Soil Environ. 36(2): 93-113, 2017
DOI:10.25252/SE/17/51346
Online ISSN: 2075-1141
Print ISSN: 2074-9546

Review

Plant-bacteria synergism: An innovative approach for the remediation of crude oil-contaminated soils

***Kaneez Fatima*[1]*, Asma Imran*[1]*, Muhammad Naveed*[2] *and Muhammad Afzal*[1]**
[1]Soil and Environmental Biotechnology Division, National Institute for Biotechnology and Genetic Engineering (NIBGE) PO Box No 577, Jhang Road, Faisalabad, Pakistan
[2]Institute of Soil and Environmental Sciences, University of Agriculture, Faisalabad, 38040, Pakistan

Abstract

The adverse ecological and socio-economic effects of oil pollution demand that eco-friendly and proficient remediation technologies be devised as countermeasures. The synergistic use of plants and bacteria is considered as one of the efficient technologies for the remediation of crude oil-contaminated soil. In plant-bacterial synergism, plants host a large number of bacteria in its rhizosphere, root and shoot by providing nutrients and space for colonization. In return, bacterial population increases in different compartments of the plant and degrade organic pollutants. This review will highlight the issues related to soil contamination with hydrocarbons and their remediation, bioremediation and phytoremediation, plant-bacterial synergism in hydrocarbons degradation with special emphasis on the role of endo/rhizospehere bacteria for the maximum remediation of hydrocarbons contaminated soil.

Keywords: Crude oil, hydrocarbons, phytoremediation, plant-bacterial synergism, rhizobacteria, endophytic bacteria

Soil is an essential life-supporting and fundamental constituent of the biosphere which offers a number of advantages to the surroundings including primary production, control of biogenic gases, water cycling, preservation of life, and biodiversity (Alexander, 1978; Kuske *et al.,* 2002). In earlier times, it was believed that our land and its resources are in abundance and will remain available for centuries. Unfortunately, due to excessive use and now misuse, half of this natural wealth is either destroyed or is at the verge of depletion (Balba *et al.,*1998; Andreoni *et al.,* 2004; Reda and Ashraf, 2010). The reasons behind continuous exhaustion of healthy soil ecosystem are the use of chemical fertilizers, release of other anthropogenic chemicals, and dumping of industrial/domestic wastes into the environment; all these activities are posing a significant threat to mankind itself (Kuske *et al.,* 2002; Srogi, 2007). In addition to other prevalent pollutants, petroleum hydrocarbons (PHs) are of specific concern because of their structural complexity, hydrophobicity, toxicity, and persistent nature (Tolosa *et al.,* 2004; Pinedo *et al.,* 2013; Brevik *et al.,* 2015; Fatima *et al.,* 2015; Tahseen *et al.,* 2017).

The world's energy sources depend greatly on petroleum oil and its products, and world-wide energy demand is expected to rise steeply over the next twenty years (Aqeel and Butt, 2001; Siddiqui, 2004). Due to their excessive use, there is a chance that these PHs may release in the environment and cause severe damage to the ecosystem. Environmental contaminants enter the environment by both natural and manmade sources leading to contamination of drinking water, diminishing water and air quality, waste of non-renewable resources, and loss of soil fertility (Sebiomo *et al.,* 2010; Janbandhu and Fulekar, 2011; Prince *et al.,* 2013; Shabir *et al.,* 2013). On the other hand, continual contact with high oil concentrations may have negative effects on human health and all other life forms as well. Even at low levels of pollution, hydrocarbon causes lethal mutations in genetic material. Thus due to its mutagenic and neurotoxic effects, the United States Environmental Protection Agency (US EPA) categorizes crude oil as a significant pollutant (Aguilera *et al.,* 2010; Ordinioha and Brisibe, 2013; Robertson and Hansen, 2015).

Considering the worldwide problem of soil pollution, more suitable treatments are necessary as compared to the conventionally used more expensive and environmentally deleterious *ex situ* techniques. Conventional technologies, based on physicochemical methods (soil washing, chemical reduction or oxidation of contaminants, and incineration), are not feasible due to high cost, environmental invasion, engineering skills, labour administration, and operational management (Pandey *et al.,* 2009). Keeping in mind the limitation of conventional technologies, a much better method is needed to destroy the pollutants or to transform them into nontoxic substances. This can be achieved by the use of efficient microbes in conjunction with suitable plants i.e., microbe-assisted phytoremediation (Weyens *et al.,*

---

*Email: afzal@nibge.org

2009; Khan *et al.,* 2013a; Ijaz *et al.,* 2015a; Fatima *et al.,* 2016). This technique provides a means of *in situ* treatment of contaminated land with high efficiency using natural biological activity. In plant-microbe synergism, plants offer nutrients and habitat to their associated bacteria and in return, microbes enhance plant growth and detoxify environmental pollutants (Chaudhry *et al.,* 2005; Compant *et al.,* 2010; Glick, 2010; Sessitsch *et al.,* 2013; Afzal *et al.,* 2014a; Ijaz *et al.,* 2015b, 2016; Ahmed *et al.,* 2017).). In this review, the contamination of environment with crude oil, remediation of soil contaminated with crude oil, plant-bacterial synergism in phytoremediation, and role of rhizo- and endophytic bacteria for the maximum remediation of the soil, are discussed.

Crude oil and environmental pollution

Crude oil primarily comprises of variable extents of carbon and hydrogen. Furthermore, it contains nitrogen, oxygen, sulfur, and a range of metal-containing compounds (Chandra *et al.,* 2013; Speight, 2014; Varjani *et al.,* 2015). It is characterized as light, moderate, or thick oil established on comparative quantities of weighty molecular components existing in it. Its configuration may differ with site, age and depth of an oil well (Bachmann *et al.,* 2014). On the basis of composition, crude oil is characterized in to four major segments: 1) aliphatics, 2) aromatics, 3) resins, and 4) asphalthenes. Some of the constituents of crude oil are shown (Figure 1). Each fraction has a distinctive chemical and physical behaviour that influences the way it spreads and undergoes biodegradation in the environment (Abbasian *et al.,* 2015). In basic prearrangement of the aforementioned constituents of crude oil, aliphatics fraction constitutes the outmost layer while asphalthenes, being the high molecular weight constituent, establish the intimate share of oil (Prince *et al.,* 2013; Robertson and Hansen, 2015).

Hydrocarbons are one of the most recalcitrant organic contaminants in the environment. Because of their toxic nature, they cause wide-ranging and permanent damage to human as well as all other life forms. Although microbes eradicate soil pollution, whereas the quantity of pollutants surpasses the buffering capability of soil, it leads to enduring undesirable effects on its value and ecology (Gan *et al.,* 2009).

Petroleum hydrocarbons pollution of soil is an anxiety for a number of causes (Figure 2). At the outset, when discharged into soil, the volatility of hydrocarbons can lead to fire or even hazardous outbursts, particularly when fumes enter restrained places (Souza *et al.,* 2014). Secondly, contaminants can adsorb on soil particles and be retained in soil for years thus leading to land degradation. Though these chemicals can profit the soil microflora as an energy basis, they still have toxic and mutagenic effects on microorganisms even at low concentrations (Walker *et al.,* 2012). PHs also destroy the aesthetics of land by inducing unpleasant odour, taste in associated groundwater, or appearance to surroundings. Persistent seepage and continuous runoffs occur due to their mobile nature which extends their impact to adjacent areas (Albaigés, 2014).

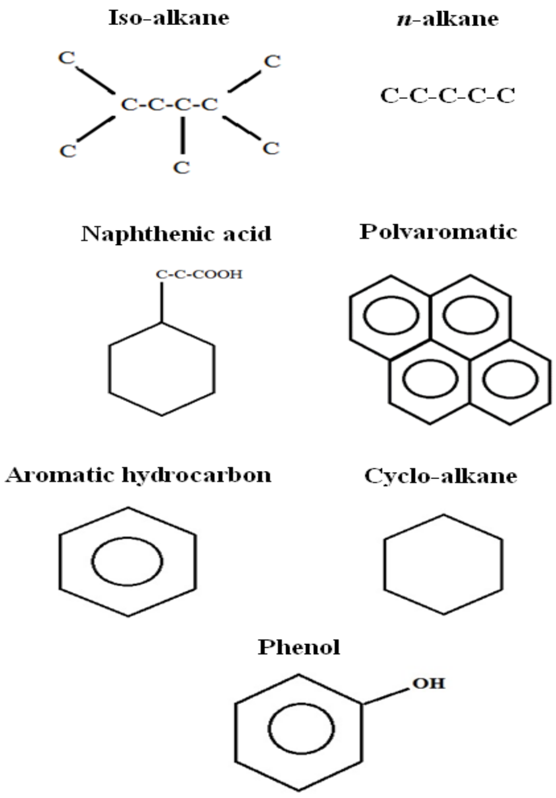

Figure 1: Chemical structure of some crude oil components

Fate of PHs in soil environment

It is essential to advance understanding about the fortune of PHs within the surroundings in order to regulate and remove pollution. The soil rhizosphere helps in structural rearrangement of hydrocarbons arriving from several sources (Varjani and Upasani, 2016). As soon as go in to the soil, the multifaceted compounds of PHs can detach into distinct amalgams dependent on their physicochemical possessions. The environmental fate of these pollutants may be dissimilar from that of distinct petroleum compounds due to the structural arrangements and interactions among hydrocarbons, soil, and microflora (Atlas, 1981; Salanitro, 2001). Resistance of hydrocarbons to soil microflora in soil/water lean towards to rise with the nature and molecular weight of hydrocarbons. Petroleum crude oil undergoes a number of weathering courses, such as sorption, degradation, vaporisation, photodestruction, emulsification, or biodegradation, which naturally degrade its constituents (Al-Majed *et al.*, 2012; Wu and Coulon, 2016). Amalgams of lower molecular weight, e.g. benzene, xylene and toluene can easily move in the atmosphere and are possibly more prone to volatilize in to the air or penetrate towards the groundwater as compared to hydrocarbons of higher molecular weight (Huang *et al.*, 2013; Li *et al.*, 2013). Commonly, hydrocarbon compounds with straight and limited chains are degraded more easily than those having five or six rings. Compounds with high molecular weight, such as polyaromatic hydrocarbons (PAHs), have a high tendency to adsorb on soil particles and persist relatively fixed at the site where they are dropped till they are dispersed into minor segments and are mineralized by microbes (Atlas, 1981; Salanitro, 2001; Glick, 2010; Sessitsch *et al.*, 2013; Fatima *et al.*, 2017).

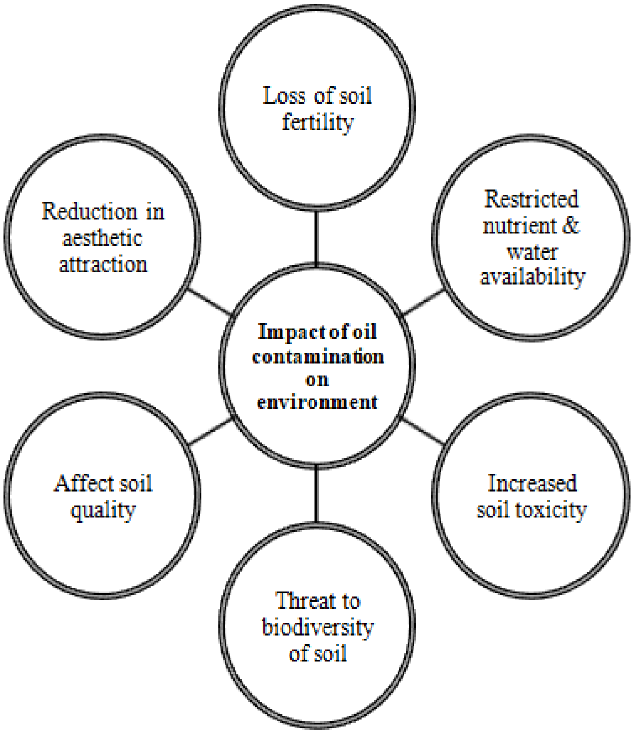

Figure 2: Concerns due to crude oil contamination of soil

Soil remediation: Preserving a precious resource

Physicochemical vs. biological methods

Many conventional physical decontamination methods, e.g., soil washing, incineration, and solvent extraction, are expensive due to diggings and moving of huge amount of contaminated material for *ex-situ* treatment (Afzal *et al.*, 2014a). Other physicochemical techniques are the use of dispersants, cleaners, emulsifiers, surfactants, soil oxidizers, abiotic transformations, and chemical inactivation (potassium permanganate/hydrogen peroxide are used as chemical oxidants to mineralize non-aqueous hydrocarbons) (Kuppusamy *et al.*, 2016). Though, there is growing discussion about the practice of these techniques as they involve the relocation of contaminants away from the original site or produce secondary pollution (Bao *et al.*, 2012; Ferradji *et al.*, 2014). Therefore, the increasing cost and limiting efficacy of these out-of-date methods have impelled the progress of innovative and substitute expertise for *in situ* remediation of contaminated lands, particularly based on biological approaches. On-site operation of biological technology is less expensive and causes minimal site disruption, therefore, it has greater public acceptance (Afzal *et al.*, 2011, 2012; Chen *et al.*, 2012; Burghal *et al.*, 2015; Athar *et al.*, 2016).

