

Alkane degrading bacterial gene dynamics in the process of oil contaminated soil bioremediation

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Abstract

© SGEM2019 All Rights Reserved. It is well known that soil polluted with different pollutants, including oil, can naturally remediate. Primarily, the process of oil utilization starts with the degradation of saturated alkanes by microorganisms. Alkane monooxygenase is the major enzyme involved in the degradation of alkanes and it is classified into three groups, each catalyzing the degradation of n-alkanes with different chain lengths. In this study, we investigated abundance of alkane monooxygenases genes in the soil contaminated with oil during the process of bioremediation that lasted for 120 days. We conducted a laboratory experiment with three oil doses – 6, 12 and 25% (P6, P12, P25). Dynamics of genes related to group I, group II, and group III alkane monooxygenases were quantified by qPCR. In addition, the total petroleum content and the content of hydrocarbon fractions were analyzed. It was found that the hydrocarbon content did not change significantly during 120 days. However, the content of saturated alkanes decreased by 9.8 and 24% for P6 and P12, respectively. It was determined that I group genes were characterized by a minimal amount in the range from 1.4×10^2 to 4.4×10^3 gene copy number g⁻¹. The number of genes belonging to the II group was in the range from 2×10^2 to 7.7×10^5 gene copy number g⁻¹, and the genes of the III group — from 9.9×10^4 to 3.2×10^6 gene copies number g⁻¹. The content of I group genes increased immediately at the 3rd day after the contamination, and further their quantity decreased in comparison with the uncontaminated soil. The content of genes from the II and III groups increased from the 1st to 3rd days and further continued to grow with the maximum amount at the 30-60 days after the contamination. Thus, it was found that the content of genes encoding alkane monooxygenase increased after oil pollution, while a decrease in the content of aliphatic hydrocarbon fractions was also observed.

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Keywords

Alkane monooxygenase, Bioremediation, Gene abundance, Oily soil

References

- [1] Powell SM, Bowman JP, Ferguson SH, Snape I. The importance of soil characteristics to the structure of alkane-degrading bacterial communities on sub-Antarctic Macquarie Island. *Soil Biol Biochem.* 2010;42: 2012–2021. doi:10.1016/j.soilbio.2010.07.027

- [2] Biktasheva LR, Shalyamova RP, Guseva UA, Galitskaya PY. Occurrence of Hydrocarbon Degrading Genes in the Soils of the Republic of Tatarstan (Russia). IOP Conference Series: Earth and Environmental Science. 2018. doi:10.1088/1755-1315/107/1/012049
- [3] Aliakbari E, Tebyanian H, Hassanshahian M. Degradation of Alkanes in contaminated sites. Int J Adv Biol Biomed Res. 2014;2: 1620-1637.
- [4] Cébron A, Norini MP, Beguiristain T, Leyval C. Real-Time PCR quantification of PAH-ring hydroxylating dioxygenase (PAH-RHD α) genes from Gram positive and Gram negative bacteria in soil and sediment samples. J Microbiol Methods. 2008;73: 148-159. doi:10.1016/j.mimet.2008.01.009
- [5] Kok M, Oldenhuis R, Van Der Linden MPG, Raatjes P, Kingma J, Van Lelyveld PH, et al. The *Pseudomonas oleovorans* alkane hydroxylase gene. Sequence and expression. J Biol Chem. 1989;264: 5435-5441.
- [6] Whyte LG, Smits THM, Labbé D, Witholt B, Greer CW, Van Beilen JB. Gene cloning and characterization of multiple alkane hydroxylase systems in *Rhodococcus* strains Q15 and NRRL B-16531. Appl Environ Microbiol. 2002;68: 5933-5942. doi:10.1128/AEM.68.12.5933-5942.2002
- [7] Hara A, Baik SH, Syutsubo K, Misawa N, Smits THM, Van Beilen JB, et al. Cloning and functional analysis of alkB genes in *Alcanivorax borkumensis* SK2. Environ Microbiol. 2004;6: 191-197. doi:10.1046/j.1462-2920.2003.00550.x
- [8] Fukuhara Y, Horii S, Matsuno T, Matsumiya Y, Mukai M, Kubo M. Distribution of hydrocarbon-degrading bacteria in the soil environment and their contribution to bioremediation. Appl Biochem Biotechnol. 2013;170: 329-339. doi:10.1007/s12010-013-0170-x
- [9] Godbout J, Comeau Y, Greer C. Soil characteristics effects on introduced bacterial survival and activity. 1995. pp. 115-120.
- [10] Oudot J, Merlin FX, Pinvidic P. Weathering rates of oil components in a bioremediation experiment in estuarine sediments. Mar Environ Res. 1998;45: 113-125. doi:10.1016/S0141-1136(97)00024-X
- [11] Margesin R, Labbé D, Schinner F, Greer CW, Whyte LG. Characterization of hydrocarbon-degrading microbial populations in contaminated and pristine Alpine soils. Appl Environ Microbiol. 2003;69: 3085-3092. doi:10.1128/AEM.69.6.3085-3092.2003
- [12] Zhang Z, Zhao X, Liang Y, Li G, Zhou J. Microbial functional genes reveal selection of microbial community by PAHs in polluted soils. Environ Chem Lett. 2013;11: 11-17. doi:10.1007/s10311-012-0370-6
- [13] Bengtsson G, Törneman N, de Liphay JR, Sørensen SJ. Microbial Diversity and PAH Catabolic Genes Tracking Spatial Heterogeneity of PAH Concentrations. Microb Ecol. 2013;65: 91-100. doi:10.1007/s00248-012-0112-0
- [14] Ding GC, Heuer H, Zühlke S, Spitteller M, Pronk GJ, Heister K, et al. Soil type-dependent responses to phenanthrene as revealed by determining the diversity and abundance of polycyclic aromatic hydrocarbon ring-hydroxylating dioxygenase genes by using a novel PCR detection system. Appl Environ Microbiol. 2010;76: 4765-4771. doi:10.1128/AEM.00047-10