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The plastic-degrading capabilities of *Pseudomonas aeruginosa*

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Abstract

The global accumulation of synthetic and bio-based plastics has intensified the demand for effective and sustainable degradation strategies. This study explores the plastic-degrading potential of *Pseudomonas aeruginosa*, focusing on its degrading enzymes, biofilm formation, and biosurfactant production. The study highlights the limited degradability of C–C backbone plastics such as polyethylene (PE), polypropylene (PP), and polystyrene (PS), in contrast to ester-containing polymers like PET, PU, and bio-based plastics (PLA, PCL, PHA), which exhibit greater microbial susceptibility. While *P. aeruginosa* demonstrates only partial surface modification of recalcitrant plastics, it achieves substantial degradation of bio-based plastics such as PCL. Genomic profiling using PlasticsDB and PAZy databases reveals homologs of plastic-active enzymes, including esterases and depolymerases, with potential roles in polyester degradation. Furthermore, the integration of chemical pretreatment methods, such as pyrolysis of PE into metabolizable alkanes, combined with microbial conversion into polyhydroxyalkanoates (PHA), underscores the importance of hybrid chemo-biotechnological approaches. Despite biosafety concerns, *P. aeruginosa* emerges as a metabolically versatile and genetically tractable candidate for precision-engineered bioremediation. This work positions *P. aeruginosa* not as a standalone solution, but as a modular component within broader strategies for next-generation plastic waste valorization and upcycling.

Keywords *P. aeruginosa*, Plastic polymers, Biodegradation, Biofilm formation, Enzymatic degradation, Rhamnolipids

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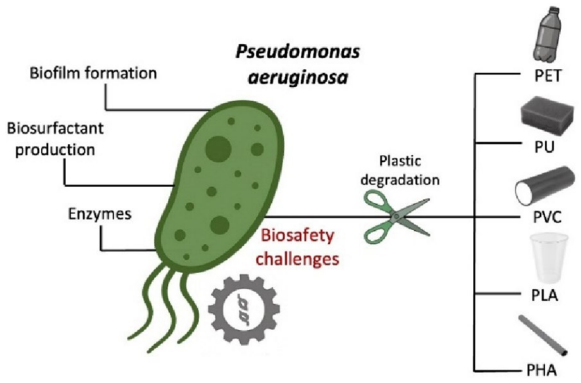
Graphical Abstract



Introduction

Plastic has become an essential material in modern society, with uses ranging from packaging and construction to healthcare and electronics. However, its durability and resistance to natural degradation have led to a global environmental crisis. Since the first synthetic plastic was made in 1907, production has risen to over 350 million tons annually [1], with the vast majority accumulating in landfills and natural ecosystems. Conventional disposal methods, such as landfilling, incineration, and chemical recycling, recover less than 10% of global plastic waste [2], underscoring the pressing need for sustainable alternatives. Microbial biodegradation has emerged as a promising solution, utilizing the metabolic capabilities of microorganisms to break down plastic polymers. Bacteria, particularly when organized in biofilms, possess enhanced resilience and enhanced enzymatic activity, making them attractive candidates for plastic degradation. Biofilms provide a protective matrix and allow horizontal gene transfer, potentially boosting the efficiency of polymer breakdown [3, 4]. Among the diverse microbial plastic degraders, *Pseudomonas aeruginosa* stands out due to its metabolic versatility, adaptability to various environments, and robust biofilm-forming capacity [5–7]. While traditionally studied for its pathogenicity and antibiotic resistance [8], more recent findings suggest that *P. aeruginosa* biofilms may alter the structure of plastics [9, 10].

The most widely used types of plastics are polyethylene terephthalate (PET), polyethylene (PE), polypropylene (PP), polyvinyl chloride (PVC), and polyurethane (PU) which dominate global production due to their durability, flexibility, and low cost (Fig. 1). Overall, polymers with inert C–C backbones (e.g., PE, PP) are less degradable than those with ester or amide linkages (e.g., PET, PU). In parallel, the use of bio-based plastics such as polylactic acid (PLA), poly(butylene succinate-co-butylene adipate) (PBSA), and polyhydroxyalkanoates (PHA)

