

Abstract

Plastic pollution is a critical global challenge driven by the persistence of polymers such as low-density polyethylene (LDPE) and polyethylene terephthalate (PET), along with associated contaminants including bisphenol A (BPA) and terephthalic acid (TPA). This study investigates environmental microorganisms and landfill-derived microbial communities for plastic bioremediation by integrating genome mining, culturomics, and metagenomics approaches to identify key taxa and enzymatic pathways involved in aerobic and anaerobic plastic degradation. Screening 48,922 bacterial genomes (retrieved from the NCBI genome database) revealed a modular distribution of plastic-degrading enzymes (PETases, MHETases, alkane monooxygenases), enabling rational designing of bacterial consortia for efficient degradation. Metagenomic analyses of ~50-year-old Pirana landfill (Gujarat) and other landfills of India (from other studies) revealed diverse communities dominated by *Methylocaldum*, *Streptomyces*, *Pseudomonas*, *Bacillus*, *Pseudoxanthomonas*, *Flavobacterium*, and *Nocardioide*s. These analyses yielded 131 high-quality metagenome-assembled genomes (MAGs), including archaea like *Methanosarcina*, *Methanoculleus*, and *Nitrososphaera*, marking one of the few reports highlighting archaeal genomes from plastic-impacted environments. Enrichment of Pirana landfill microbial communities with LDPE and PET elucidated potential for plastic biodegradation. LDPE enrichments were dominated by *Rubrivivax*, *Burkholderia*, *Pseudomonas*, and *Illumatobacter*, whereas PET enrichments were dominated by *Methyloversatilis*, *Stutzerimonas*, *Cupriavidus*, and *Hypomicrobium*. MAGs reconstructed from these enrichment microcosms showed robust genetic potential for LDPE, PET, TPA, and BPA degradation, along with pathways supporting biofilm formation, biosurfactant production, and central metabolism carbon, nitrogen, sulfur, and methane, highlighting metabolically versatile plastic-degrading communities. Microcosm studies showed substantial LDPE and PET biodegradation without pretreatment. Nearly 60% LDPE weight loss over 120 days (rate 0.00766 mg/day) under aerobic conditions and ~6% under anaerobic conditions were observed. Nearly 16% of PET biodegradation was achieved in 120 days. LDPE and PET biodegradation by landfill microorganisms was confirmed by Fourier transform infrared (FTIR) spectroscopy, showing oxidative chain scission. Scanning electron microscopy (SEM) revealed surface cracks and biofilm formation, and atomic force microscopy (AFM) indicated increased surface roughness. Gas chromatography-mass spectrometry (GC-MS) detected long-chain alkanes, volatile fatty acids, and methane in anaerobic systems, confirming microbial biodegradation. Mixed-pollutant conditions enhanced LDPE degradation through bacterial synergy and metabolic flexibility, whereas PET degradation was not improved significantly. This work not only deepens our scientific understanding of how diverse landfill-derived bacteria and archaea participate in plastic transformation but also translates these insights into tangible biotechnological opportunities. By characterizing the organisms, pathways, and interactions that drive plastic degradation in landfill and enrichment systems, the study provides a mechanistic basis for predicting and enhancing microbial plastic breakdown, leading to environmental cleanup.

Keywords: Landfill, bacterial communities, polyethylene terephthalate (PET), low-density polyethylene (LDPE), Bisphenol A (BPA), terephthalate (TPA), biodegradation, plastics