

Study of Microbial Diversity Associated with Tarballs and Their Exploitation in Crude Oil Degradation

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Abstract : Tarballs are crude oil remnants found in oceans after long term weathering process and are a global concern since several decades as potential marine pollutant. Being complicated in structure microbial remediation of tarballs in natural environment is a slow process. They are rich in high molecular weight alkanes and poly aromatic hydrocarbons which are resistant to microbial attack and other environmental factors, therefore remain in environment for long time. However, it has been found that many bacteria and fungi inhabit on tarballs for nutrients and shelter. Many of them are supposed to be oil degraders, while others are supposed to be getting benefited by byproducts formed during hydrocarbon metabolism. Thus tarballs are forming special interesting ecological niche of microbes. This work aimed to study diversity of bacteria and fungi from tarballs and to see their potential application in crude oil degradation. The samples of tarballs were collected from Betul beach of south Goa (India). Different methods were used to isolate culturable fraction of bacteria and fungi from it. Those were sequenced for 16S rRNA gene and ITS for molecular level identification. The 16S rRNA gene sequence analysis revealed the presence of 13 bacterial genera/clades (Alcanivorax, Brevibacterium, Bacillus, Cellulomonas, Enterobacter, Klebsiella, Marinobacter, Nitratireductor, Pantoea, Pseudomonas, Pseudoxanthomonas, Tistrella and Vibrio), while the ITS sequence analysis placed the fungi in 8 diverse genera/ clades (Aspergillus, Byssochlamys, Monascus, Paecilomyces, Penicillium, Scytalidium/ Xylogone, Talaromyces and Trichoderma). All bacterial isolates were screened for oil degradation capacity. Potential strains were subjected to crude oil degradation experiment for quantification. Results were analyzed by GC-MS-MS.

Keywords : bacteria, biodegradation, crude oil, diversity, fungi, tarballs

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