Avicenna J Environ Health Eng. 2017 Dec;4(2):38-39 http://ajehe.umsha.ac.ir

Letter to Editor

doi 10.15171/ajehe.2017.08

The Role of Mycobacteria in Biodegradation

Masoud Keikha*

Department of Microbiology, School of Medicine, Isfahan University of Medical Sciences, Isfahan, Iran

***Correspondence to:** Masoud Keikha, Tel: +989386836425, Email: Masoud.keykha90@gmail.com

Received September 30, 2017; **Revised** October 25, 2017; **Accepted** November 29, 2017 **Published online** December 20, 2017

Crude oil- and petrochemical-induced contamination of the environment has gained considerable attention in recent decades. Today, leakage and spread of oil contamination due to inefficient extraction, transmission and crude oil refinery processes along with occurrence of different incidents in various sections of oil industry like oil production site, oil refineries and transmission lines are inevitable (1). Crude oil product may enter into the environmental resources and exert harmful effects such as health risks, contamination of natural resources and underground water. In addition to their effects on the environment, these compounds have harmful effects on human. Studies have shown that oil compounds can cause mutation and cancer, and negatively affect human neonates (1,2). Therefore, cleaning the oil-contaminated areas is one of the main environmental concerns. For this purpose, different physical, chemical, and biological methods have been proposed (1,3). Biodegradation is one of the most important solutions to clean these compounds from the environment. During this natural process, microorganisms break the organic chemicals into simpler forms. Chemical and mechanical methods, in addition to being costly, do not clean these compounds effectively and can transmit the contamination to other areas. While biodegradation is a cost-effective and efficient method in comparison with the two mentioned methods, it is now recognized as one of the important strategies in environmental protection (4,5). Presence of microorganisms in contaminated site is another advantage of this method. So far, more than 200 microorganisms with such capabilities have been identified among which *Pseudomonas*, *Actinomyces* (especially mycobacteria), *Flavobacterium*, *Bacillus*, *Alcaligenes* and *Micrococcus* can be mentioned (6).

Non-tuberculous mycobacteria live in the environmental resources including soil, water, dust, milk, and animals. Today, this group of bacteria are known as one of the important biodegrading bacteria and can degrade pollutants. Based on the literature, various species of environmental mycobacteria have been reported with biodegradation properties (4,7). The most important molecular method used for the identification of mycobacterial species is gene sequence investigation of 16S rRNA in A (125-270), B (408-502) positions and *rpoB* gene in V (2581-3300) position and also the sequence of *hsp65* in 624-664 and 683-725 positions (8). Among non-tuberculous mycobacteria, the species with profound biodegradation properties are: *M. fredriksbergense, M. austroafricanum, M. obuense, M. phocaicum, M. paragordonae, M. lentiflavum*, *M. ratisbonense* and *M. fortuitum* (4,7,8). Presence of fatty acid-saturated cell wall and also presence and expression of biodegradation genes such as *nidA*, ABC transporter, *alkB* and so on have enabled the mycobacteria to biodegrade the pollutants (9,10).

Among the methods used to evaluate the biodegradation, methods such as chromatography (i.e. HPLC), enrichment technique, spray plate technique and gibbs and turbidometric methods can be mentioned. Among them, enrichment method is one of the most accurate ones in which a salt-based varied medium of methylsulfonylmethane (MSM), which contains the minimum mineral and the studied pollutant, is used as the only source of carbon (9-13). Recently, by advancement in genetic sciences and achievements in getting information of genomics of organisms, researchers are now able to identify the biodegrading bacteria by means of whole genome sequencing (14).

In general, previous studies have shown that mycobacteria are one of the bacterial species which possess biodegradation properties. Moreover, presence of fatty acid-saturated cell wall has enhanced the resistance of this bacterium against toxic and harsh environmental conditions; which helps this microorganism to survive in contaminated ecosystems. As non-tuberculous mycobacteria exist in various environments such as water and soil, these bacteria can be used for contamination removal from water and soil.

Conflict of Interest Disclosures

There is no conflict of interests.

