



Response of soil bacterial communities to high petroleum content in the absence of remediation procedures

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Received: 29 May 2020 / Accepted: 18 October 2020 / Published online: 5 November 2020
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Abstract

Oil spills are events that frequently lead to petroleum pollution. This pollution may cause stress to microbial communities, which require long adaptation periods. Soil petroleum pollution is currently considered one of the most serious environmental problems. In the present work, processes occurring in the bacterial communities of three soil samples with different physicochemical characteristics, artificially polluted with 12% of crude oil, were investigated in 120-day laboratory experiment. It was found that the total petroleum hydrocarbon content did not decrease during this time; however, the proportion of petroleum fractions was altered. Petroleum pollution led to a short-term decrease in the bacterial 16S rRNA gene copy number. On the basis of amplicon sequencing analysis, it was concluded that bacterial community successions were similar in the three soils investigated. Thus, the phyla Actinobacteria and Proteobacteria and candidate TM7 phylum (Saccaribacteria) were predominant with relative abundances ranging from 35 to 58%, 25 to 30%, and 15 to 35% in different samples, respectively. The predominant operational taxonomic units (OTUs) after pollution belonged to the genera *Rhodococcus* and *Mycobacterium*, families Nocardioideae and Sinobacteraceae, and candidate class TM7-3. Genes from the alkIII group encoding monooxygenases were the most abundant compared with other catabolic genes from the alkI, alkII, GN-PAH, and GP-PAH groups, and their copy number significantly increased after pollution. The copy numbers of expressed genes involved in the horizontal transfer of catabolic genes, *FlgC*, *TraG*, and *OmpF*, also increased after pollution by 11–33, 16–63, and 11–71 times, respectively. The bacterial community structure after a high level of petroleum pollution changed because of proliferation of the cells that initially were able to decompose hydrocarbons, and in the second place, because proliferation of the cells that received these catabolic genes through horizontal transfer.

Keywords Soil petroleum pollution · Bacterial structure · Alkane monooxygenase · Dioxygenase · Horizontal gene transfer · Sequencing

Introduction

Petroleum hydrocarbons are main pollutants of the environment (Margesin et al. 2003; Deppe et al. 2005; Antônio Marcondes de Souza et al. 2014; Gong et al. 2014; Sajna et al. 2015; Ossai et al. 2020). Petroleum contains aliphatic, aromatic, and polyaromatic compounds of different C-lengths and skeletons (Zhang et al. 2011; Chen et al. 2015; Galitskaya

et al. 2015; Varjani and Upasani 2017), and the majority of these compounds are toxic to soil biota (Sikkema et al. 1995; ATSDR 1999; Wang et al. 2017; Khan et al. 2018a).

When introduced to soil, petroleum hydrocarbons cause stress to the soil microbial community (Galitskaya et al. 2016; Morais et al. 2016; Khan et al. 2018a). One of the ways microbes overcome stress is the intensive activation and decomposition of hydrocarbons. Many species are able to decompose not only aliphatic but also aromatic compounds. The bacterial genera that actively attack hydrocarbons include *Acinetobacter*, *Pseudomonas*, *Streptomyces*, *Arthrobacter*, *Bacillus*, *Achromobacter*, *Acinetobacter*, *Azoarcus*, *Brevibacterium*, *Cellulomonas*, *Corynebacterium*, *Rhodococcus*, *Flavobacterium*, *Marinobacter*, *Micrococcus*, *Nocardia*, *Ochrobactrum*, *Stenotrophomonas*, *Vibrio*, *Thalassolituus*, *Alcanivorax*, and *Sphingobacterium* (Khan

Responsible Editor: Robert Duran

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