

## **Microbial Community Structure and Distribution Characteristics in Oil Contaminated Soil**

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In order to understand the impact of oil pollution on soil microbial community structure, oil contaminated soil samples were collected from different locations in a refinery in Dongying, China, and the microbial community structures of bacteria in those soil samples were determined by a high-throughput sequencing method. The results showed that the OTU numbers of the microbial community increased with the increase of oil content in the soil samples. The beta diversity of the microbial communities correlated significantly with oil content in the soil samples. Proteobacteria was the predominant phylum in bacterial communities, with the relative abundance of 44.8%-79.5%. Cluster analysis showed that with the increase of the oil content in the soil samples, the relative abundance of *Stenotrophomonas* in bacterial communities increased from 0.1% to 1.9%. The RDA analysis between physico-chemical properties and the bacterial communities in the oil contaminated soil samples indicated that the bacterial communities correlated most significantly with pH and oil content of the soil samples. The findings make an important contribution to better understand the microbial characteristics of the oil contaminated soil, and the relationship with its physico-chemical properties, providing important implications for the bioremediation of oil contaminated soil and groundwater environment.