Biological methods are efficient, versatile, cost-effective, and environmentally safe (Abhilash and Yunus, 2011; Abhilash *et al.*, 2012; Shabir *et al.*, 2016; Ahsan *et al.*, 2017; Arslan *et al.*, 2017). Different biotic apparatuses that can be applied for soil clean-up are: 1) use of microbes (fungi/bacteria) to degrade carbon-based chemicals, 2) usage of plants, particularly fast-growing plants with huge biomass and 3) soil fauna (e.g., earthworms) to store or stabilize the non-degradable pollutants in their body or in the soil; and 4) the combined use of plants and bacteria i.e., microbe-assisted phytoremediation (Singh, 2009; Hodson, 2010; Banwart, 2011; Yousaf *et al.*, 2011; Ahmad *et al.*, 2012; Shehzadi *et al.*, 2014; Tara *et al.*, 2014).

Bioremediation: A natural method for the restoration of polluted sites

Bioremediation utilizes biological agents (green plants and microorganisms) or their metabolic capabilities to degrade or transform many environmental pollutants in both terrestrial and aquatic ecosystems (Ron and Rosenberg, 2014). Due to the abundance of microorganisms, their capacity to grow even in anaerobic conditions, and large biomass relative to different residing organisms inside the Earth, they make a suitable means for bioremediation. In biodegradation, microbes utilize chemical contaminants within soil as sole carbon source and degrade the desired contaminant into carbon through redox reactions (Singh, 2009; Yousaf *et al.*, 2010; Abhilash *et al.*, 2012; Hassanshahian *et al.*, 2012; Ron and Rosenberg, 2014). Byproducts are released again into the environment usually in a lesser toxic form. Microorganisms present in contaminated areas adjust themselves in keeping with the situation accordingly of which genetic transformations are activated in next generations organising them to emerge them as hydrocarbon degraders (Beškoski *et al.,* 2017). It is a well-known fact that hydrocarbon-degrading microbes in uncontaminated ecosystem constitute less than 0.1% of the total microscopic microbes. This quantity may rise up to 1-10% of the whole inhabitants in PHs contaminated site. However, overall microbial diversity in a polluted environment is declined (Nazina *et al.,* 2005; Ferradji *et al.,* 2014; Mnif *et al.,* 2014; Varjani *et al.,* 2015). Aerobic environment and suitable microorganisms are necessary for an optimal rate of bioremediation of soils contaminated with PHs. Therefore, hydrocarbon-degrading bacteria are the best candidate to be used in bioremediation of soil contaminated with crude oil because they can adapt rapidly to the contaminated environment and release variety of enzymes to detoxify pollutants (Khan *et al.,* 2013a).

Biodegradative bacteria

Hydrocarbons might be degraded completely within couple of hours, days, or months by action of microbes. A number of investigation reports indicated that low molecular weight alkanes are degraded more quickly by soil microorganisms than high molecular weight alkanes (Fuentes *et al.,* 2011; Hamzah *et al.,* 2013). Petroleum is a combination of various compounds and no individual bacterium can utilize all components present inside petroleum because single bacterium can degrade only a narrow range of hydrocarbons (Mukred *et al.,* 2008; Alkhatib *et al.,* 2011). Bioremediation requires the dynamic synergy of different microbes to treat a wide ranging environmental contaminants such as pesticides and complex hydrocarbons (Mittal and Singh, 2009; Varjani and Upasani, 2013; Sajna *et al.,* 2015). It has been suggested that certain microorganisms may make PHs more bioavailable. This could happen through the development of a bacterial biofilm specifically on PHs (Norman *et al.,* 2002; Flemming and Wingender, 2010). Several microbes have the tendency to form multi-cellular aggregates joined together to form biofilms (Dasgupta *et al.,* 2013). Biofilms can be formed by single type of bacteria or even by different species of bacteria. The potential of microbial aggregates in the biofilm communities for bioremediation is always a safer method than free-living microorganisms as the biofilm protects them during stress giving the bacterial cells a better chance of adaptation to harsh environments (Decho, 2000; Klein *et al.,* 2010).

Specific microbes have the capability to degrade aliphatics, certain can degrade monoaromatics or polyaromatics, whereas others degrade resins (Khan *et al.,* 2013a). Hydrocarbons degrading microbes and the nature of hydrocarbons degraded by them is enlisted in Figure 3.

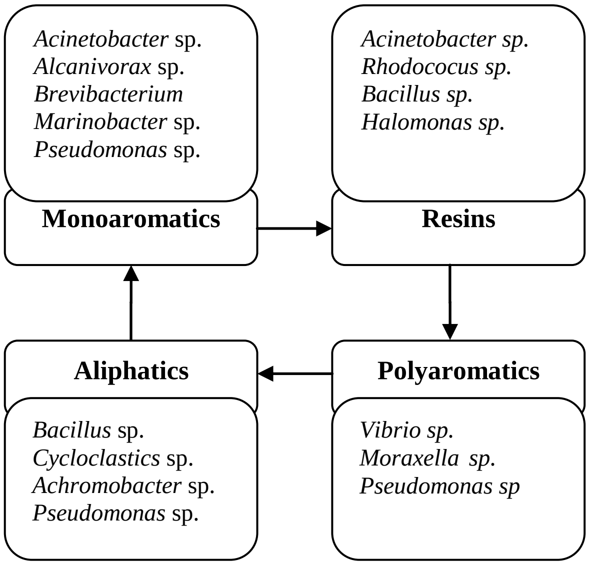

Figure 3: Bacterial species involved in the degradation of different types of PHs

Concerns associated with bioremediation

Bioremediation of PHs is thought to be a complicated phenomenon due to the lethal and hydrophobic nature of the contaminants, changes in microbial surroundings, and certain biotic and abiotic factors of soil including temperature, pH, composition, and moisture (Boopathy, 2000; Klein *et al.,* 2010). Certain factors modify the rate of microbial uptake and alter the rate of movement of contaminant to the bacteria (bioavailability) (Shukla *et al.,* 2010; Adams *et al.,* 2014; Afzal *et al.,* 2014a; Adams *et al.,* 2015). Important factors that have a significant impact on the effectiveness of bioremediation process are shown in Figure 4.

Contaminant concentration and characteristics

The type and concentration of environmental contaminants have a direct influence on microbial growth and activity. When the concentration is too high, it may have a toxic effect on bacteria. On the other hand, low concentration may prevent induction of pollutant-degrading genes present in bacteria (Bhatnagar and Kumari, 2013; Nandal *et al.,* 2015).

Bioavailability of contaminants

Bioremediation efficiency to a great extent relies upon the degree of the bioavailability of the contaminant and consequent metabolism by the microorganisms. It is generally believed that bioavailability of hydrocarbons decreases with increasing molecular mass. Moreover, the rate of bioremediation in soil decreases with increase in residence time of PHs. Aging hinders the movement of pollutants into soil leading to the alteration and/or absorption of pollutants on soil particles. This practice restrains the release of PHs into the liquid phase making them unavailable to microorganisms, thus lowering their biodegradation rate (Tang *et al.*, 1998).

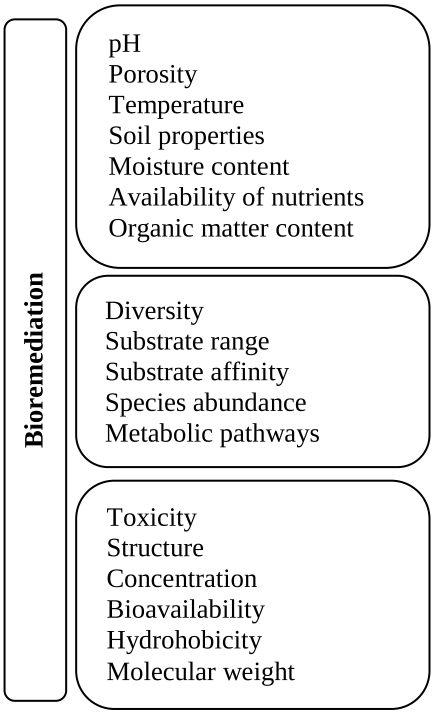

Figure 4: Factors influencing the process of bioremediation of soil contaminated with PHs

Soil properties

Another significant aspect that affects the rate of biodegradation is the chemical/physical/biological properties of soil. Due to the hydrophobic nature of PHs, they become hypothetically inaccessible for microbial degradation. Their degradation occurs when they come in contact with aqueous material as only small fraction of these mixtures become in water-dissolved condition. Additionally, the rate of biodegradation largely depends upon the soil type. Low fractions of clay and slit in soil have been associated with higher availability of hydrocarbon (Mohan *et al.*, 2006).

Temperature

It also influences the biodegradation of hydrocarbons. Despite the fact that hydrocarbon biodegradation can occur over an extensive range of temperatures, the rate of biodegradation usually declines with the diminishing temperature. It also has a major effect on microbial metabolism and consequently on microbial activity in the environment (Srivastava *et al.*, 2014).

Nutrients

Nutrients (nitrogen, phosphorus and/or iron) play an essential role in biodegradation of PHs. Appropriate amounts of these nutrients are already present in the soil but with high concentrations of pollutants there, they become limiting factors thus affecting the process of biodegradation. To overcome this limitation, nutrients can be added in useable form or with organic amendments (Foght *et al.*, 1996).

Moisture content

For efficient microbial activity, optimum amount of water in soil environment is essential. For optimal growth and development, microorganisms require approximately 25% of moisture contents in the soil (Das and Chandran, 2010).

Redox potential

It is influenced by the presence of electron acceptors including manganese and iron oxides in soil. It is suggested that redox potential increases the degradation of PHs by expanding their bioavailability thus increasing microbial metabolism (Varjani and Upasani, 2016).

Phytoremediation: Using green technology to restore contaminated environment

In general, it was believed that plants can only supply fibre, energy, and food. However, their promising role in eliminating contaminants from environment have been documented in the past two eras (Khan *et al.*, 2013a). Phytoremediation is a promising phenomenon where green plants are used to diminish, eliminate, detoxify, and immobilize toxins with the purpose of restoration of a site to a condition that can be used for private or public applications (Ijaz *et al.*, 2015). It provides a solution to the problem of sites contaminated with organic and inorganic contaminants which includes metals, insecticides, solvents, explosives, and PHs. Growth of plants and their capacity to tolerate high concentrations of pollutants are the factors responsible for their efficiency in phytoremediation (Chen *et al.*, 2015). The benefits and limitations of phytoremediation are listed in Table 1.

Plants use various mechanisms to remove and/or uptake organic and inorganic contaminants that forms the basis of phytoremediation technology. For removal of environmental contaminants, they utilize dynamic processes including rhizofiltration, phytovolatilization, phytostabilization, phytodegradation, and rhizodegradation (Meagher, 2000; Liang *et al.,* 2017). The initial step of efficient phytoremediation is plant uptake of hydrocarbons. Contaminant uptake and transport takes place in the two-vessel system of xylem and phloem for subsequent accumulation and degradation within the plant (Chen *et al.*, 2015; Patowary *et al.*, 2017; Wei *et al.*, 2017). The pathway by which pollutants enter the plants depends upon their physicochemical properties including hydrophobicity, water solubility, and vapour pressure. Hydrophobicity is usually expressed as coefficient of octanol/water partition (K_{ow}), wherein a log of K_{ow} value (0.5-3.5) make sure take-up of pollutants by plants whereas higher values mainly result in sorption to roots and insignificant translocation in aerial parts of plants (Gerhardt *et al.*, 2017; Kuppusamy *et al.*, 2017; Thomas *et al.*, 2017).

Table 1: Pros and cons of phytoremediation

Pros	Cons
In situ, proficient and environment friendly technology	Technology is limited to shallow ground water and soils. Highly dependent on soil properties and environmental conditions
Applicable on moderate and low levels of contamination	Not applicable in high concentrations of contaminants
Fast and beneficial for breaking down diverse organic pollutants	Slower than physico-chemical treatments and often in need of supplementary treatments such as nutrient supply
High public acceptance	Toxicity and nature of biodegradation products are not known
Aesthetically pleasant	Results are variable
Reduces landfill wastes	Effects to food web might be unknown
Harvestable plant material	Contaminant fates might be anonymous

Plant selection for phytoremediation

Selection of appropriate plant species is critical consideration for implementing phytoremediation strategies. Common factors for selection of trees or grasses generally include: 1) resistance to contaminants, 2) tolerance to environmental conditions, 3) high productivity, 4) low bioaccumulation, 5) suitability for various soil types, and 6) native to avoid the introduction of invasive species. Several reports indicated that shrubs, grasses, herbs and trees are suitable candidates that can be utilized for phytoremediation (Farraji *et al.*, 2017; Patel and Patra, 2017; Singha and Pandey, 2017; Shahsavari *et al.*, 2016). Legumes (e.g. alfalfa, clover, and peas), grasses (e.g. ryegrass, kallar grass, and para grass), and trees (e.g. *Populus* sp., *Conocarpus erectus* and *Acacia nilotica*) have been proven to be tolerant to hydrocarbon pollutants (Yousaf *et al.*, 2010).

