus	Polychlorinated biphenyls	Mouhamadou *et al*. [123]
Doratomyces verrucisporus	Polychlorinated biphenyls	Mouhamadou *et al*. [123]
Fusarium chlamydosporium	Tannery Wastewater	Sharma, Malaviya [124]
Fusarium oxysporum	Oil mixture	Marchand *et al*. [125]
Fusarium sambucinum	Pulp and paper mill effluent	Malaviya, Rathore [126]
Fusarium solani	DDT	Mitra *et al*. [127]
Ganoderma austral	Lindane	Rigas *et al*. [128]
Gongronella butleri	Uranium	Coelho *et al*. [129]
Hypocrea lixii	Pyrene	Hong *et al*. [130]
Irpex lacteus	Remazol Brilliant Blue R	Novotný *et al*. [131]
Lecanicillium lecanii	Polychlorinated dibenzo-p-dioxins	Delsarte *et al*. [106]
Merulius aureus	Pulp and paper mill effluent	Malaviya, Rathore [126]
Mortierella minutissima	Polychlorinated dibenzo-p-dioxins	Delsarte *et al*. [106]
Mucor circinelloides	Heavy metals	Cui *et al*. [132]
Mucor racemosus	Pyrene, benzo[a]pyrene	Passarini *et al*. [112]
Myceliophthora thermophile	Polychlorinated biphenyls	Mouhamadou *et al*. [123]
Paecilomyces carneus	Polychlorinated dibenzo-p-dioxins	Delsarte *et al*. [106]
Paecilomyces variotii	Tannery wastewaters	Prigione *et al*. [115]
Penicillium chrysogenum	Crude Oil	Maamar *et al*. [133]
Penicillium citreonigrum	Oil spills	Bovio *et al*. [134]
Penicillium citrinum	Chromium	Zapana-Huarache *et al*. [135]
Penicillium coffeae	Arsenic	Bhargavi, Savitha [136]

(Contd...)

Table 2: *(Continued)*

Fungal strains	Compounds	References
Penicillium cyclopium	Crude Oil	Maamar *et al*. [133]
Penicillium digitatum	Polychlorinated biphenyls	Tigini *et al*. [137]
Penicillium expansum	Wheat straw, cattle/chicken mature	Wang *et al*. [13]
Penicillium funiculosum	Hydrocarbon	Mancera-López *et al*. [138]
Penicillium piscarium	Uranium	Coelho *et al*. [129]
Penicillium polonicum	Crude Oil	Maamar *et al*. [133]
Pestalotiopsis maculans	Textile mill effluents	Verma *et al*. [118]
Phanerochaete chrysosporium	Olive mill wastewater	Mann *et al*. [139]
Phoma eupyrena	Polychlorinated biphenyls	Mouhamadou *et al*. [123]
Pleurotus ostreatus	Nylon Blue, Cotton Yellow	Skariyachan *et al*. [140]
Purpureocillium lilacinum	Petroleum hydrocarbons	Benguenab, Chibani [116]
Saccharomyces cerevisiae	Cu	Geva *et al*. [72]
Scedosporium apiospermum	Polychlorinated biphenyls	Tigini *et al*. [137]
Scheffersomyces stipites	Apple pomace	Pathania *et al*. [82]
Scopulariopsis brevicaulis	PAH	Godoy *et al*. [141]
Talaromyces amestolkiae	Uranium	Coelho *et al*. [129]
Talaromyces islandicus	Lead	Sharma *et al*. [142]
Thermoascus crustaceus	Polychlorinated biphenyls	Mouhamadou *et al*. [123]
Tolypocladium geodes	Acetochlor	Erguven [121]
Trichoderma asperellum	*n*-Alkanes	Husaini *et al*. [143]
Trichoderma atroviride	Phenolic compounds	Chakroun *et al*. [119]
Trichoderma harzianum	Oil spills	Bovio *et al*. [134]
Trichoderma koningii	Reactive Violet-5, Red HE7B, and Red Black-B	Gajera *et al*. [14]
Trichoderma lixii	As, Ni, Zn, Cu, and Cr	Kumar, Dwivedi [144]
Trichoderma longibrachiatum	PAH	Rosales *et al*. [117]
Trichoderma tomentosum	Oil mixture	Marchand *et al*. [125]
Trichoderma viride	Cr, Cd, Pb, and Ni	Joshi *et al*. [145]
Xerocomus chrysenteron	DDT	Huang, Wang [146]

