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Bio-surfactant-mediated Surface Conditioning Enhances the Microbial Colonization on Polyethylene Terephthalate (PET) Surface: Implication for the Development of Microbial Enhanced Biodegradation of PET

A Kulakalaharan[1] and HS Jayasinghearachchi[1#]

[1]Institute for Combinatorial Advance Research and Education, General Sir John Kotelawala Defence University, Sri Lanka

[#]jayasinghearachchihs@kdu.ac.lk

Microbial degradation of Polyethylene Terephthalate (PET) holds promise for bioremediation efforts. The process can be slow, yet sustainable and have long-term implications for environmental health and stability. This study focused on the bio-surfactant-mediated PET colonization and degradation by the indigenous microbial species. PET debris from marine coastal waste and the open environment were collected. Then plastic debris was first washed with running water and then washed with sterile distilled water. Minimal salt medium (MSM) supplemented with 0.05% crude oil and plastic debris were used as potential carbon sources. The incubation period for cultures extended up to 3 months and microbial colonizers on the PET surface were recovered and grown on the Luria Brentani broth (LB). Mix microbial cultures were further evaluated for PET degradation on standard PET granules (Sigma Aldrich, Germany). Weight losses were measured after specific incubation periods (2-3 months). Bio-surfactant production was determined by drop collapse, oil displacement, emulsification index, and interfacial tension assays. Microbial strains colonized on PET were identified using nucleotide sequences of 16S rDNA and ITS1-ITS2 region. Nucleotide sequences were compared using BLAST search and 99% sequence similarities were found with *Pseudomonas alkaligenes, Rodococcus sp. Shewenella sp., Acromobacter sp* and *Candida sp.* to the GenBank. SEM images showed dense microbial colonization on PET particles and about 30% weight losses were observed. The microbial degradation of PET and heavy colonization of PET highlight the importance of bio-surfactant production leading to surface conditioning of the PET surface. Further studies are currently underway to determine PET metabolites in the supernatant.

Keywords: *bio-surfactant, PET, microbial degradation, Pseudomonas alkaligenes, Rodococcus sp., Shewenella sp., Acromobacter sp,, and Candida sp.*