Benefits of grasses, legumes, and trees in phytoremediation

Grass species are excellent contenders for phytoremediation because of their widespread fibrous root structure that result in increased rhizosphere and ultimately abundant area for microbial activity and growth (Shahsavari *et al.*, 2016). Additionally, grasses can proficiently eradicate hydrocarbons from polluted soil, without any nutrient requirement, and show broad usage to the harms associated with hydrocarbon pollution (Yi and Crowley, 2007).

The other important factor to be considered in phytoremediation is the level of nutrients in polluted soils. Soils contaminated with elevated amounts of crude oil are often deficient in nitrogen. Legumes might be utilized in phytoremediation because of their symbiotic-association with nitrogen fixers (bacteria and fungi) and arbuscularmycorrhizal fungi (Farraji *et al.*, 2017; McIntosh *et al.*, 2017). The root system of leguminous plants generally is not as flourished as grasses to reach deeper soil layers (Safronova *et al.*, 2011). Legumes have preference over non-leguminous plants on account of their inherent capacity to fix nitrogen. Moreover, legumes do not need to contend with microorganisms and different plants for accessible soil nitrogen at oil-contaminated sites; they additionally stimulate attached microorganisms by discharging nutrients into the rhizosphere (Brígido and Glick, 2015). Legumes, such as *Medicagosativa*, *Vulpiamyuros,Elymus* sp., *Trifolium* sp. and *Phalarisarundinacea* have been effectively applied to clean polluted places, particularly petrochemical waste polluted sites (Minoui *et al.*, 2015).

Trees additionally play an essential role in the process of phytoremediation. Proper selection of tree species and variety/genotype is important criteria to predict the phytoremediation efficacy (Hussain *et al.*, 2017; Luo *et al.*, 2017). Trees typically have greater root biomass and deeper root systems than grasses, thereby occupying a greater soil volume than grasses. Common reasons behind the excessive use of trees in phytoremediation are their easy propagation, fast growth, deep root systems that stretch out to the water table, high water take-up rates, maximum absorption surface areas, perennial growth, and/or tolerance to contaminants (Iori *et al.,* 2017). For instance, poplar and willows have been carefully chosen as potential contestants in phytoremediation of both organic and inorganic contaminants (Mathur *et al.*, 2010).

Microbe-assisted phytoremediation: An optimal approach to revitalize ecosystem

The efficacy of plant-based remediation is often restricted by two factors: (1) the toxic nature of environmental contaminants, and (2) loss of soil fertility in the form of unavailability of nutrients and modification of soil texture. In contrast, microbial degradation often faces difficulty due to the inability of existing microflora to degrade the contaminants, insufficient nutrients in contaminated soil, and low bioavailability of pollutants (Noroozi *et al.,* 2017; Patel and Patra, 2017). Therefore, an optimal system is obligatory in order to overcome these constraints. Dynamic synergy between plant roots and soil microorganisms has received great attention due to the possible role of bacteria in plant development and degradation of PHs (Kamath *et al.,* 2004; Vaziri *et al.,* 2013). The inoculation of specific bacteria increases plant resistance to pollutant stress and enhances plant biomass. In response, vegetation, through its rhizospheric effects, supports the proliferation of hydrocarbon degrading microbes, which results in the mineralization of recalcitrant organic pollutants (Kuiper *et al.,* 2004; Glick, 2010). The combined use of phytoremediation and microbial augmentation techniques develop a more effective strategy for the restoration of recalcitrant pollutants, predominately polyaromatic hydrocarbons (Afzal *et al.,* 2013; Khan *et al.,* 2013b; Arslan *et al.,* 2014).

While it is broadly accepted that bacteria and fungi are chief mediators in hydrocarbon degradation, bacteria have been revealed to be more versatile than fungi (Weyens *et al.,* 2009; Khan *et al.,* 2013a; Sessitsch *et al.,* 2013). Bacteria are ubiquitous -living in the rhizosphere, rhizoplane/ phyllosphere, and plant interior, thus can be considered active players in the cleanup strategy for hydrocarbon remediation (Truu *et al.,* 2015; Pandey *et al.,* 2016a). Microbes having both hydrocarbon-degrading and plant growth promoting (PGP) abilities more actively reduce stress symptoms in plants and detoxify soil pollutants as compared to microorganisms having just contaminant degrading/PGP capabilities (Ma *et al.,* 2011). Plant growth promoting bacteria actively stimulate the growth via different mechanisms, such as fixation of N_2, P-solubilization, siderophores, and production of 1-amino cyclopropane 1-carboxylate (ACC) deaminase, thus assisting plants to overcome stress, enhance plant defense towards pathogens, and stimulate biodegradation process (Figure 5) (Compant *et al.,* 2010). Ethylene (plant hormone) assumes a vital part in root initiation, extension, fruit ripening, and in stress signaling too. The inhibition of growth that occurs as a result of environmental stress is the outcome of the plant reaction to increased amounts of ethylene (Belimov *et al.,* 2001). However, bacteria producing ACC deaminase can bring down levels of ethylene by cleaving the ethylene precursor ACC and mitigate stress in developing plant (Saleem *et al.,* 2007; Rai *et al.,* 2016). Numerous bacteria produce indole 3-acetic acid (IAA) which plays an important role in the development of extensive root system and prompting enhanced uptake of nutrient that, thus, stimulates bacterial propagation in root zone (Saleem *et al.,* 2007). It has been recommended that bacterium producing IAA might prevent the deleterious impacts of environmental stresses on plant development. Thus, the collective application of vegetation and such microorganisms may be an important alternative for remediation of oil-polluted soils (Benson *et al.,* 2017; Salam *et al.*, 2017; Spada *et al.*, 2017).

The adequacy of plant-bacteria partnership relies to a great extent upon the persistence and metabolic capability of bacteria harboring catabolic genes necessary for the enzymatic degradation of PHs (McGenity *et al.,* 2012; Shankar *et al.,* 2014). It is additionally essential to screen the abundance and expression of specific genes during remediation of oil-polluted soil to get proof of the survival and metabolic activity of the inoculated microbes (Afzal *et al.,* 2011, 2012, 2013). Culture-dependent techniques are classical means of determining microbial population changes. Though, less than 1% of environmental bacteria are cultivable (Andria *et al.,* 2009). Culture-independent procedures have opened gateways for a deeper understanding of microbial communities enlightening information about gene abundance and expression (Yan *et al.,* 2016). Culture-independent approaches give molecular insights of the bacteria present in a particular site at a definite time (Gandolfi *et al.,* 2017; Wang *et al.,* 2017). Nucleic acids are also analyzed by way of fingerprinting of functional genes (e.g., *alkB* gene) or a quantitative PCR (*q*PCR) to reveal the presence of specific bacteria in an environment (Blain *et al.,* 2017; Li *et al.,* 2017).

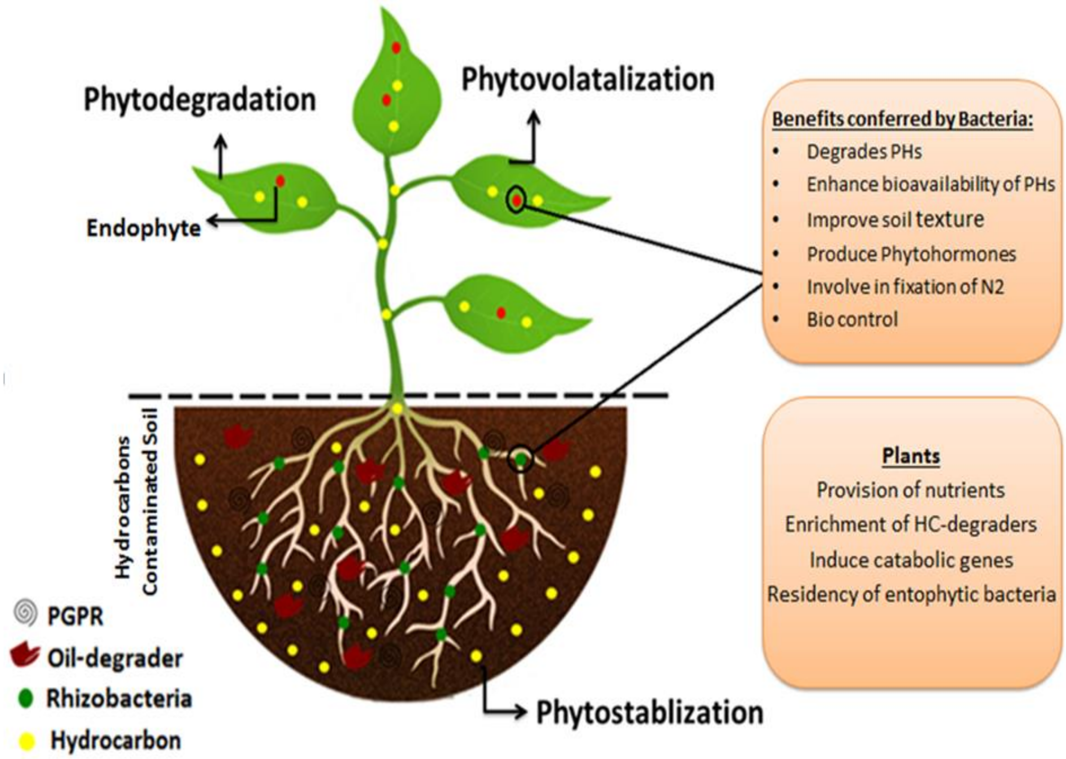

Figure 5: Plant-microbe interactions that lead to remediation of soils contaminated with PHs

Rhizoremediation: Use of rhizobacteria to enhance hydrocarbon phytoremediation

Rhizoremediation is described as the use of plants and their root-associated microorganisms to decontaminate oil-polluted soils. This beneficial association relies on the fact that bacteria increase the bioavailability and degradation of organic pollutants, in turn, plants provide residency and food to the bacteria (Muratova *et al.*, 2003; Weyens *et al.*, 2009).Despite the fact that rhizoremediation happens naturally, but through deliberate manipulation (inoculating the soil with contaminant degrading and/or PGP bacteria) in rhizosphere it can be enhanced (Hernández-Vega *et al.*, 2017; Vergani *et al.*, 2017).

The rhizosphere is a densely-populated zone wherein enhanced microbial activities are witnessed and plant roots have interaction with soil-borne microorganisms by exchange of essential supplements, growth factors and so forth (Abioye *et al.*, 2017; Kong and Glick, 2017). Increased removal of persistent contaminants in the rhizosphere is perhaps the consequence of greater microbial populations and functional actions around the roots of plants. Growing plants release a diversity of chemicals in root exudates. Following root exudation, the proliferation of specific group of bacteria is 10-1000 folds more prominent in the rhizosphere than in the bulk soil; this occurs due to excessive level of nutrients found in exudates (Adam, 2016; Maddela *et al.*, 2016; Wu *et al.*, 2017). The properties, amount and timing of root exudation are critical for rhizoremediation process (Kang, 2014). In soil, plants may react to chemical stress with the aid of changing the composition of nutrients that, thus, adjust the metabolic potential of microorganisms. The microbial activity in the close vicinity of the root seems to offer a promising environment for degradation of obstinate chemicals (Hassanshahian *et al.*, 2012; Hassanshahian *et al.*, 2014). These activities also increase the bioavailability of soil-bound nutrients and degradation of phytotoxic soil contaminants in the rhizosphere (Gkorezis *et al.*, 2016).

Rhizobacteria with plant growth-promoting capability have been conventionally used in agricultural science to improve crop yields. Nevertheless, prospective role in the remediation of environmental pollutants have been sightseen in recent times (Dong *et al.*, 2014; Ajuzieogu *et al.*, 2015; Hou *et al.*, 2015). Organic compounds including PHs, pesticides, chlorinated compounds (polychlorinated biphenyl), explosives, organophosphate insecticides (diazinon and parathion), and surfactants (detergents) are more rapidly degraded by rhizospheric bacteria (PizarroTobías *et al.*, 2015; Thijs and Vangronsveld, 2015).

The successful application of rhizoremediation largely depends upon survival and establishment of bacteria in the rhizosphere. This phenomenon has been widely studied, but the complete mechanism is as yet not clear; it has been suggested that it may be because of the secretion of certain compounds (e.g. polysaccharides) and other phenomenon such as chemotaxis (Afzal *et al.*, 2013; Fester *et al.*, 2014).

It is supposed that a plant and its related bacteria establish bacterial colonization on root surface through complex chemical signals which includes hydrogen peroxide, superoxide anion and especially flavonoids (Lugtenberg *et al.,* 2001; De Weert *et al.,* 2002; Kamilova *et al.,* 2006; Nadeem *et al.,* 2016). This communication is of extreme significance for the persistence and colonization of applied bacteria in the plant rhizosphere. Numerous investigations have been executed to see persistence of inoculated bacteria, especially through labelling of inoculated bacterial strains with a marker gene, for example *gfp* encoding green fluorescent protein, *gusA* encoding ß-glucuronidase and so forth (Swamy *et al.,* 2016).

