



Review

A new look on factors affecting microbial degradation of petroleum hydrocarbon pollutants



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ABSTRACT

In recent years, there has been increasing concern over public health threat presented by introduction of petroleum hydrocarbon pollutants in environment due to anthropogenic activities to a greater extent and natural processes to some extent. Many countries all over the world are currently facing severe problem due to these pollutants as they are one of the persistent organic pollutants (POPs). Remediation of polluted sites by biodegradation is a viable option as conventional physico-chemical methods for remediation seems technically as well as economically challenging. Biodegradation is non-invasive and could be cost-effective in removal of petroleum hydrocarbon pollutants. It is considered as ultimate mechanism for pollutants removal. Immobilized microbial cells give advantage over free microbial cells to improve the survival and retention of the bioremediation agents in polluted sites. However, current biodegradation approaches suffer from a number of limitations, which include pollutant characteristics, poor capabilities of microbial communities in the field, lesser bioavailability of pollutants, growth conditions, etc. Understanding the factors affecting microbial degradation is of great research interest in present scenario. This review selectively examines and provides a critical view on bioavailability of the substrates, microorganisms in petroleum hydrocarbon pollutants degradation and the molecular techniques for their characterization, degradation mechanisms under aerobic and anaerobic conditions, commercially available bioremediation agents and factors affecting biodegradation of these pollutants. Role of genetically modified organisms and biodegradation of petroleum hydrocarbon pollutants by immobilized will also be discussed.

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1. Introduction

The rapid economic growth achieved in last decade has been paralleled by an increase in global petroleum oil consumption (Ghazali et al., 2004; Varjani and Upasani, 2016a), which is attributable to the fact that petroleum oil serves as the most indispensable energy source as well as a raw material in petroleum oil refineries and petrochemical industries for several products such as fuel, synthetic polymers and petrochemicals (Atlas, 1981; Varjani et al., 2015). According to the Toxic Release Inventory (EPA) report (2005), the oil refining industry is one of ten major sources releasing/emitting toxic chemicals into the environment. In past few years, petroleum hydrocarbon pollution has become one of the most serious global concerns due to its toxicity to microorganisms as well as to higher forms of life including humans (Hasanuzzaman et al., 2007; Saeki et al., 2009; Varjani and Upasani, 2016c). Among petroleum hydrocarbon pollutants sixteen polycyclic aromatic hydrocarbons (PAHs) are listed as priority pollutants due to high stability in the environment (Zhang et al., 2011; Abdel-Shafy and Mansour, 2016; Lamichhane et al., 2016; Varjani, 2017). There has been an increasing concern about the human health and environmental risk of petroleum industry activities associated with crude oil exploration as well as accidental and intentional oil discharges during transportation, production and refining of petroleum oil (Baderna et al., 2011; Ghosh et al., 2015; Varjani et al., 2015).

Petroleum is a complex mixture of hydrocarbons and other organic compounds, including some organo-metallo constituents, most notably complexing vanadium and nickel (Van Hamme et al., 2003; Varjani et al., 2013; Lamichhane et al., 2016). Bioremediation involves the use of micro-organisms to degrade hazardous organic constituents to harmless substances, such as carbon dioxide and water (Zhao et al., 2011; Varjani and Upasani, 2012). With rapid progress in the field of molecular genetics, PCR-based approaches have emerged to study specific microorganisms or groups of microorganisms and specific genes to evaluate overall community profiles (Van Elsas et al., 1998). Molecular methods to evaluate community profiles include denaturing and temperature gradient gel electrophoresis, single-strand conformation polymorphism, restriction fragment length polymorphism, DNA microarrays, random amplified polymorphic DNA, and amplified ribosomal DNA restriction analysis (Pieper and Reineke, 2000; Kasai et al., 2001; Weelink et al., 2009; Peixoto et al., 2011; Tong et al., 2013). Techniques and tools of modern molecular biology have increased our current knowledge about non-cultured microorganisms (Pieper and Reineke, 2000; Urgun-Demirtas et al., 2006). Due to this

development of new strains with desirable properties viz. degradation pathway construction, modification of enzyme specificity, substrate affinity, cellular localization, and expression for bioremediation of petroleum hydrocarbon pollutant degraders has become possible (Urgun-Demirtas et al., 2006; Peixoto et al., 2011; Sana, 2015). Immobilization method is very widely used in case of marine oil spills in which microbes or their enzyme is immobilized in a limited space by chemical or physical methods, which make them keeping it active and allowing its reuse (Cunningham et al., 2004; Gentili et al., 2006; Nunal et al., 2014; Zhang et al., 2016). The immobilized live cells can offer many advantages over application of free cells such as avoid microbial cell wash-out, ensure higher cell concentration in small volumes, embed nutrients and resist external disadvantages to microbes that are immobilized (Zhao et al., 2006; Shen et al., 2015). Petroleum hydrocarbon utilization by microorganisms can be phototrophic, anoxygenic; chemotrophic, aerobic and chemotrophic, anaerobic (Varjani, 2017). The anaerobic degradation pathways of some compounds such as phenol, toluene and ethylbenzene, xylene, naphthalene, pyrene, phenanthrene and anthracene have been well studied at the enzyme level in many reviews in last decades (Heider, 2007; Fuchs et al., 2011; Boll et al., 2014; Waigi et al., 2015; Meckenstock et al., 2016; Wilkes et al., 2016). Biodegradation of pollutants involve sequential metabolic reactions catalyzed by enzymes (Heider, 2007; Peixoto et al., 2011; Varjani, 2017). Surfactants produced by microorganisms are termed as biosurfactants (Rahman et al., 2003; Kavitha et al., 2014; Varjani et al., 2014a; Sajna et al., 2015). They promote hydrocarbon pollutants cracking, micelle formation, increasing their mobility, bioavailability and exposure to bacteria, thus favoring hydrocarbon biodegradation (Rahman et al., 2003; Kavitha et al., 2014; Souza et al., 2014; Varjani and Upasani, 2016a). The mode of action in bioremediation of petroleum hydrocarbon pollutants for biosurfactants has been extensively studied and reviewed earlier (Desai and Banat, 1997; Varjani, 2017). Extent of biodegradation activity depends on growth conditions of microbes such as nutrient and substrate bioavailability, oxygen availability, electron acceptors, temperature, pH, salinity and pressure (Chandra et al., 2013; Varjani et al., 2014b).

This review article provides an overview about microbial abilities and pathways used for degradation of petroleum hydrocarbon pollutants in both aerobic and anaerobic conditions. This article focuses on molecular techniques for characterization of hydrocarbon degrading microorganisms and factors influencing microbial degradation of these pollutants. Attention has been paid to bioremediation agents, genetically modified organisms and

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