

Metagenomic profiling of bacterial community in assam crude oil treated microcosms

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Abstract

Environmental pollution caused by crude oil and its fractions has been a major concern in today's world due to its adverse ecological impact. This has necessitated the development of eco-friendly and cost-effective biodegradation methods. Here we examined the crude oil biodegradation and 16S rDNA metagenomics of the bacterial consortia developed from the crude oil contaminated sediments of Noonmati Refinery, Assam. The biodegradation was assessed at 3% and 1% concentrations of Assam crude oil at different intervals at 25°C. Analysis of 16S rDNA metagenomics revealed the abundance of unclassified species of bacteria under the genus *Pseudomonas*, *Flavobacterium*, *Sphingobium*. The functional annotation of the 16S amplicons was performed using PICRUSt to derive relative KEGG and COG abundance, which predicted a total of 5587 different genes out of which 423 were unclassified genes. Further, 45 and 271 genes were exclusively present at 3% and 1% crude oil treated microcosms respectively. This analysis also showed the abundance of both alkane and aromatic hydrocarbon degrading genes.

Keyword: Crude oil, 16S rDNA metagenomics, bioremediation, KEGG, COG, PICRUSt

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Biography

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