Endophyte-assisted phytoremediation

In addition to rhizobacteria, plants are internally colonized by bacteria, fungi, and actinomycetes. Endophytes can be defined as pathogenic and nonpathogenic microbes living inside plant organs (root/shoot). They are ubiquitous (found in all plant species), diverse in nature, and residing in a dormant or active state in the plant tissues (Compant *et al.,* 2010). Endophytes interact more closely with the host while savoring a less competitive environment which has high amount of nutrients and is highly protective against wide-ranging fluctuations than the environment that rhizo- or phyllospheric bacteria usually face. Endophytes gain entry in plant tissue through the roots, followed by habitation in the root cortex or aerial parts of plants via plant vascular system. Additionally, cell wall-degrading enzymes favor the entrance of such microbe into plants. Endophytes have to proliferate in the rhizosphere before entering the plant (Afzal *et al.,* 2014a). Additionally, cell wall-degrading enzymes favour the entrance of such microbe into plants. Endophytes have to proliferate in the rhizosphere before entering the plant (Blain *et al.,* 2017; Oliveira *et al.,* 2017). During endophytic colonization, bacteria move to the plant roots either inertly by soil water oscillations or actively through particular stimulation of flagella. In addition, root exudates, act as indicators for chemotactic movements and provide a nutrient-rich environment for active colonization (Shehzadi *et al.,* 2016; Zhu *et al.,* 2017a).

Despite the fact that rhizoremediation seems promising, the contaminant is not accessible to the rhizospheric microflora because its residence time is very much lower in the rhizosphere (Pandey *et al.,* 2016b; Su *et al.,* 2016; Zhu *et al.,* 2017b). Here, endophytic bacteria get the chance to breakdown the contaminants with the assistance of their intracellular enzymes before than the contaminants are evapotranspired. Additionally, a most important advantage of endophytic bacteria over rhizobacteria is that they are living inside the tissues of the host plant and consequently have lesser competition for nutrients and space (Shehzadi *et al.,* 2016; Goodwin and Gao, 2017).

Endophytes assume a key role in plant's adaptation to contaminated surroundings and furthermore improve phytoremediation by transforming contaminants, stimulating plant growth, subsiding phytotoxicity, and improving overall plant's health (Compant *et al.,* 2005; Compant *et al.,* 2008).Many endophytic bacteria exhibit PGP activities, for example nitrogen fixation, production of phytoharmones (IAA and ACC deaminase) and hydrolytic enzymes (HCN and siderophores) (Weyens *et al.,* 2009).These PGP actions of endophytic bacteria improve the plant growth in contaminated soils and eventually phytoremediation efficiency. Further to modify the phytohormone intensities in plants, some endophytes can speed up plant growth via fixation of nitrogen (Naveed *et al.,* 2014). An outstanding illustration is the nitrogen-fixing endophytes of sugarcane, which provides ample nitrogen to the plant and enhance plant growth. Moreover, some endophytes enhance plant growth by enhancing mineral nutrition or increasing resilience to biotic and abiotic stresses (Compant *et al.,* 2016).

Metabolic pathways for biodegradation of PHs

Most microbial species do not contain all the appropriate enzymes so degradation is a collective function of a consortium of microorganisms belonging to different genera. Microbes either catabolize organic contaminants to get energy or integrate them into cell biomass (Rahman *et al.,* 2003).

Hydrocarbon-degrading bacteria may be categorized into two groups: 1) aerobic, and 2) anaerobic. Aerobic conditions facilitate the fastest and complete degradation of most hydrocarbons because during metabolic activities oxygen is available as an electron acceptor (Abbasian *et al.,* 2015; Pugazhendi *et al.,* 2016). Conceivable exterior pathways for aerobic biodegradation of *n*-alkanes and aromatic hydrocarbons are described in Figure 6.

Aerobic biodegradation

In aliphatic hydrocarbons, the crucial step for aerobic degradation involves the addition of oxygen by oxygenases and peroxidases (Tolosa *et al.,* 2004). Peripheral degradation pathways (terminal/sub-terminal oxidation) convert activated molecules to intermediates in a step-by-step process followed by conversion into a fatty acid. This molecule is then conjugated to coenzyme A which forms an acyl-CoA which is then converted into acetyl-CoA (final product). Acetyl-CoA enters in the Krebs cycle and eventually completely oxidized to CO_2 (Chandra *et al.,* 2013). Other oxidation pathways include di- and sub-terminal oxidation of *n*-alkanes. In di-terminal pathway, oxidation of both ends of alkane molecule takes place through x-hydroxylation (x position represents terminal methyl group) of fatty acids. It is then further converted into dicarboxylic acid and processed by ß-oxidation pathway. Cell biomass is produced from the central precursor metabolites (acetyl-CoA and pyruvate).

Polyaromatic hydrocarbons such as biphenyls and naphthalene are more persistent in the environment than saturated hydrocarbons (Field *et al.*, 1995). Due to their toxic nature, they are the priority pollutants in bioremediation programs. For initial activation, four different enzymes are involved; 1) the non-heme iron oxygenases, 2) the soluble di-iron multi component, 3) the flavoproteinmonooxygenases, and 4) the CoA ligases (Nishino *et al.*, 2000). Unlike aliphatic hydrocarbon degradation, activated molecule is not transformed to alkanol but rather to intermediates of phenol (catechol). (Kulkarni and Chaudhari, 2007). Intradiol or extradioldioxygenases will further convert these phenol intermediates to di or tri-hydroxylated aromatic compounds that may be enters into the Krebs cycle and completely metabolized into CO_2 (Abramowicz, 1990).Hydrocarbon degrading bacteria cleave benzene ring in diverse ways by

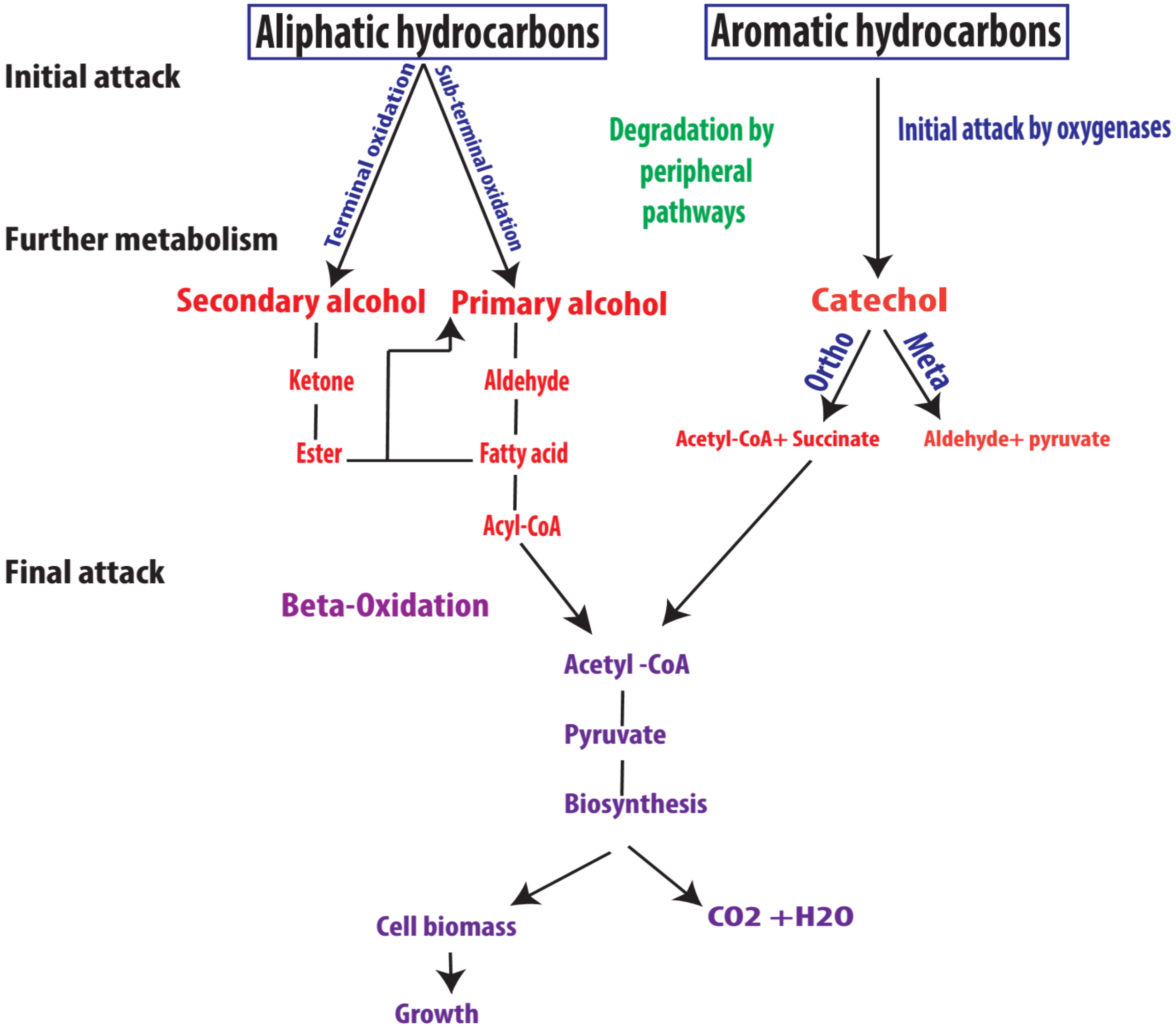

Figure 6: Schematic overview of metabolic pathways for hydrocarbons (aliphatic and aromatic) utilization by aerobic bacteria. Ortho: ortho cleavage pathway, meta: meta cleavage pathway, CoA: coenzyme A

appropriate enzymes. In PAHs, benzene rings are degraded one after the other. But in case of cyclic alkanes, transition from alkane to alcohol takes place which is further dehydrogenated to ketones by an oxidase system. Alkenes may be attacked by (a) terminal oxygenase, (b) sub-terminal oxygenase, and (c) oxidation of double bond to resultant epoxide/diol.

Anaerobic biodegradation

Microbial degradation of various substrates, specifically obstinate hydrocarbons, is restricted under anaerobic conditions because O_2 is prerequisite for this process (Varjani and Upasani, 2017). Understanding of the mechanism of anaerobic degradation is more recent as compared to aerobic degradation. Therefore, less information is available about the genes and enzymes involved in these pathways. During degradation of PHs, anaerobic bacteria offer nutrients required for the growth of other catabolizing bacteria (Varjani, 2017). A large variety of microorganisms (bacteria and archaea) have been identified with the capability to degrade hydrocarbon molecules anaerobically. These bacteria exploit anaerobic respiration via nitrate, nitrite, and metal ions or fermentation during substrate catabolism (Lueders, 2017; Portugal *et al.*, 2017).

Table 2: Bacterial and plant enzymes involved in alkane degradation

Enzyme	Catalytic action	Origin/Reference
Dehalogenase	Involved in release of chlorine and fluorine from halogenated straight chain and ring compounds	*Xantho bacterautotrophicus*, *Populus* spp and *Protobacteria* (Compant *et al.*, 2010)
Lacasse	Degrade numerous aromatic hydrocarbons	*Alfalfa, Trametesversicolor* and *Coriolopsispolyzona* (Alaxender 1978; Reda *et al.*, 2010)
Dioxygenase	Degrade specific aromatic rings	*Pseudomonas* sp., *Mycobacterium* sp. (Mohan *et al.*, 2006)
Peroxidase	Involved in degradation of several aromatic compounds; dehalogenation of various n-alkanes	*Armoraciarusticana, Phaneroc haetechrysosporidium, Phanerochaetelaevis, Medicago sativa* (Foght *et al.*, 1996)
Nitrilase	Cleaves cyanide group from aliphatic and aromatic nitriles	*Salix* spp., *Aspergillusniger* (Klein *et al.*, 2010)
Nitroreductase	Reduces nitro groups on nitro-aromatic compounds; removes N from ring structures	*Comamonas*sp, *Pseudomonas putida, Populus*spp (Ijaz *et al.*, 2015)
Phosphatase	Cleaves phosphate groups from pesticides	*Spirodelapolyrhiza* (Bhatnagar and Kumari 2013)
Cytochrome p450 monooxygenase	Hydroxylation of ring and straight chain hydrocarbons	Bacteria, fungi and plants (Iori *et al.*, 2017)

For anaerobic bacteria, alkanes with smaller chain length are difficult to degrade than alkanes having mid- to long-chain lengths. In anaerobic conditions, short-length hydrocarbons (up to n-C17) do not dissipate easily, so these compounds can develop and exert a harmful effect on the cell wall of bacteria, thus inhibiting their growth. Moreover, sulphate reducing bacteria degrade branched alkanes more efficiently than straight chain alkanes (Arulazhagan *et al.*, 2017; Ghattas *et al.*, 2017).