yeast *Cyberlindnera samutprakarnensis* was reported for acid red B decolorization by 97% in 18 h after incubation [122]. *Lysinibacillus fusiformis* was reported for methyl red degradation in study of Sari, Simarani [49]. Ali *et al*. [151] reported the degradation of reactive azo dyes by the consortium containing three different species of yeast, that is, *Barnettozyma californica, Sterigmatomyces halophilus*, and *Yarrowia* sp. In another study, consortium of cyanobacteria and green algae, that is, *Scenedesmus obliquus* and *Oscillatoria* sp., was reported for the decolorization of azo dyes including reactive orange 122 and reactive red 194 [152].

3.4. Remediation of Heavy Metal Contamination

Heavy metals (HM) are the group of metallic elements that are abundantly present in the earth crust and have density >5 g/cm^3. They owe various applications in the multiple areas as metalloenzyme and also cause a systemic toxicity [153,154]. Its removal is considered as priority especially arsenic, chromium, cadmium, lead, and mercury [155]. Microbial remediation is the cheap and environmental friendly technique for the removal of HM in comparison to conventional methods that are high in cost and eco-unfriendly as it can remove HMs below 100 mg/L and cause secondary pollution [156,157]. The microbial remediation has gained great attention from the past 3–4 decades and it has been widely researched. Multiple species of microbes have been found in the bioremediation of HM including bacteria and fungi [158]. Microbes having capability to remediate were reported from various habitats and some of them are plant associated. Microbial species association with the plants could be rhizospheric and endophytic that help in the detoxification of the HM [159]. In a report, *Bacillus* sp., the bacterial endophyte of the plant *Solanum nigrum* L. growing in cadmium accumulated soil, was reported for the bioremediation of three different divalent HM including Cu (21.25%), Cd (75.78%), and Pb (80.48%) having initial concentration 10 mg/L [160].

In a report by Joshi *et al*. [145], four different fungi sorted out from the HM contaminated site was reported for the remediation of Cr, Cd, Pb, and Ni. The fungal strains remediating the HM were identified as *Aspergillus awamori, A. flavus, Phanerochaete chrysosporium,* and *Trichoderma viride* and all the strains were able to tolerate 400 ppm concentration of all the HM. An investigation reported *Paenibacillus validus* from industrial effluent polluted soil for adsorption of Cd, Cu, Cr, Pb, Ni, and Zn [55]. Kamika and Momba [161] reported two bacterial and a protozoa species for the remediation of different HM and they were identified as *Bacillus licheniformis* (Al and Zn)

Pseudomonas putida (Co, Ni, Mn, V, Pb, Ti, and Cu) and *Peranema* sp. (Cd). This study has also reported HM resistant genes from both bacteria and protozoa, that is, *copC* (Cu), *chrB* (Cr), *cnrA3* (Co-Ni), and *nccA* (Cd-Ni-Co). In another study, the bacterial consortium of strains *Aeromonas veronii, Bacillus barbaricus,* and *Stenotrophomonas maltophilia* isolated from the hot spring was reported for the bioremediation of Cd and Pb [162].

Bacillus sp. was reported for the detoxification of HM such as Co, Cr, Cu, Fe, Li, Ni, Pb, V, and Zn [163]. In a report, the HM remediation was reported by the fungal strains *Actinomucor* sp., *Mucor circinelloides*, and *Mortierella* sp. [132]. The synergistic combination of bacterial strains *Bacillus cereus* and plant *Vetiveria zizanioides* L. was reported for the phytoremediation of the Cr, Fe, Mn, Zn, Cd, Cu, and Ni [164]. Teng *et al*. [165] reported *Leclercia adecarboxylata* and *Pseudomonas putida* for the biomineralization of Pb metal. Similarly, another study has reported the urease producing bacterial strains, namely, *Variovorax boronicumulans* and *Stenotrophomonas rhizophila* for the bioremediation of Cd, Pb, and Zn [166]. Bacterial strain, namely, *Paenibacillus* sp. and *Morganella* sp. isolated from the PB-Zn mining site, was reported for biomineralization of copper, mercury, nickel lead, and zinc [167]. In another report, the arsenic biodetoxification was reported by the *Klebsiella pneumonia* species which was isolated from the contaminated soil and water [168].