References

1. Megharaj M, Ramakrishnan B, Venkateswarlu K, Sethunathan

N, Naidu R. Bioremediation approaches for organic pollutants: a critical perspective. Environ Int. 2011;37(8):1362-75. doi: 10.1016/j.envint.2011.06.003.
2. Roy TA, Johnson SW, Blackburn GR, Mackerer CR. Correlation of mutagenic and dermal carcinogenic activities of mineral oils with polycyclic aromatic compound content. Fundam Appl Toxicol. 1988;10(3):466-76.
3. Bogan BW, Sullivan WR. Physicochemical soil parameters affecting sequestration and mycobacterial biodegradation of polycyclic aromatic hydrocarbons in soil. Chemosphere. 2003;52(10):1717-26. doi: 10.1016/s0045-6535(03)00455-7.
4. Azadi D, Dibaj R, Pourchangiz M, Naser A, Shojaei H. Isolation and molecular identification of biodegrading Mycobacteria from water supplies of Iranian hospitals. Iran J Microbiol. 2014;6(4):240-5.
5. Haritash AK, Kaushik CP. Biodegradation aspects of polycyclic aromatic hydrocarbons (PAHs): a review. J Hazard Mater. 2009;169(1-3):1-15. doi: 10.1016/j.jhazmat.2009.03.137.
6. Rashid Ashmagh F, Rezaei Kalantary R, Farzadkia M, Joneidy Jafari A, Nabizadeh R. Survey of Phenantherene Biodegradation's Model in Contaminated Soils by Acinetobacter sp. Iran J Health Environ. 2009;2(3):196-203.
7. Berekaa MM, Steinbuchel A. Microbial degradation of the multiply branched alkane 2,6,10,15,19, 23-hexamethyltetracosane (Squalane) by *Mycobacterium fortuitum* and *Mycobacterium ratisbonense*. Appl Environ Microbiol. 2000;66(10):4462-7.
8. Hashemi-Shahraki A, Bostanabad SZ, Heidarieh P, Titov LP, Khosravi AD, Sheikhi N, et al. Species spectrum of nontuberculous mycobacteria isolated from suspected tuberculosis patients, identification by multi locus sequence analysis. Infect Genet Evol. 2013;20:312-24. doi: 10.1016/j.meegid.2013.08.027.
9. Stingley RL, Khan AA, Cerniglia CE. Molecular characterization of a phenanthrene degradation pathway in *Mycobacterium vanbaalenii* PYR-1. Biochem Biophys Res Commun. 2004;322(1):133-46. doi: 10.1016/j.bbrc.2004.07.089.
10. Vila J, Lopez Z, Sabate J, Minguillon C, Solanas AM, Grifoll M. Identification of a novel metabolite in the degradation of pyrene by *Mycobacterium* sp. strain AP1: actions of the isolate on two- and three-ring polycyclic aromatic hydrocarbons. Appl Environ Microbiol. 2001;67(12):5497-505. doi: 10.1128/aem.67.12.5497-5505.2001.
11. Murray AP, Gibbs CF, Longmore AR, Flett DJ. Determination of chlorophyll in marine waters: intercomparison of a rapid HPLC method with full HPLC, spectrophotometric and fluorometric methods. Mar Chem. 1986;19(3):211-27. doi: 10.1016/0304-4203(86)90024-1.
12. Kiyohara H, Nagao K, Yana K. Rapid screen for bacteria degrading water-insoluble, solid hydrocarbons on agar plates. Appl Environ Microbiol. 1982;43(2):454-7.
13. Nuhu AA. Bio-catalytic desulfurization of fossil fuels: a mini review. Rev Environ Sci Biotechnol. 2013;12(1):9-23. doi: 10.1007/s11157-012-9267-x.
14. Nelson KE, Weinel C, Paulsen IT, Dodson RJ, Hilbert H, Martins dos Santos VA, et al. Complete genome sequence and comparative analysis of the metabolically versatile *Pseudomonas putida* KT2440. Environ Microbiol. 2002;4(12):799-808.