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Extended Abstract

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10th International Congress on Clinical Virology, Fungal Infections & Infectious Diseases, December 04-05, 2017 Dubai, UAE-Stimulated rhizoremediation of petroleum hydrocarbons in aged and spiked contaminated soil using compost, biochar and bacterial consortia

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Petroleum hydrocarbons are extensively utilized in petrochemical industries and cause soil deterioration during exploration, transportation, refining and making petroleum products. Toxicity to plants depends on the availability of contaminant. In aged contaminated soil total petroleum hydrocarbon are not available to plants, but suppress the plant growth by disrupting the physico-chemical characteristics of soil. The present study focused on phytoremediation of hydrocarbons in aged and spiked contaminated soil amended with biochar (5%), compost (5%). Both soils were inoculated with consortia of four hydrocarbon degrading bacterial strains (Pseudomonaspoae, Actinobacterbouvetii, Stenotrophomonasrhizosphere and Pseudomans japonica). Initial hydrocarbon concentration in aged soil was 37 g/kg and fresh soil was also spiked with same concentration. Italian ryegrass seeds (60/pot) were sown in both soils. The plants were harvested after 75 days. The highest hydrocarbon removal (85.1%) was observed in spiked soil amended with compost, biochar and consortia. Bacterial inoculation with biochar and compost showed significantly higher hydrocarbon degradation as compared to all other treatments. Hydrocarbon removal in spiked soil was higher than in aged soil. Highest TPH degrading bacteria (2.96×108 cells/g) were also observed in rhizosphere of spiked soil amended with compost, biochar and consortia. Maximum fresh and oven dry root and shoot biomass was produced in spiked soil as compared aged soil. The organic amendments improved plant growth and bacterial count which resulted in higher degradation of hydrocarbons. Most petroleum hydrocarbons encountered in the environment are ultimately degraded or metabolized by indigenous bacteria because of their energetic and carbon needs for growth and reproduction, as well as the requirement to relieve physiological stress caused by the presence of petroleum hydrocarbons in the microbial bulk environment (Hazen et al., 2010; Kleindienst et al., 2015a). The development of microbial biotechnology and high-throughput sequencing technology, such as microfluidic techniques (Jiang et al., 2016; Guerra et al., 2018), is beneficial for screening and identifying functional microorganisms from petroleum hydrocarbon-contaminated environments. Indeed, many studies have revealed that there is a large number of hydrocarbon-degrading bacteria in oil-rich environments, such as oil spill areas and oil reservoirs (Hazen et al., 2010; Yang et al., 2015), and that their abundance and quantity are closely related to the types of petroleum hydrocarbons and the surrounding environmental factors (Fuentes et al., 2015; Varjani and Gnansounou, 2017).

Many normal and extreme bacterial species have been isolated and utilized as biodegraders for dealing with petroleum hydrocarbons. The degradation pathways of a variety of petroleum hydrocarbons (e.g., aliphatics and polyaromatics) have been shown to employ oxidizing reactions; however, these pathways differ greatly because of the specific oxygenases found in different bacterial species. For instance, some bacteria can metabolize specific alkanes, while others break down aromatic or resin fractions of hydrocarbons. This phenomenon is related to the chemical structure of petroleum hydrocarbon components. Petroleum hydrocarbon-degrading bacteria and the type of petroleum components they degrade are listed in thus, their roles in oil-contaminated.

Recent studies have identified bacteria from more than 79 genera that are capable of degrading petroleum hydrocarbons; several of these bacteria such as Achromobacter, Acinetobacter, Alkanindiges, Alteromonas, Arthrobacter, Burkholderia, Dietzia, Enterobacter, Kocuria, Marinobacter, Mycobacterium, Pandoraea, Pseudomonas, Staphylococcus, Streptobacillus, Streptococcus, and Rhodococcus have been found to play vital roles in petroleum hydrocarbon degradation. Interestingly, "conditionally rare taxa" in soil, such as Alkanindiges sp., have been reported to exhibit rare-to-dominant bacterial shifts that are strongly affected by environmental constrains such as diesel pollution (Fuentes et al., 2015). Similarly, some obligate hydrocarbonoclastic bacteria (OHCB), including Alcanivorax, Marinobacter, Thallassolituus, Cycloclasticus, Oleispira and a few others (the OHCB), showed a low abundance or undetectable status before pollution, but were found to be dominant after petroleum oil contamination. These phenomena suggest that these microorganisms are crucial to the degradation of petroleum hydrocarbons, and that they significantly influence the transformation and fate of petroleum hydrocarbons in the environment. Although some bacteria have been reported to have a broad spectrum of petroleum hydrocarbon degradation ability, Dietzia sp. DQ12-45-1b utilizes n-alkanes (C6–C40) and other compounds as the sole carbon and Achromobacter xylosoxidans DN002 works well on a variety of monoaromatic and polyaromatic hydrocarbons almost no bacteria can degrade the entire petroleum hydrocarbon fraction. Indeed, petroleum hydrocarbons most bacteria can only effectively degrade or utilize certain petroleum hydrocarbon components, while others are completely unavailable. This can be attributed to the fact that different indigenous bacteria have different catalytic enzymes; thus petroleum hydrocarbons their roles in oil-contaminated sites also vary widely. This also implies that the remediation of petroleum hydrocarbon contamination requires the joint action of multiple functional bacteria to achieve the best environmental purification effect. Based on this view,constructed a halotolerant Hydrocarbon Utilizing Bacterial Consortium (HUBC) consisting of the bacterial isolates Ochrobactrum sp., Stenotrophomonas maltophilia and Pseudomonas aeruginosa that was found to be good at degrading crude oil (3% v/v), with a degradation percentage as high as 83.49%, utilized a defined co-culture of an indigenous bacterial consortium and exogenous Bacillus subtilis to effectively accelerate the degradation of crude oil. Found that an aboriginal bacterial consortium based on the Penglai 19-3 oil spill accident, thus, their roles in oil-contaminated had higher oil degradation efficiency compared to individual bacteria and demonstrated that this indigenous consortium had the potential for bioremediating crude oil dispersed in the marine ecosystem. A field study showed that bioaugmentation with an artificial consortium containing Aeromonas hydrophila, Alcaligenes xylosoxidans, Gordonia sp., Pseudomonas fluorescens, Pseudomonas putida, Rhodococcus equi, S. maltophilia, and Xanthomonas sp. contributed to high biodegradation efficiency (89%) in a 365-day treatment of diesel oil-contaminated soil. Taken together, these studies indicate that improving the biodegradation potential via the application of bacterial consortia possessing multiple catabolic genes is a reasonable and feasible strategy for accelerating the removal efficiency of petroleum hydrocarbons from contaminated environments.