3.5. Remediation of Xenobiotic Compounds

Xenobiotics are group of compounds which are chemical in nature and manufactured by the human. There are different types of xenobiotics such as pesticides, fuels, solvents, alkanes, antibiotics, oil mixture, azo dyes and polyaromatic, and nitro and chlorinated aromatic compounds. These xenobiotics are used in the different areas and have zero possibility of degradation. There non-degradable property causes adverse effect on the environment and health of humans [169]. Remediation of xenobiotics with the help of microbes (singly culture and microbial consortium) is an appropriate technology for their degradation in less time and without having any other adverse effect [Table 3]. Microbes in the surrounding contaminated soils are specialized in degrading xenobiotic compounds such as chlorobiphenyls and chlorobenzenes by utilizing them as substrates by secreting enzymes. Diverse group of microbes has been found to decontaminate the polluted soils [44]. In a report, fungal strain *Hypocrea lixii* and *Fusarium solani* isolated from petrol station soil was reported for bioremediating pyrene [130]. An investigation reported *Bacillus cereus* for the remediation of pentachlorophenol along with Cr metal. This strain was isolated from the tannery effluent of a effluent treatment plant [170]. In a report of Dubey and Fulekar [171], xenobiotic chlorpyrifos was degraded up to 33.3% by the novel strain *Stenotrophomonas maltophilia* within the 72 h of incubation. DDT (1,1,1-trichloro-2,2-bis(4-chlorophenyl) ethane, the one of the most deleterious pesticide was degraded by ectomycorrhizal fungi, *Xerocomus chrysenteron* [146]. In a similar report, DDT and chlorobenzoate degradation were reported by *Rhodococcus* sp. which was isolated pesticide contaminated soil [172]. Marco-Urrea *et al*. [173] reported the bioremediation of another hazardous xenobiotic, that is, chlorinated and polycyclic aromatic hydrocarbons with the help of white-rot fungi that belongs to phylum Ascomycota and Zygomycota. In a report, the bioremediation of the oil mixture was reported by the salt tolerant bacteria *Corynebacterium variabile*. This strain was isolated from the oilfield of China and also helps in the degradation of *n*-alkanes and polycyclic aromatic hydrocarbons mixture [43]. Similarly, the oil mixture was degraded by the bacterial and fungal strains, namely, *Rhodococcus* sp., *Fusarium oxysporum,* and *Trichoderma tomentosum* [125].

In a similar report, the oil contaminated saline soil microbial consortium was reported for the bioremediation of oil based drill cutting. The microbial consortium used for the bioremediation of oil drills contains species of genera *Arthrobacter*, *Dietzia, Halomonas, Marinobacter*, *Propionibacterium,* and *Salinimicrobium* [174]. An investigation has reported that the microbial consortium prepared from the bacterial cultures *Bacillus cereus* and *Ochrobactrum pseudintermedium* was helpful in the remediation of crude oil [175]. In a study, the biodegradation of two environmental contaminant, that is, *n*-alkanes and PAH, was reported to be biodegraded by bacterial species *Bacillus subtilis, B. atrophaeus, Pseudomonas resinovorans, Plantibacter auratus,* and *Staphylococcus pasteuri* [12]. Liu *et al*. [176] reported bacterial strains *Acinetobacter lwoffii, Bacillus cereus,* and *Pseudomonas aeruginosa* for the aerobic degradation of *n*-alkanes. In a report, the xenobiotic nitrophenol degraded by the bacterial strains *Pseudomonas* sp*., Bacillus* sp*., and Arthrobacter* sp*.* These bacterial strains were having paranitrophenol monooxygenase gene which is responsible for the biodegradation of nitrophenol [177]. A study has reported antibiotic (ampicillin, erythromycin, chloramphenicol, and penicillin) resistant strain *Kocuria assamensis* which have capability to biodegrade chlorpyrifos and malathion [47].

