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Occurrence of Hydrocarbon Degrading Genes in the Soils of the Republic of Tatarstan (Russia)

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Oil production can lead to many ecological problems, particularly to contamination of the soil by crude oil. Soil self-purification depends on the presence of microorganisms that have the ability to utilize hydrocarbons. Alkane-degrading bacteria are widespread and thus they are considered as an important tool in the clean-up of polluted environments. One of the key enzymes involved in bacterial alkane degradation is the alkane monooxygenase (alk): gene alkB present, for example, in Pseudomonas spp. which encodes the enzymes to decompose short-chain alkanes 6-12, genes alkM found, for example, in Acinetobacter spp. are responsible for the synthesis of enzymes which are responsible for decomposing alkanes C10-C40, genes alkB1 and alkB2 found in Rhodococcus spp. encode enzymes to decompose alkanes 8-32. The alk genes can be used as a biomarker to monitor the presence and diversity of alkane-degrading bacteria in the environment. Also, it is well-known that alkane-degraders are common in pristine environments.

In this study, we investigated the occurrence of three groups of different alk genes (alkB, alkM and alkB1) in pristine soils of the Republic of Tatarstan (Russia). Samples were collected from 25 locations with pristine soil but which differ in their physicochemical properties. In all the samples the study of the proportions of alk-genes and the number of 16S rRNA gene copies was carried out using the qPCR method. Percentages of alk gene copy numbers were calculated in proportion to 16S rRNA gene copy numbers.

The relative abundance of genes belonging to first group, associated with the alkB gene from Pseudomonas putida and Stenotrophomonas spp. varied within a range of 0.01% to 0.07%. In five samples genes of this group were not detected. Genes belonging to second group, being the gene of alk and the genus of Acinetobacter were not detected in any of the pollution-free samples under analysis. The third group of alk genes was the most highly represented in all the samples, being 10 to 100 times higher than the presence of first group. AlkB and alkB1 genes responsible for the synthesis of alkane monooxygenases enzyme in third group are more often found in the representatives of Pseudomonas (Ps. fluorescens, Ps. aeruginosa), Rhodococcus, Burkholderia and Amycolatopsis genera. Relative abundance of alk genes varied from 0.06% to 7.25%. The abundance of genes of the group connected with the presence of certain representatives of Pseudomonas, Rhodococcus, Burkholderia, and Amycolatopsis genera can be explained by the variety within the group presented and the wide occurrence of the carriers of such genes in the soil. Representatives of Pseudomonas and Rhodococcus genera are widespread in soil communities in cold and temperate climate zones.

Thus, alkane monooxygenase encoding genes were found in pristine soils of Republic of Tatarstan. Particularly, the greatest amount of genes detected belonging to the third group (alkB and alkB1). Genes belonging to first group (alkB) were also found while alk genes from Acinetobacter spp. were not detected in any of the 25 samples.