Anaerobic degradation is commonly established in deep and anoxic environments for example natural oil seeps on land/ocean and the sites polluted with oil. Likewise, this kind of biodegradation can happen beneath the surface of areas where aerobic biological activity has been ceased as all the oxygen is used. After oxygen exhaustion, there may be a consecutive employment of the electron acceptors (nitrate, ferric iron, sulphate, and hydrogen) to supply energy from the hydrocarbon mineralization (Aktas *et al.*, 2017; Arulazhagan *et al.*, 2017; Ghattas *et al.*, 2017; Lueders, 2017).

Enzymatic biodegradation

In order to explore functional genes involved in degradation of hydrocarbons, one must have knowledge about the enzymes involved in biodegradation. Though there are few bacteria that can fully mineralize the particular organic pollutant, single species usually do not have the capability to degrade PHs or lack entire degradation pathways (Peixoto *et al.*, 2011). However, consortium of heterogeneous bacterial strains can effectively degrade these recalcitrant compounds fully.

Details of bacterial and plant based degradative enzymes (Van Beilen and Funhoff, 2007) are depicted in Table 2.

The prokaryotic monooxygenases isolated are catalogued into two sets on the basis of their electron transport system and the microorganisms in which they are available: (a) enzyme dependent on rubredoxin (2FeO), in most of bacteria this enzyme is encoded by *alkB* gene and *alkM* specifically in *Acinetobacter* sp., (b) cytochrome P450 monooxygenase belonging to CYP153 family of microbes. Alkane hydroxylase enzyme was firstly described in *Pseudomonas putida*GPo1 where it was located on the OCT plasmid and was reported to be organized in two operons: *alkBFGHJKL*and *alkST* (Throne-Holst *et al.,* 2007).

The cytochrome P450 enzymes are set of heme (iron protoporphyrin IX) comprising monooxygenase enzymes that work in association with sub-atomic oxygen, and an electron-transfer system to oxidize diverse range of compounds (Muangchinda *et al.,* 2015). Rather than eukaryotes, the bacterial cytochrome P450 are soluble in the cytoplasm. The structures of these enzymes vary from species to species.

Moving on, with extensive distribution ranges, various genotypes, and sufficient previous research results, *alkB* gene is considered an encouraging useful biomarker to monitor potential of bioremediation at a site of oil pollution. A number of studies attempted to communicate the degradation practices or contaminant mineralization to kinetic changes of *alkB* gene diversity, abundance, or expression *in situ* (Van Beilen and Funhoff, 2007; Peixoto *et al.,* 2011; Muangchinda *et al.,* 2015).

Conclusion and future prospects

Soil pollution might increase in coming years due to speedy population growth and as a result an enhancement in industrialization, urbanization and intensive agriculture all over the world. To alleviate the harsh belongings of soil pollution by organic chemicals, phytoremediation might be an efficient and inexpensive methodology to remediate contaminated soil and water. Nevertheless, several features still need to be studied to make this technology effective. In particular, consideration should be paid to the exploitation of plant-endophyte synergisms for the clean-up of polluted soil and water. In the case of remediation of soil and water polluted with organic chemicals, endophytes harboring the suitable degradation pathway(s) can support their host plant by degrading pollutants that are freely absorbed by plants. To investigate the whole microbial diversity in a particular environment, the isolation and identification of microorganisms is not an appropriate technique. The modern metagenomic approach facilitate scientists to analyze the complete bacterial diversity, and the genetic capability for the active metabolic pathways existing in a specified environment. This practice is particularly effective for the study of the biodiversity and genome analysis of complex environmental samples where most of microorganisms cannot be cultured under normal laboratory conditions.

References

Abbasian, F., R. Lockington, M. Mallavarapu and R. Naidu. 2015. A comprehensive review of aliphatic hydrocarbon biodegradation by bacteria. *Applied Biochemistry and Biotechnology* 176: 670-699.

Abhilash, P., J.R. Powell, H.B. Singh and B.K. Singh. 2012. Plant-microbe interactions: Novel applications for exploitation in multipurpose remediation technologies. *Trends in Biotechnology* 30: 416-420.

Abhilash, P. and M. Yunus. 2011. Can we use biomass produced from phytoremediation? *Biomass Bioenergy* 35: 371-1372.

Abioye, O., U. Ijah and S. Aransiola. 2017. Phytoremediation of soil contaminants by the biodiesel Plant *Jatropha curcas*, phytoremediation potential of bioenergy plants. *Springer* 12: 97-137.

Abramowicz, D.A. 1990. Aerobic and anaerobic biodegradation of PCBs: *Critical Review in Biotechnology* 10: 241-251.

Adam, M. 2016. Biodegradation of marine crude oil pollution using a salt-tolerant bacterial consortium isolated from Bohai Bay, China. *Marine Pollution Bulletin* 105: 43-50.

Adams, G., P. Tawari-Fufeyin and E. Igelenyah. 2014. Bioremediation of spent oil contaminated soils using poultry litter. *Research Journal of Applied Sciences* 3: 124-130.

Adams, G.O., P.T. Fufeyin, S.E. Okoro and I. Ehinomen. 2015. Bioremediation, biostimulation and bioaugmention. *International Journal of Environmental Bioremediation and Biodegradation* 3: 28-39.

Afzal, M., Q.M. Khan and A. Sessitsch. 2014. Endophytic bacteria: Prospects and applications for the phytoremediation of organic pollutants. *Chemosphere* 117: 232-242.

Afzal, M., S. Khan, S. Iqbal, M.S. Mirza and Q.M. Khan. 2013. Inoculation method affects colonization and activity of *Burkholderia phytofirmans* PsJN during phytoremediation of diesel-contaminated soil. *International Biodeterioration and Biodegradation* 85: 331-336.

Afzal, M., S. Yousaf, T.G. Reichenauer, A. Sessitsch. 2012. The inoculation method affects colonization and performance of bacterial inoculant strains in the phytoremediation of soil contaminated with diesel oil. *International Journal of Phytoremediation* 14: 35-47.

Afzal, M., S. Yousaf, T.G. Reichenauer, M. Kuffner, A. Sessitsch. 2011. Soil type affects plant colonization, activity and catabolic gene expression of inoculated bacterial strains during phytoremediation of diesel. *Journal of Hazardous Materials* 186: 1568-1575.

Aguilera, F., J. Méndez, E. Pásaro, B. Laffon. 2010. Review on the effects of exposure to spilled oils on human health. *Journal of Applied Toxicology* 30: 291-301.

Ahmad, F., S. Iqbal, S. Anwar, M. Afzal, E. Islam, T. Mustafa, Q.M. Khan. 2012. Enhanced remediation of chlorpyrifos from soil using ryegrass (*Lollium multiflorum*) and chlorpyrifos-degrading bacterium *Bacillus pumilus* C2A1. *Journal of Hazardous Materials* 237-238: 110-115.

Ahmed, M.M.M., M.B.D. Mazen, N.A. Nafady and O.A. Monsef. 2017. Bioavailability of cadmium and nickel to *Daucus carota* L. and *Corchorus olitorius* L. treated by compost and microorganisms. *Soil & Environment* 36: 1-12.

Ahsan, M.T., M. Najam-ul-haq, M. Idrees, I. Ullah, M. Afzal. 2017. Bacterial endophytes enhance phytostabilization in soils contaminated with uranium and lead. *International Journal of Phytoremediation* 19(10): 937-946.

Ajuzieogu, C.A., A.A. Ibiene, H.O. Stanley. 2015. Laboratory study on influence of plant growth promoting rhizobacteria (PGPR) on growth response and tolerance of *Zea mays* to petroleum hydrocarbon. *African Journal of Biotechnology* 14: 2949-2956.

Aktas, D.F., K.R. Sorrell, K.E. Duncan, B. Wawrik, A.V. Callaghan and J.M. Suflita. 2017. Anaerobic hydrocarbon biodegradation and biocorrosion of carbon steel in marine environments: The impact of different ultra low sulfur diesels and bioaugmentation. *International Biodeterioration and Biodegradation* 118: 45-56.

Al-Majed, A.A., A.R. Adebayo and M.E. Hossain. 2012. A sustainable approach to controlling oil spills. *Journal of Environmental Management* 113: 213-227.

Albaigés, J. 2014. Ecotoxicology: Effects of pollutants on the natural environment. 2014 edition, USA: Taylor Francis.

Alexander, M., 1978. Introduction to soil microbiology. *Soil Science* 125: 331.

Alkhatib, M.A.F., Z. Alam, S.A. Muyibi and A. Husain, 2011. An isolated bacterial consortium for crude oil biodegradation. *African Journal of Biotechnology* 10: 18763-18767.

Andreoni, V., L. Cavalca, M. Rao, G. Nocerino, S. Bernasconi, E. Dell Amico, M. Colombo, L. Gianfreda. 2004. Bacterial communities and enzyme activities of PAHs polluted soils. *Chemosphere* 57: 401-412.

Andria, V., T.G. Reichenauer and A. Sessitsch. 2009. Expression of alkane monooxygenase (*alkB*) genes by plant-associated bacteria in the rhizosphere and endosphere of Italian ryegrass (*Lolium multiflorum* L.) grown in diesel contaminated soil. *Environmental Pollution* 157: 3347-3350.

Aqeel, A and M.S. Butt. 2001. The relationship between energy consumption and economic growth in Pakistan. *Asia-Pacific Development Journal* 8: 101-110.

Arslan, M., M. Afzal, I. Amin, S. Iqbal and Q.M. Khan. 2014. Nutrients can enhance the abundance and expression of alkane hydroxylase CYP153 gene in the rhizosphere of ryegrass planted in hydrocarbon-polluted soil. *PloS One* 9: 111-208.

Arslan, A., A. Imran, Q.M. Khan and M. Afzal. 2017. Plant-bacteria partnerships for the remediation of persistent organic pollutants. *Environmental Science and Pollution Research* 24(5): 4322-4336.

Arulazhagan, P., S. Mnif, J.R. Banu, Q. Huda and M. Jalal. 2017. Biodegradation of hydrocarbons by extremophiles, biodegradation and bioconversion of hydrocarbons. *Springer* 18: 137-162.

Athar, H.R., S. Ambreen, M. Javed, M. Hina, S. Rasool, Z.U. Zafar, H. Manzoor, C.C. Ogbaga, M. Afzal, F. Al-Qurainy and M. Ashraf. (2016). Influence of sub-lethal crude oil concentration on growth, water relations and photosynthetic capacity of maize (*Zea mays* L.) plants. *Environmental Science and Pollution Research* 23: 18320-18331.

Atlas, R.M. 1981. Microbial degradation of petroleum hydrocarbons: An environmental perspective. *Microbiological Reviews* 45: 180.

Bachmann, R.T., A.C. Johnson and R.G. Edyvean. 2014. Biotechnology in the petroleum industry. *International Biodeterioration and Biodegradation* 86: 225-237.

Balba, M., N. Al-Awadhi and R. Al-Daher. 1998. Bioremediation of oil-contaminated soil: Microbiological methods for feasibility assessment and field evaluation. *Journal of Microbiological Methods* 32: 155-164.

Banwart, S. 2011. Save our soils. *Nature* 474: 151-152.

Bao, M.T., L.N. Wang, P.Y. Sun, L.X. Cao, J. Zou, Y.M. Li. 2012. Biodegradation of crude oil using an efficient microbial consortium in a simulated marine environment. *Marine Pollution Bulletin* 64: 1177-1185.

Belimov, A.A., V.I. Safronova, T.A. Sergeyeva, T.N. Egorova, V.A. Matveyeva, V.E. Tsyganov, A.Y.

Borisov, I.A. Tikhonovich, C. Kluge, A. Preisfeld. 2001. Characterization of plant growth promoting rhizobacteria isolated from polluted soils and containing 1-aminocyclopropane-1-carboxylate deaminase. *Canadian Journal of Microbiology* 47: 642-652.

Benson, A., G. Ram, A. John and M. Melvin Joe. 2017. Inoculation of 1-aminocyclopropane-1-carboxylate deaminase–producing bacteria along with biosurfactant application enhances the phytoremediation efficiency of *Medicago sativa* in hydrocarbon-contaminated soils. *Bioremediation Journal* 21: 20-29.

Beškoski, V.P., S. Miletić, M. Ilić, G. Gojgić Cvijović, P. Papić, N. Marić Šolević T. Knudsen, B.S. Jovančićević, T. Nakano, M.M. Vrvić. 2017. Biodegradation of isoprenoids, steranes, terpanes, and phenanthrenes during *in situ* bioremediation of petroleum contaminated groundwater. *Clean Soil Air Water* 45: 189-195.

Bhatnagar, S., R. Kumari. 2013. Bioremediation: A sustainable tool for environmental management. *Annual Research and Review in Biology* 3: 974-993.

Blain, N.P., B. Helgason, J.J. Germida. 2017. Endophytic root bacteria associated with the natural vegetation growing at the hydrocarbon contaminated bitumount provincial historic site. *Canadian Journal of Microbiology* doi/10.1139/cjm-2017-0039.