In a report by Gupta *et al*. [29], *Bacillus circulans* and *B. brevis were reported for* having degradation efficiency of hexachlorocyclohexane (HCH; α, β, γ, and δ). Gupta *et al*. [11] isolated from HCH contaminated soil using selective media, screened for (HCH) degradation and identified as *Alcaligenes faecalis*. Bioremediation is a potential field and requires considerable interest directed toward exploitation of diverse microbial isolates from the contaminated areas showing differential capacity of pesticide degradation. Many bacterial strains have been sorted out through enrichment technique and identified as *Burkholderia cocovenenans* using Biolog system. *Burkholderia cocovenenans* demonstrated to be a feasible strain for phenanthrene degradation having initial concentration of 1000 mg L^{-1}at a neutral pH. Böltner *et al*. [65] reported three novel HCH-degrading bacteria from soil contaminated with HCH using noble agar containing γ HCH (μg/mL) and identified as *Sphingomonas taejonensis* DS31 degradating βHCH, *Sphingomonas flava* DS2 and DS2-2 degardating α, γ, and δ isomers of HCH using 16S rRNA gene sequencing. The gene, that is, *lin* genes involved in the degradation of HCH, has been also reported in isolated bacterial strains *Sphingomonas taejonensis* and *Sphingomonas flava.* The excessive use of HCH has possessed very serious environmental issues [202]. The use of lindane and HCH has been banned all around the globe, while some countries including India are still producing lindane. The microbial groups such as archaea, bacteria, and fungi are useful for degradation of HCH isomers. The bacterial genera *Sphingobium indicum*, belonging to the Sphingomonads, has been isolated and found to degradate HCH isomers. The lin genes have been reported from *Sphingobium indicum* B90A which is responsible to degradation of HCH isomers through bioaugmentation process. A bacterial strain *Bacillus pumilus* isolated from soil was found highly effective in degrading chlorpyrifos (90%) within incubation 8 days Anwar *et al*. [203]. A Gram-positive bacterium *Bacillus* sp. having capability to degrade 2.99 mg/L of microcystin-RR and 2.15 mg/L of microcystin-LR was isolated from algae heap in a study by Hu *et al*. [204].

Table 3: Microbial consortia for bioremediation.

Microbial consortium	Pollutant	References
Mycobacterium spp., + *Novosphin-gobium pentaromativorans,* + *Ochrobactrum* sp. + *Bacillus* sp.	Pyrene	Wanapaisan *et al*. [101]
Arthrobacter sp. + *Bacillus subtilis* + *Variovorax* sp. + *Arthrobacter* sp.	Atrazine	Zhang *et al*. [178]
Rhodococcus sp. +*Acinetobacter* sp. +*Pseudomonas* sp.	PAHs	Yu *et al*. [179]
Bacillus sp. + *Ralstonia eutropha*	Cd and 2,4-D	Roane *et al*. [180]
Aspergillus niger + *A. terreus* + *A. fumigatus* + *A. flavus*	Petroleum hydrocarbons	Hernández-Adame *et al*. [181]
Aspergillus lentulus+ *A. terreus*+ *Rhizopus oryzae*	Metal–dye mixtures	Mishra, Malik [182]
Perenniporia subtephropora + *Cerrena aurantiopora* + *Aspergillus niger* + *A. fumigatus*+ *Paecilomyces lilacinus* + *Trematesversicolor* + *Fusarium chlamydosporum* + *Antrodia serialis* + *Polyporales sp.* + *Penicillium cataractum* + *Fusarium equiseti* + *Phanerochaete concrescens* + *Daldinia starbaeckii*	Ni, Pb, and Zn	Hassan *et al*. [183]
Aspergillus flavus + *Aspergillus fumigatus*	Cr and Cd	Talukdar *et al*. [184]
Cladosporeum perangustum +*Penicillium commune* + *Paecilomyces lilacinus* +*Fusarium equiseti*	Tannery wastewater	Sharma, Malaviya [185]
Ochrobactrum sp. + *Pseudomonas citronellolis*	Pesticide	Góngora-Echeverría *et al*. [186]
Sphingobacterium sp.+ *Bacillus cereus* + *Achromobacter insolitus*	Phenanthrene	Janbandhu, Fulekar [187]
Flavobacterium +*Aspergillus*	Hydrocarbons	Salinas-Martínez *et al*. [188]
Enterobacter + *Pseudomonas* + *Stenotrophomonas*	PAH	Molina *et al*. [189]
Ochrobactrum pseudintermedium + *Bacillus cereus*	Crude oil spill	Bhattacharya *et al*. [175]
Acinetobacter oleivorans +*Corynebacterium* sp. + *Pseudomonas* sp. + *Rhodococcus* sp. + *Micrococcus* sp. + *Yarrowia* sp.	Diesel Fuel	Lee *et al*. [190]
Sphingomonas cloacae + *Rhizobium* sp. + *Pseudomonas aeruginosa* + *Achromobacter xylosoxidans*	Phenanthrene	Wang *et al*. [191]
Mycobacterium fortuitum + *Bacillus cereus* +*Microbacterium* sp. + *Gordonia polyisoprenivorans* + *Fusarium oxysporum*	PAH	Jacques *et al*. [192]
Bacillus +*Pseudomonas* sp.	Hydrocarbon	Ghazali *et al*. [193]
Proteus vulgaris + *Micrococcus glutamicus*	Scarlet R	Saratale *et al*. [194]
Bacillus subtilis +*Pseudomonas aeruginosa*	Petroleum hydrocarbons	Mukherjee, Bordoloi [195]
Pseudomonas aeruginosa + *Candida albicans* +*Aspergillus flavus* +*Fusarium* sp.	Benzo[a]Pyrene	Waszak *et al*. [196]
Ochrobactrum sp. + *Brevibacillus parabrevis*	Crude oil	Bao *et al*. [197]
Acinetobacter radioresistens + *Bacillus subtilis*	Diesel oil	Mnif *et al*. [198]
Serratia marcescens + *Streptomyces rochei* + *Phanerochaete chrysosporium*	PAH	Sharma *et al*. [199]
Achromobacter sp., + Rhodanobacter spp.	PAH	Bacosa *et al*. [200]
Pseudomonas putida + *Shewanella oneidensis*	Congo red	Wang *et al*. [201]

