

Isolation and characterization of plastic waste degrading microorganisms from Landfill soil

Abstract:

The pervasive issue of plastic pollution poses a grave risk to planetary health. Current methods like landfilling, incineration, and conventional recycling are either environmentally detrimental or inadequate. Therefore, biodegradation by microbes emerges as an attractive and sustainable solution. This study focused on finding plastic-degrading microbes within landfill environments, using soil samples and enriching them with plastic as the sole carbon. Through three consecutive 15-day cycles of enrichment, potential degraders were isolated and subjected to various tests, including microscopy, biochemical assays, PEG plate clearance, enzyme production assessment, and identification via 16S rRNA Sanger sequencing.

Over the course of the year, 28 distinct isolates were obtained across seven enrichment rounds. These isolates exhibited varied morphological and biochemical characteristics, displayed capacity for PEG clearance, and produced lipase and esterase enzymes. However, different isolates showed different levels of PEG clearance and/or enzyme activity. The sequencing of 16S rRNA primarily grouped the isolates into four genera: *Pseudomonas*, *Brevibacillus*, *Bacillus*, and *Bordetella*. A smaller, miscellaneous group also contained green or mixed species isolates.

Selected *Brevibacillus* and *Pseudomonas* isolates showed promising results in plastic weight loss experiments across four different polymer types. Intriguingly, subsequent 16S rRNA metagenomic analysis through next generation sequencing platform of the top enzyme-producing strains revealed that the apparent single-species cultures were actually mixed microbial communities (consortia)—for example, the *Brevibacillus* isolate was only 78% *Brevibacillus*.

The results indicate that these microbial isolates show potential for plastic degradation. However, their true efficiency may rely on collaborative action within their consortia. Future research using in-depth whole-genome metagenomics can help fully understand the identity and complex mechanisms behind this degradation process.