Boopathy, R. 2000. Factors limiting bioremediation technologies. *Bioresource Technology* 74: 63-67.

Brevik, E., A. Cerdà, J. Mataix-Solera, L. Pereg, J. Quinton, J. Six and K.V. Oost. 2015. The interdisciplinary nature of soil. *Soil* 1: 117.

Brígido, C., B.R. Glick. 2015. Phytoremediation Using Rhizobia. In: Ansari A., Gill S., Gill R., Lanza G., Newman L. (eds) Phytoremediation. Springer, Cham, pp. 114-120.

Burghal, A.A., N.A. Al-Mudaffar and K.H. Mahdi. 2015. *Ex situ* bioremediation of soil contaminated with crude oil by use of actinomycetes consortia for process bioaugmentation. *European Journal of Experimental Biology* 5: 24-30.

Chandra, S., R. Sharma, K. Singh, A. Sharma. 2013. Application of bioremediation technology in the environment contaminated with petroleum hydrocarbon. *Annals of Microbiology* 63: 417-431.

Chaudhry, Q., M. Blom-Zandstra, S.K. Gupta, E. Joner. 2005. Utilising the synergy between plants and rhizosphere microorganisms to enhance breakdown of organic pollutants in the environment. *Environmental Science and Pollution Research* 12: 34-48.

Chen, B., M. Yuan, L. Qian. 2012. Enhanced bioremediation of PAH-contaminated soil by immobilized bacteria with plant residue and biochar as carriers. *Journal of Soils and Sediments* 12: 1350-1359.

Chen, Z.X., H.G., Ni, X. Jing, W.J. Chang, J.L. Sun and H. Zeng. 2015. Plant uptake, translocation, and return of polycyclic aromatic hydrocarbons via fine root branch orders in a subtropical forest ecosystem. *Chemosphere* 131: 192-200.

Compant, S., C. Clément and A. Sessitsch. 2010. Plant growth-promoting bacteria in the rhizo-and endosphere of plants: their role, colonization, mechanisms involved and prospects for utilization. *Soil Biology and Biochemistry* 42: 669-678.

Compant, S., H. Kaplan, A. Sessitsch, J. Nowak, E.A. Barka and C. Clément. 2008. Endophytic colonization of *Vitis vinifera* L. by *Burkholderia phytofirmans* strain PsJN: From the rhizosphere to inflorescence tissues. *FEMS Microbiology and Ecology* 63: 84-93.

Compant, S., B. Reiter, A. Sessitsch, J. Nowak, C. Clément and E.A. Barka. 2005. Endophytic colonization of *Vitis vinifera* L. by plant growth-promoting bacterium *Burkholderia* sp. strain PsJN. *Applied and Environmental Microbiology* 71: 1685-1693.

Compant, S., K. Saikkonen, B. Mitter, A. Campisano and J. Mercado-Blanco. 2016. Editorial special issue: soil, plants and endophytes. *Plant Soil* 405: 1-11.

Das, N., P. Chandran. 2010. Microbial degradation of petroleum hydrocarbon contaminants: An overview. *Biotechnology Research International* 2011: 1-13.

Dasgupta, D., R. Ghosh and T.K. Sengupta. 2013. Biofilm-mediated enhanced crude oil degradation by newly isolated *Pseudomonas* species. ISRN Biotechnology. 2013: 250749.

De Weert, S., H. Vermeiren, I.H. Mulders, I. Kuiper, N. Hendrickx, G.V. Bloemberg, J. Vanderleyden, R. De Mot and B.J. Lugtenberg. 2002. Flagella-driven chemotaxis towards exudate components is an important trait for tomato root colonization by *Pseudomonas fluorescens*. *Molecular Plant-Microbe Interactions* 15: 1173-1180.

Decho, A.W. 2000. Microbial biofilms in intertidal systems: An overview. *Continental Shelf Research* 20: 1257-1273.

Dong, R., L. Gu, C. Guo, F. Xun and J. Liu. 2014. Effect of PGPR *Serratia marcescens* BC-3 and AMF Glomus intraradices on phytoremediation of petroleum contaminated soil. *Ecotoxicology* 23: 674-680.

Farraji, H., N.Q. Zaman, M.A. Zahed and H. Faraji. 2017. Role of rhizoremediation in decontaminating some hazardous pollutants, *Handbook of Research on*

Inventive Bioremediation Techniques. IGI Global, pp. 213-246.

Fatima, K., A. Imran, Q.M. Khan and M. Afzal. 2015. Bacterial rhizosphere and endosphere populations associated with grasses and trees to be used for phytoremediation of crude oil contaminated soil. *Bulletin of Environmental Contamination and Toxicology* 94: 314-320.

Fatima, K., A. Imran, I. Amin, Q.M. Khan and M. Afzal. 2016. Plant species affect colonization patterns and metabolic activity of associated endophytes during phytoremediation of crude oil-contaminated soil. *Environmental Science and Pollution Research* 23: 6188-6196.

Fatima, K., A. Imran, I. Amin, Q.M. Khan and M. Afzal. 2017. Successful phytoremediation of crude-oil contaminated soil at an oil exploration and production company by plants-bacterial synergism. *International Journal of Phytoremediation* (in press).

Ferradji, F.Z., S. Mnif, A. Badis, S. Rebbani, D. Fodil, K. Eddouaouda and S. Sayadi. 2014. Naphthalene and crude oil degradation by biosurfactant producing *Streptomyces* spp. isolated from Mitidja plain soil (North of Algeria). *International Biodeterioration and Biodegradation* 86: 300-308.

Fester, T., J. Giebler, L.Y. Wick, D. Schlosser and M. Kästner. 2014. Plant-microbe interactions as drivers of ecosystem functions relevant for the biodegradation of organic contaminants. *Current Opinion in Biotechnology* 27: 168-175.

Field, J.A., A.J. Stams, M. Kato and G. Schraa. 1995. Enhanced biodegradation of aromatic pollutants in cocultures of anaerobic and aerobic bacterial consortia. *Antonie van Leeuwenhoek* 67: 47-77.

Flemming, H.C. and J. Wingender. 2010. The biofilm matrix. *Nature Reviews Microbiology* 8: 623-633.

Foght, J.M., D.W. Westlake, W.M. Johnson and H.F. Ridgway. 1996. Environmental gasoline-utilizing isolates and clinical isolates of *Pseudomonas aeruginosa* are taxonomically indistinguishable by chemotaxonomic and molecular techniques. *Microbiology* 142: 2333-2340.

Fuentes, M.S., J.M. Sáez, C.S. Benimeli and M.J. Amoroso. 2011. Lindane biodegradation by defined consortia of indigenous Streptomyces strains. *Water Air and Soil Pollution* 222: 217-231.

Gan, S., E. Lau and H. Ng. 2009. Remediation of soils contaminated with polycyclic aromatic hydrocarbons (PAHs). *Journal of Hazardous Materials* 172: 532-549.

Gandolfi, I., C. Canedoli, V. Imperato, I. Tagliaferri, P. Gkorezis, J. Vangronsveld, E.P. Schioppa, M. Papacchini, G. Bestetti and A. Franzetti. 2017. Diversity and hydrocarbon-degrading potential of epiphytic microbial communities on *Platanus x acerifolia* leaves in an urban area. *Environmental Pollution* 220: 650-658.

Gerhardt, K.E., G.J. MacNeill, P.D. Gerwing and B.M. Greenberg. 2017. Phytoremediation of salt-impacted soils and use of plant growth-promoting rhizobacteria (PGPR) to enhance phytoremediation. In: Ansari A., Gill S., Gill R., R. Lanza G. and Newman L. (eds) Phytoremediation. Springer, Cham. pp. 19-51.

Ghattas, A.K., F. Fischer, A. Wick and T. Ternes. 2017. Anaerobic biodegradation of (emerging) organic contaminants in the aquatic environment. *Water Research* 13: 189-196.

Gkorezis, P., M. Daghio, A. Franzetti, J.D. Van Hamme. W. Sillen and J. Vangronsveld. 2016. The interaction between plants and bacteria in the remediation of petroleum hydrocarbons: An environmental perspective. *Frontiers in Microbiology* 7: 1836-1848.

Glick, B.R. 2010. Using soil bacteria to facilitate phytoremediation. *Biotechnological. Advances* 28: 367-374.

Goodwin, P. and W. Gao. 2017. Increased bacterial endophyte populations in *Nicotiana benthamiana* with a branched chain alkane mixture. *Plant Pathology* 23: 15-25.

Hamzah, A., C.W. Phan, N.F. Abu Bakar and K.K. Wong. 2013. Biodegradation of crude oil by constructed bacterial consortia and the constituent single bacteria isolated from Malaysia. *Bioremediation Journal* 17: 1-10.

Hassanshahian, M., G. Emtiazi and S. Cappello. 2012. Isolation and characterization of crude-oil-degrading bacteria from the Persian Gulf and the Caspian Sea. *Marine Pollution Bulletin* 64: 7-12.

Hassanshahian, M., M.S. Zeynalipour and F.H. Musa. 2014. Isolation and characterization of crude oil degrading bacteria from the Persian Gulf (Khorramshahr provenance). *Marine Pollution Bulletin* 82: 39-44.

Hernández-Vega, J.C., B. Cady, G. Kayanja, A. Mauriello, N. Cervantes, A. Gillespie, L. Lavia, J. Trujillo, M. Alkio and A. Colón-Carmona. 2017. Detoxification of polycyclic aromatic hydrocarbons (PAHs) in *Arabidopsis thaliana* involves a putative flavonol synthase. *Journal of Hazardous Materials* 321: 268-280.

Hodson, M.E. 2010. The need for sustainable soil remediation. *Elements* 6: 363-368.

Hou, J., W. Liu, B. Wang, Q. Wang, Y. Luo and A.E. Franks. 2015. PGPR enhanced phytoremediation of petroleum contaminated soil and rhizosphere microbial community response. *Chemosphere* 138: 592-598.

Huang, Y., J. Wei, J. Song, M. Chen and Y. Luo. 2013. Determination of low levels of polycyclic aromatic hydrocarbons in soil by high performance liquid chromatography with tandem fluorescence and diode-array detectors. *Chemosphere* 92: 1010-1016.

Hussain, S., M. Akram, G. Abbas, B. Murtaza, M. Shahid, N.S. Shah, I. Bibi and N.K. Niazi, 2017. Arsenic tolerance and phytoremediation potential of *Conocarpus erectus* L. and *Populus deltoides* L. *International Journal of Phytoremediation* 91: 101-106.

Ijaz, A., A. Imran, M.A. Haq, Q.M. Khan and M. Afzal. 2015a. Phytoremediation: Recent advances in plant-endophytic synergistic interactions. *Plant and Soil* 12: 1-17.

Ijaz, A., G. Shabir, Q.M. Khan and M. Afzal. 2015b. Enhanced remediation of sewage effluent by endophyte-assisted floating treatment wetlands. *Ecological Engineering* 84: 58-66.

Ijaz, A., Z. Iqbal and M. Afzal. 2016. Remediation of sewage and industrial effluent using bacterially-assisted floating treatment wetlands vegetated with *Typha domingensis. Water Science and Technology* 74: 2192-2201.

Iori, V., F. Pietrini, D. Bianconi, G. Mughini, A. Massacci and M. Zacchini. 2017. Analysis of biometric, physiological, and biochemical traits to evaluate the cadmium phytoremediation ability of *eucalypt* plants under hydroponics. *iForest-Biogeosciences and Forestry* 10: 416-420.

Janbandhu, A. and M. Fulekar. 2011. Biodegradation of phenanthrene using adapted microbial consortium isolated from petrochemical contaminated environment. *Journal of Hazardous Materials* 187: 333-340.

Kamath, R., J. Rentz, J.L. Schnoor and P. Alvarez. 2004. Phytoremediation of hydrocarbon-contaminated soils: Principles and applications. *Studies in Surface Science and Catalysis* 151: 447-478.

Kamilova, F., L.V. Kravchenko, A.I. Shaposhnikov, T. Azarova, N. Makarova and B. Lugtenberg. 2006. Organic acids, sugars, and L-tryptophane in exudates of vegetables growing on stonewool and their effects on activities of rhizosphere bacteria. *Molecular Plant-Microbe Interactions* 19: 250-256.

Kang, J.W. 2014. Removing environmental organic pollutants with bioremediation and phytoremediation. *Biotechnology Letters* 36: 1129-1139.

Khan, S., M. Afzal, S. Iqbal and Q.M. Khan. 2013a. Plant–bacteria partnerships for the remediation of hydrocarbon contaminated soils. *Chemosphere* 90: 1317-1332.

Khan, S., M. Afzal, S. Iqbal, M.S. Mirza and Q.M. Khan. 2013b. Inoculum pretreatment affects bacterial survival, activity and catabolic gene expression during phytoremediation of diesel contaminated soil. *Chemosphere* 91: 663-668.