4. FACTORS LIMITING BIOREMEDIATION

Microbial activity and growth are voluntarily changed by pH, moisture, and temperature. Even though microbiomes were isolated in adverse situation, most of them survive and grow optimally in a limited series that it is vital to accomplish most favorable situation. Temperature greatly fluctuates the rates of biochemical reactions, and the reaction rate may also increases with each 10°C temperature increase. Beyond a definite temperature, the cells may decrease. Water availability is vital for the entire living systems and irrigation is desirable to attain the most favorable moisture height. The quantity of accessible oxygen will establish whether the system is anaerobic or aerobic. Hydrocarbons are eagerly tarnished in aerobic situation, whereas chlorinate compounds are remediate only in anaerobic conditions. To amplify the oxygen quantity in the soil, it is likely to sparge air. However, in some situations, magnesium peroxide or hydrogen peroxide can be added in the ecosystem. Soil structure maintains the efficient release of water, air, and nutrients. To get better soil organization, materials such as organic matter likes gypsum can be useful. Low permeability of soil can hamper progression of water, oxygen, and nutrients; therefore, soils having low permeability may not be suitable for clean-up technology *in situ* [205].

4.1. Energy Sources

Energy source is the chief fluctuating disturbing factor that fluctuates the activity, accessibility, and capability of bacteria. Regardless, a pollutant will give out as an efficient source of energy for an aerobic heterotrophic organism is a purpose of the typical carbon oxidation state in the material. In common, higher oxidation states relate to lesser yields of energy which thus supply less energetic inducement for microbe's degradation. The conclusion of all degradation practice depends on microbial enzyme activities, population diversity, and biomass concentration; substrate physicochemical characteristics, molecular structure, and concentration; and a series of environmental factors such as moisture content, pH, temperature, electron acceptors availability, and carbon and energy sources. These parameters act as the acclimation period of the microbiome to the substrate. The molecular structure and contaminant concentration have been revealed to robustly influence the viability of bioremediation and the kind of microbial alteration taking place, and whether the compound will give out as a cometabolic substrate primary or secondary [205].