Klein, B., P. Bouriat, P. Goulas and R. Grimaud. 2010. Behavior of *Marinobacter hydrocarbonoclasticus* SP17 cells during initiation of biofilm formation at the alkane–water interface. *Biotechnology and Bioengineering* 105: 46-468.

Kong, Z., B.R. Glick. 2017. The Role of Bacteria in Phytoremediation. *Applied Bioengineering: Innovations and Future Directions* 5: 121-134.

Kuiper, I., E.L. Lagendijk, G.V. Bloemberg and B.J. Lugtenberg. 2004. Rhizoremediation: A beneficial plant-microbe interaction. *Molecular Plant-Microbe Interactions* 17: 6-15.

Kulkarni, M. and A. Chaudhari. 2007. Microbial remediation of nitro-aromatic compounds: An overview. *Journal of Environmental Management* 85: 496-512.

Kuppusamy, S., T. Palanisami, M. Megharaj, K. Venkateswarlu and R. Naidu. 2016. *Ex-situ* remediation technologies for environmental pollutants: A critical perspective, *Reviews of Environmental Contamination and Toxicology* 236: 117-192.

Kuppusamy, S., P. Thavamani, K. Venkateswarlu, Y.B. Lee, R. Naidu and M. Megharaj. 2017. Remediation approaches for polycyclic aromatic hydrocarbons (PAHs) contaminated soils: Technological constraints, emerging trends and future directions. *Chemosphere* 168: 944-968.

Kuske, C.R., L.O. Ticknor, M.E. Miller, J.M. Dunbar, J.A. Davis, S.M. Barns and J. Belnap. 2002. Comparison of soil bacterial communities in rhizospheres of three plant species and the interspaces in an arid grassland. *Applied and Environmental Microbiology* 68: 1854-1863.

Li, J., C. Luo, M. Song, Q. Dai, L. Jiang, D. Zhang and G. Zhang. 2017. Biodegradation of phenanthrene in polycyclic aromatic hydrocarbon-contaminated wastewater revealed by coupling cultivation-dependent and-independent approaches. *Environmental Science and Technology* 45: 123-135.

Li, S., U. Turaga, B. Shrestha, T.A. Anderson, S. Ramkumar, M.J. Green, S. Das and J.E. Cañas-Carrell. 2013. Mobility of polyaromatic hydrocarbons (PAHs) in soil in the presence of carbon nanotubes. *Ecotoxicology and Environmental Safety* 96: 168-174.

Liang, X., C. Guo, C. Liao, S. Liu, L.Y. Wick, D. Peng, X. Yi, G. Lu, H. Yin and Z. Lin. 2017. Drivers and applications of integrated clean-up technologies for surfactant-enhanced remediation of environments contaminated with polycyclic aromatic hydrocarbons (PAHs). *Environmental Pollution* 225: 129-140.

Lueders, T. 2017. The ecology of anaerobic degraders of BTEX hydrocarbons in aquifers. *FEMS Microbiology Ecology*. 93: 220-234.

Lugtenberg, B.J., L. Dekkers and G.V. Bloemberg. 2001. Molecular determinants of rhizosphere colonization by *Pseudomonas*. *Annual Review of Phytopathology* 39: 461-490.

Luo, J., S. Qi, L. Peng and X. Xie. 2017. Enhanced phytoremediation capacity of a mixed-species plantation of *Eucalyptus globulus* and Chickpeas. *Journal of Geochemical Exploration* 34: 23-45.

Ma, Y., M. Prasad, M. Rajkumar and H. Freitas. 2011. Plant growth promoting rhizobacteria and endophytes accelerate phytoremediation of metalliferous soils. *Biotechnology Advances* 29: 248-258.

Maddela, N.R., R. Burgos, V. Kadiyala, A.R. Carrion and M. Bangeppagari. 2016. Removal of petroleum hydrocarbons from crude oil in solid and slurry phase by mixed soil microorganisms isolated from Ecuadorian oil fields. *International Biodeterioration and Biodegradation* 108: 85-90.

Mathur, N., J. Singh, S. Bohra, A. Bohra and A. Vyas. 2010. Phytoremediation potential of some multipurpose tree species of Indian Thar Desert in oil contaminated soil. *Advances in Environmental Biology* 23: 131-138.

McGenity, T.J., B.D. Folwell, B.A. McKew and G.O. Sanni. 2012. Marine crude-oil biodegradation: a central role for interspecies interactions. *Aquatic Biosystems* 1: 8-10.

McIntosh, P., C.P. Schulthess, Y.A. Kuzovkina and K. Guillard. 2017. Bio-and phytoremediation of total petroleum hydrocarbons (tph) under various conditions. *International Journal of Phytoremediation*, 2: 12-20.

Meagher, R.B. 2000. Phytoremediation of toxic elemental and organic pollutants. *Current Opinion in Plant Biology* 3: 153-162.

Minoui, S., D. Minai-Tehrani and M.H. Shahriari. 2015. Phytoremediation of crude oil-contaminated soil by medicago sativa (alfalfa) and the effect of oil on its growth, phytoremediation for green energy. *Springer* 23: 123-129.

Mittal, A., P. Singh. 2009. Isolation of hydrocarbon degrading bacteria from soils contaminated with crude oil spills.*Indian Journal of Experimental Biology* 47: 760-765.

Mnif, S., S. Sayadi and M. Chamkha. 2014. Biodegradative potential and characterization of a novel aromatic-degrading bacterium isolated from a geothermal oil field under saline and thermophilic conditions. *International Biodeterioration & Biodegradation* 86: 258-264.

Mohan, S.V., T. Kisa, T. Ohkuma, R.A. Kanaly and Y. Shimizu. 2006. Bioremediation technologies for treatment of PAH-contaminated soil and strategies to enhance process efficiency. *Reviews in Environmental Science and Biotechnology* 5: 347-374.

Muangchinda, C., S. Chavanich V. Viyakarn, K. Watanabe, S. Imura, A. Vangnai and O. Pinyakong. 2015. Abundance and diversity of functional genes involved in the degradation of aromatic hydrocarbons in Antarctic soils and sediments around Syowa Station. *Environmental Science and Pollution Research* 22: 4725-4735.

Mukred, A.M., A.A. Hamid, A. Hamzah and W.W. Yusoff. 2008. Development of three bacteria consortium for the bioremediation of crude petroleum-oil in contaminated water. *The Journal of Biological Sciences* 8: 73-79.

Muratova, A.Y., O. Turkovskaya, T. Hübner and P. Kuschk. 2003. Studies of the efficacy of alfalfa and reed in the phytoremediation of hydrocarbon-polluted soil. *Applied Biochemistry and Microbiology* 39: 599-605.

Nadeem, S.M., M. Naveed, M. Ayyub, M.Y. Khan, M. Ahmad and Z.A. Zahir. 2016. Potential, limitations and future prospects of *Pseudomonas* spp. for sustainable agriculture and environment: A Review. *Soil & Environment* 35: 106-145.

Nandal, M., P. Solanki, M. Rastogi and R. Hooda. 2015. Bioremediation: A sustainable tool for environmental management of oily sludge. nature environment and pollution technology 14: 181-187.

Naveed, M., B. Mitter, S. Yousaf, M. Pastar, M. Afzal and A. Sessitsch. 2014. The endophyte *Enterobacter* sp. FD17: A maize growth enhancer selected based on rigorous testing of plant beneficial traits and colonization characteristics. *Biology and Fertility of Soils* 50: 249-262.

Nazina, T.N., D.S. Sokolova, A.A. Grigoryan, N.M. Shestakova, E.M. Mikhailova, A.B. Poltaraus, T.P. Tourova, A.M. Lysenko, G.A. Osipov and S.S. Belyaev. 2005. *Geobacillus jurassicus* sp. nov., a new thermophilic bacterium isolated from a high-temperature petroleum reservoir, and the validation of the Geobacillus species. *Systematic and Applied Microbiology* 28: 43-53.

Nishino, S.F., J.C. Spain and Z. He. 2000. Strategies for aerobic degradation of nitroaromatic compounds by bacteria: process discovery to field application. *Biodegradation of Nitroaromatic Compounds and Explosives*, 7: 61-65.

Norman, R.S., R. Frontera-Suau and P.J. Morris. 2002. Variability in *Pseudomonas aeruginosa* lipopolysaccharide expression during crude oil degradation. *Applied and Environmental Microbiology* 68: 5096-5103.

Noroozi, M., M.A. Amozegar, , R. Rahimi, S.A.S. Fazeli and G.B. Khaniki. 2017. The isolation and preliminary characterization of native cyanobacterial and microalgal strains from lagoons contaminated with petroleum oil in Khark Island. *Biological Journal of Microorganism* 5: 12-15.

Oliveira, V., N.C. Gomes, M. Santos, A. Almeida, A.I. Lillebø, J. Ezequiel J. Serôdio, A.M. Silva, M.M. Simões, S.M. Rocha. and A. Cunha. 2017. Effects of the inoculant strain *Pseudomonas* sp. SPN31 nah+ and of 2-methylnaphthalene contamination on the rhizosphere and endosphere bacterial communities of *Halimione portulacoides*. *Current Microbiology* 74(5) 575-583.

Ordinioha, B and S. Brisibe. 2013. The human health implications of crude oil spills in the Niger delta, Nigeria: An interpretation of published studies. *Nigerian Medical Journal* 54: 10.

Pandey, P., H. Pathak and S. Dave. 2016a. Microbial ecology of hydrocarbon degradation in the soil: A Review. *Research Journal of Environmental Toxicology*10: 1-12.

Pandey, P.K., S. Singh, A.K. Singh, R. Samanta, R.N.S. Yadav and M.C. Singh. 2016b. Inside the plant: Bacterial endophytes and abiotic stress alleviation. *Journal of Applied Natural Sciences* 8: 1899-1904.

Pandey, V.C., P. Abhilash and N. Singh. 2009. The Indian perspective of utilizing fly ash in phytoremediation, phytomanagement and biomass production. *Journal of Environmental Management* 90: 2943-2958.

Patel, A., D. Patra. 2017. A sustainable approach to clean contaminated land using terrestrial grasses, phytoremediation potential of bioenergy plants. *Springer*, 12: 305-331.

Patowary, R., K. Patowary, A. Devi, M.C. Kalita and S. Deka. 2017. Uptake of total petroleum hydrocarbon (tph) and polycyclic aromatic hydrocarbons (PAHs) by *Oryza sativa* L. grown in soil contaminated with crude oil. *Bulletin of Environmental Contamination and Toxicology* 98: 120-126.

Peixoto, R., A. Vermelho and A. Rosado. 2011. Petroleum-degrading enzymes: Bioremediation and new prospects. *Enzyme Reserch* 2: 11-15.

Pinedo, J., R. Ibanez, J. Lijzen and A. Irabien. 2013. Assessment of soil pollution based on total petroleum hydrocarbons and individual oil substances. *Journal of Environmental Management* 130: 72-79.

Pizarro, P., J.L. Niqui, A. Roca, J. Solano, M. Fernández, F. Bastida, C. García and J.L. Ramos. 2015. Field trial on removal of petroleum hydrocarbon pollutants using a microbial consortium for bioremediation and rhizoremediation. *Environmental Microbiology Reports* 7: 85-94.

Portugal, F.S., J.M. Dias, H. Ribeiro, C. Magalhães, A.P. Mucha and A.S. Danko. 2017. Anaerobic biodegradation of ethylic and methylic biodiesel and their impact on benzene degradation. *Clean Soil Air Water* (in press).

Prince, R.C., K.M. McFarlin, J.D. Butler, E.J. Febbo, F.C. Wang and T.J. Nedwed. 2013. The primary biodegradation of dispersed crude oil in the sea. *Chemosphere* 90: 521-526.

Pugazhendi, A., H. Wazin, H. Qari, J.M. Basahi, J.J. Godon and J. Dhavamani. 2016. Biodegradation of low and high molecular weight hydrocarbons in petroleum refinery wastewater by a thermophilic bacterial consortium. *Environmental Technology* 7: 1-11.

Rahman, K., T.J. Rahman, Y. Kourkoutas, I. Petsas, R. Marchant and I. Banat. 2003. Enhanced bioremediation of n-alkane in petroleum sludge using bacterial consortium amended with rhamnolipid and micronutrients. *Bioresource Technology* 90: 159-168.

Rai, S.B., A. Khalid, S. Qadeer, S. Mahmood and I. Aziz. 2016. Reduction in phytotoxicity of chromium using ACC-deaminase containing bacteria. *Soil & Environment* 35: 155-160.

Reda, A.B. and T. Ashraf. 2010. Optimization of bacterial biodegradation of toluene and phenol under different nutritional and environmental conditions. *Journal of Applied Sciences Research* 34: 1086-1095.

Robertson, L.W. and L.G. Hansen. 2015. PCBs: Recent advances in environmental toxicology and health effects. University Press of Kentucky.

Ron, E.Z. and E. Rosenberg. 2014. Enhanced bioremediation of oil spills in the sea. *Current Opinion in Biotechnology* 27: 191-194.

Safronova, V., G. Piluzza, S. Bullitta and A. Belimov. 2011. Use of legume-microbe symbioses for phytoremediation of heavy metal polluted soils: Advantages and potential problems. Handbook of Phytoremediation. Nova Science Publishers, Inc, 443-469.

Sajna, K.V., R.K. Sukumaran, L.D. Gottumukkala and A. Pandey. 2015. Crude oil biodegradation aided by biosurfactants from *Pseudozyma* sp. NII 08165 or its culture broth. *Bioresource Technology* 191: 133-139.

Salam, J.A., M.A. Hatha and N. Das. 2017. Microbial-enhanced lindane removal by sugarcane (Saccharum officinarum) in doped soil-applications in phytoremediation and bioaugmentation. *Journal of Environmental Management* 193: 394-399.

Salanitro, J.P. 2001. Bioremediation of petroleum hydrocarbons in soil. *Advances in Agronomy* 72: 53-105.

Saleem, M., M. Arshad, S. Hussain and A.S. Bhatti. 2007. Perspective of plant growth promoting rhizobacteria (PGPR) containing ACC deaminase in stress agriculture. *Journal of Industrial Microbiology & Biotechnology* 34: 635-648.

Sebiomo, A., S. Bankole and A. Awosanya. 2010. Determination of the ability of microorganisms isolated from mechanic soil to utilise lubricating oil as carbon source. *African Journal of Microbiology Research* 4: 2196-2201.

Sessitsch, A., M. Kuffner, P. Kidd, J. Vangronsveld, W.W. Wenzel, K. Fallmann and M. Puschenreiter. 2013. The role of plant-associated bacteria in the mobilization and phytoextraction of trace elements in contaminated soils. *Soil Biology and Biochemistry* 60: 182-194.

Shabir, G., M. Afzal, R. Tahseen, S. Iqbal, Q.M. Khan and Z.M. Khalid. 2013. Detoxification of oil refinery wastewater by pilot scale fed batch reactor followed by coagulation and filtration. *American Journal of Environmental Protection* 1: 10-13.

Shabir, G., M. Arslan, K. Fatima, I. Amin, Q.M. Khan and M. Afzal. 2016. Effects of inoculum density on plant growth and hydrocarbon degradation. *Pedosphere* 26: 774-778.

Shahsavari, E., A. Aburto-Medina, M. Taha and A.S. Ball. 2016. Phytoremediation of PCBs and PAHs by Grasses: A Critical Perspective. In: Ansari A., Gill S., Gill R., Lanza G., Newman L. (eds) Phytoremediation. Springer, Cham. pp. 3-19.

Shankar, S., C. Kansrajh, M. Dinesh, R. Satyan, S. Kiruthikaand A. Tharanipriya. 2014. Application of indigenous microbial consortia in bioremediation of oil-contaminated soils. *International Journal of Environmental Science and Technology* 11: 367-376.

Shehzadi, M., K. Fatima, A. Imran, M. Mirza, Q. Khan and M. Afzal. 2016. Ecology of bacterial endophytes associated with wetland plants growing in textile effluent for pollutant-degradation and plant growth-promotion potentials. *Plant Biosystems* 150: 1261-1270.

Shehzadi, M., M. Afzal, M.U. Khan, E. ulIslam, A. Mobin, S. Anwar and Q.M. Khan. 2014. Enhanced degradation of textile effluent in constructed wetland system using *Typha domingensis* and textile effluent-degrading endophytic bacteria. *Water Research* 58: 152-159.

Shukla, K.P., N.K. Singh and S. Sharma. 2010. Bioremediation: Developments, current practices and perspectives. *Genetic Engineering and Biotechnology* 3: 1-20.

Siddiqui, R. 2004. Energy and economic growth in Pakistan. *The Pakistan Development Review*, 1: 175-200.

Singh, B.K. 2009. Organophosphorus-degrading bacteria: Ecology and industrial applications. *Nature Reviews Microbiology* 7: 156-164.

Singha, L.P and P. Pandey. 2017. Glutathione and glutathione-S-transferase activity in Jatropha curcas in association with pyrene degrader *Pseudomonas aeruginosa* PDB1 in rhizosphere, for alleviation of stress induced by polyaromatic hydrocarbon for effective rhizoremediation. *Ecological Engineering* 102: 422-432.

Souza, E.C., T.C. Vessoni-Penna and R.P. de Souza Oliveira. 2014. Biosurfactant-enhanced hydrocarbon bioremediation: An overview. *International Biodeterioration & Biodegradation* 89: 88-94.

Spada, V., P. Iavazzo, R. Sciarrillo and C. Guarino. 2017. Phytoremediation of PCBs and PAHs by Grasses: A Critical Perspective. In: Ansari A., Gill S., Gill R., Lanza G., Newman L. (eds) Phytoremediation. Springer, Cham. pp. 53-76.

Speight, J.G. 2014. The chemistry and technology of petroleum. CRC press.

Srivastava, J., R. Naraian, S. Kalra and H. Chandra. 2014. Advances in microbial bioremediation and the factors influencing the process. *International Journal of Environmental Science and Technology* 11: 1787-1800.

Srogi, K. 2007. Monitoring of environmental exposure to polycyclic aromatic hydrocarbons: A review. *Environmental Chemistry Letters* 5: 169-195.

Su, J., W. Ouyang, Y. Hong, D. Liao, S. Khan and H. Li. 2016. Responses of endophytic and rhizospheric bacterial communities of salt marsh plant (Spartina alterniflora) to polycyclic aromatic hydrocarbons contamination. *Journal of Soils and Sediments*. 16: 707-715.

Swamy, M.K., M.S. Akthar and U.R. Sinniah. 2016. Root Exudates and Their Molecular Interactions with Rhizospheric Microbes. *Plant, Soil and Microbes Springer* 12: 59-77.

Tahseen, R., M. Afzal, S. Iqbal, G. Shabir, Q.M. Khan, Z.M. Khalid and I.M. Banat. 2016. Rhamnolipids and nutrients boost remediation of crude oil-contaminated soil by enhancing bacterial colonization and metabolic activities. *International Biodeterioration and Biodegradation* 115: 192-198.

Tara, N., M. Afzal, T.M. Ansari, R. Tahseen, S. Iqbal and Q.M. Khan. 2014. Combined use of alkane-degrading and plant growth-promoting bacteria enhanced phytoremediation of diesel contaminated soil. *International Journal of Phytoremediation* 16: 1268-1277.

Tang, J., M. Carroquino, B. Robertson and M. Alexander. 1998. Combined effect of sequestration and bioremediation in reducing the bioavailability of polycyclic aromatic hydrocarbons in soil. *Environmental Science & Technology* 32: 3586-3590.

Thijs, S. and J. Vangronsveld. 2015. Rhizoremediation, Principles of Plant-Microbe Interactions. *Springer* 12: 277-286.

Thomas, J.C., D.K. Russell and C.L. Rugh. 2017. Polyaromatic hydrocarbon phytoremediation stimulated by root exudates. *International Journal of Environmental Bioremediation & Biodegradation* 5: 1-7.

Throne-Holst, M., A. Wentzel, T.E. Ellingsen, H.K. Kotlar and S.B. Zotchev. 2007. Identification of novel genes involved in long-chain n-alkane degradation by *Acinetobacter* sp. strain DSM 17874. *Applied and Environmental Microbiology* 73: 3327-3332.

Tolosa, I., S. de Mora, M.R. Sheikholeslami, J.P. Villeneuve, J. Bartocci and C. Cattini. 2004. Aliphatic and aromatic hydrocarbons in coastal Caspian Sea sediments. *Marine Pollution Bulletin* 48: 44-60.

Truu, J., M. Truu, M. Espenberg, H. Nõlvak and J. Juhanson. 2015. Phytoremediation and plant-assisted bioremediation in soil and treatment wetlands: *Open Biotechnology Journal* 9: 85-92.

Van Beilen, J.B. and E.G. Funhoff. 2007. Alkane hydroxylases involved in microbial alkane degradation. *Applied Microbiology and Biotechnology* 74: 13-21.

Varjani, S.J. 2017. Microbial degradation of petroleum hydrocarbons. *Bioresource Technology* 223: 277-286.

Varjani, S.J. D.P. Rana, A.K. Jain, S. Bateja and V.N. Upasani. 2015. Synergistic ex-situ biodegradation of crude oil by halotolerant bacterial consortium of indigenous strains isolated from on shore sites of Gujarat, India. *International Biodeterioration & Biodegradation* 103: 116-124.

Varjani, S.J. and V.N. Upasani. 2013. Comparative studies on bacterial consortia for hydrocarbon degradation. *International journal of Innovative Research in Science, Engineering and Technology* 2: 12-23.

Varjani, S.J. and V.N. Upasani. 2016. Biodegradation of petroleum hydrocarbons by oleophilic strain of *Pseudomonas aeruginosa* NCIM 5514. *Bioresource Technology* 222: 195-201.

Varjani, S.J. and V.N. Upasani. 2017. A new look on factors affecting microbial degradation of petroleum hydrocarbon pollutants. *International journal of Biodeterioriation and. Biodegradation* 120: 71-83.

Vaziri, A., E. Panahpour and M. Mirzaee Beni. 2013. Phytoremediation: A method for treatment of petroleum hydrocarbon contaminated soils. *International Journal of Farming and Allied Sciences* 2: 909-913.

Vergani, L., F. Mapelli, E. Zanardini, E. Terzaghi, A. Di Guardo, C. Morosini, G. Raspa and S. Borin. 2017. Phyto-rhizoremediation of polychlorinated biphenyl contaminated soils: An outlook on plant-microbe beneficial interactions. *Science of The Total Environment* 575: 1395-1406.

Walker, C.H., R. Sibly, S. Hopkin and D.B. Peakall. 2012. *Principles of Ecotoxicology*. CRC press.

Wang, B., W. Liu, X. Liu, A.E. Franks, Y. Teng and Y. Luo. 2017. Comparative analysis of microbial communities during enrichment and isolation of DDT-degrading bacteria by culture-dependent and-independent methods. *Science of The Total Environment*. 570: 1395-1406.

Wei, R., J. Ni, X. Li, W. Chen and Y. Yang. 2017. Dissipation and phytoremediation of polycyclic aromatic hydrocarbons in freshly spiked and long-term field-contaminated soils. *Environmental Science and Pollution Research* (in press).

Weyens, N., D. van der Lelie, S. Taghavi and J. Vangronsveld. 2009. Phytoremediation: Plant–endophyte partnerships take the challenge. *Current Opinion in Biotechnology*. 20: 248-254.

Wu, G. and F. Coulon. 2016. Modelling the Environmental Fate of Petroleum Hydrocarbons During Bioremediation. Hydrocarbon and Lipid Microbiology Protocols: Statistics, Data Analysis, Bioinformatics and Modelling, 165-180.

Wu, M., X. Ye, K. Chen, W. Li, J. Yuan and X. Jiang. 2017. Bacterial community shift and hydrocarbon transformation during bioremediation of short-term petroleum-contaminated soil. *Environmental Pollution* 223: 657-664.

Yan, L., H. Sinkko, P. Penttinen and K. Lindström. 2016. Characterization of successional changes in bacterial community composition during bioremediation of used motor oil-contaminated soil in a boreal climate. *Science of the Total Environment* 542: 817-825.

Yi, H and D.E. Crowley. 2007. Biostimulation of PAH degradation with plants containing high concentrations of linoleic acid. *Environmental Science & Technology* 41: 4382-4388.

Yousaf, S., V. Andria, T.G. Reichenauer, K. Smalla and A. Sessitsch. 2010. Phylogenetic and functional diversity of alkane degrading bacteria associated with Italian ryegrass (*Lolium multiflorum*) and Birdsfoot trefoil (*Lotus corniculatus*) in a petroleum oil-contaminated environment. *Journal of Hazardous Materials* 184: 523-532.

Yousaf, S., M. Afzal, T.G. Reichenauer, C.L. Brady and A. Sessitsch. 2011. Hydrocarbon degradation, plant colonization and gene expression of alkane degradation genes by endophytic *Enterobacter ludwigii* strains. *Environmental Pollution* 159: 2675-2683.

Yousaf, S., K. Ripka, T. Reichenauer, V. Andria, M. Afzal and A. Sessitsch. 2010. Hydrocarbon degradation and plant colonization by selected bacterial strains isolated from Italian ryegrass and birdsfoot trefoil. *Journal of Applied Microbiology* 109: 1389-1401.

Zhu, X., W. Wang, D.E. Crowley, K. Sun, S. Hao, M.G. Waigi and Y. Gao. 2017a. The endophytic bacterium Serratia sp. PW7 degrades pyrene in wheat. *Environmental Science and Pollution Research* 12: 1-9.

Zhu, X., W. Wang, K. Sun, X. Lin, S. Li, M.G. Waigi and W. Ling. 2017b. Inoculating wheat (*Triticum aestivum* L.) with the endophytic bacterium *Serratia* sp. PW7 to reduce pyrene contamination. *Intenational Journal of Phytoremediation* 13: 12-19.