4.2. Bioavailability

The microbial cells rate to transform contaminants during the process of bioremediation depends on the contaminant uptake and metabolism rate and the rate of transfer to the cell. When mass transfer is a restrictive feature, it does not result in elevated biotransformation rates of increased microbial alteration capacities. The contaminant bioavailability is restricted by a several number of physicochemical methods such as desorption, sorption dissolution, and diffusion. A lessen contaminants bioavailability in soil is due to by the slow mass transfer to the biodegrading microbes. Contaminants become inaccessible when the mass transfer rate is 0. The bioavailability the course of time decline in is regularly called as weathering or aging. It might be due to: i) Chemical oxidation reactions including contaminants into natural organic matter, ii) slow diffusion into extremely minute pores and assimilation into organic matter, and iii) the arrangement of semi-rigid films around non-aqueous-phase liquids (NAPL) with an elevated resistance near NAPL-water mass transfer. These bioavailability troubles can be surmount by the employ of food-grade surfactants, which raise the accessibility of contaminants for microbial degradation [206].

4.3. Bioactivity and Biochemistry

The word bioactivity is use to point out the microbiological methods operating state. Enhancing bioactivity revealed that system situation is in tune to improve biodegradation [207]. The utilize of bioremediation needed assembly a definite minimum rate, modification of situation to recover biodegradation action becomes significant and a bioremediation arrangement that allow this control likely has an lead over one that does not. In environment, the capability of organisms to transmit contaminants of both simpler and more composite molecules is extremely different. Due to of our existing inadequate capability to assess and manage biochemical pathways in composite environments, approving or unapproving biochemical changes are considered in circumstances of whether single or groups of parent compounds are detached, whether amplified toxicity is a consequence of the bioremediation procedure, and occasionally whether the parent compound elements are changed to quantifiable metabolites. These biochemical actions can be proscribed in an *in situ* process when one can manage and optimize the situation to attain a advantageous product [205].

4.4. Economic and Liability Factor

Contrasting other industry, bioremediation does not consequence in the manufacture of elevated value-added yield. Consequently, scheme resources have been sluggish to provide in the knowledge and, as an outcome, marketable action in investigate and progress has fall behind other developed sectors. As bioremediation is measured pioneering skill, consumers and authoritarian organization seldom examine bioremediation very strictly than usual technology. Accordingly, tighter limitations and presentation principles are regularly obligatory on bioremediation compare to other remediation technology. This can eventually direct to a better jeopardy from an accountability perspective if the bioremediation agenda does not completed the programmed aims [205].

5. CONCLUSION

Environmental risks which have occurred due to the build-up of lethal biological or chemicals micropollutants could be eliminated through the various technologies application. It could be complete in the form of remediation of disinfection of water resources, present historic pollution, and current agricultural/industrial practices through prevention and control. At present, it is hard to trace all the chemicals, and then removed or minimized, mostly because of insufficient information. This highlights the need for research and development for the assessment and emerging pollutant treatment and the tools, equipment's and to know how much contribute to the fulfillment of these needs. An integrated approach is required which can receive into deliberation the whole life cycle of the pollutants, from the foundation of release to their elimination during dealing and bioremediation techniques, and not ignoring the results and threat which may pose to the environment and human being well-being. The contaminant bioavailability is restricted by a number of physicochemical methods such as sorption and desorption, dissolution, and diffusion. A lessen bioavailability of contaminants in soil is due to the slow transfer of mass to the degrading microbes. The recruitment of hetrotrophic bacteria seems to be quiet helpful for the intermediate metabolites degradation and produced during nitrification. There is a requirement of scientifically validated and innovative process and many more tools are necessary to tackle the environmental problems.

6. AUTHORS' CONTRIBUTIONS

All authors made substantial contributions to conception and design, acquisition of data, or analysis and interpretation of data; took part in drafting the article or revising it critically for important intellectual content; agreed to submit to the current journal; gave final approval of the version to be published; and agreed to be accountable for all aspects of the work. All the authors are eligible to be an author as per the International Committee of Medical Journal Editors (ICMJE) requirements/guidelines.

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8. CONFLICTS OF INTEREST

The authors report no financial or any other conflicts of interest in this work.

9. ETHICAL APPROVALS

This study does not involve experiments on animals or human subjects.

10. DATA AVAILABILITY

All data generated and analyzed are included within this research article.

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