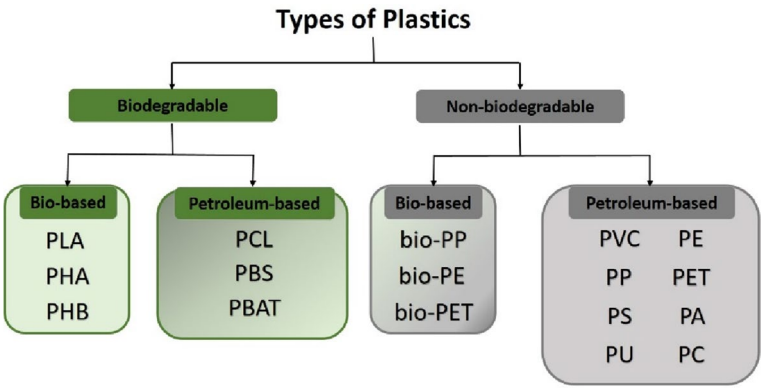


Fig. 1 Schematic representation of different types of plastics

has significantly increased, reaching approximately 2.18 million tons in 2023, and it is projected to increase to about 7.43 million tons by 2028 [11]. That highlight is the transition toward environmentally responsible polymer design.

Molecular weight, crystallinity, and surface hydrophobicity further affect microbial attachment and enzymatic activity, and these structural differences are central to evaluating *P. aeruginosa* as a plastic degrader [12]. Its metabolic adaptability, biofilm-forming abilities, and biosurfactant production may allow more effective interaction with inert polymers. Understanding both polymer barriers and microbial strategies is key to assessing its biodegradation potential. Advanced analytical methods such as Fourier-transform infrared spectroscopy (FTIR), nuclear magnetic resonance (NMR), high-performance liquid chromatography (HPLC), and Thermally Assisted Hydrolysis and Methylation–Gas Chromatography (THM-GC) enable precise monitoring of polymer bond cleavage and metabolite formation [13]. Stable isotope-tracing approaches provide direct evidence of carbon flow from polymers into microbial biomass or CO_2 [14, 15]. Omics-driven studies (genomics, transcriptomics, proteomics, and metabolomics) have revealed the genetic and enzymatic networks underpinning microbial plastic degradation, offering system-level insights into microbial consortia [16, 17]. As AI tools rapidly advance, computational enzyme discovery workflows, including machine learning and protein language models, are accelerating the identification of novel biocatalysts capable of degrading diverse polymers [18, 19]. The integration of classical approaches and modern tools in exploring polymer biodegradation processes emphasizes the interdisciplinary character of biodegradation research.

Pseudomonas aeruginosa and plastic degradation

P. aeruginosa thrives in diverse environments such as soil, water, and industrial waste. Its survival under nutrient limitation and resistance to antimicrobials make it suitable for biotechnological applications, including plastic degradation. As a metabolically versatile organism, it can use hydrocarbons, alcohols, and amino acids as carbon and energy sources [20]. This adaptability depends on extracellular hydrolases, oxygenases, and peroxidases that transform complex substrates [21]. These enzymes are crucial for oxidative transformations and cleavage of polymer chains. Also, *P. aeruginosa* can form thick biofilms, which can further support survival and nutrient access. In plastic degradation, biofilms enable adhesion to hydrophobic surfaces like PE and PET and localize enzymes and biosurfactants, promoting surface modification.

A number of studies have demonstrated the potential of *P. aeruginosa* to degrade both synthetic and bio plastics, particularly through biofilm-mediated surface modification and enzymatic activity.

Polyethylene terephthalate (PET) is a thermoplastic polymer with outstanding physical and chemical characteristics, and it is fully recyclable, making it a key material in sustainable plastic management. Its high crystallinity and hydrophobicity make it highly resistant to environmental and enzymatic degradation. *P. aeruginosa* biofilms can colonize PET surfaces and induce minor physicochemical changes, such as altered crystallinity and surface roughness, but substantial degradation has not been consistently achieved [12, 22]. Recent studies have highlighted the role of esterases in cleaving ester linkages found in polyesters like PET, enabling partial depolymerization under mild conditions [23]. Of particular interest is the leaf-branch compost cutinase (LCC) enzyme, originally isolated from leaf-branch compost, which has demonstrated exceptional activity against polyethylene terephthalate (PET) [24]. Bioinformatic analyses suggest that homologous esterases within *P. aeruginosa*, with similar catalytic domains such as the newly identified Pap1 enzyme, may exist in certain clinical isolates, offering promising avenues for horizontal gene transfer or recombinant expression [25]. Additionally, the same clinical isolate of *P. aeruginosa* (PA-W23) was capable of degrading the medically relevant plastic polycaprolactone (PCL), achieving 78% mineralization within 7 days. This finding highlights the remarkable plastic-degrading potential of *P. aeruginosa* and underscores its relevance in both environmental and clinical contexts.

Polyurethane (PU) contains ester and urethane bonds that are susceptible to enzymatic hydrolysis by esterases and proteases secreted by *P. aeruginosa*. Laboratory experiments using PU films have documented significant degradation over 20–30 days, with up to 30% weight loss and clear evidence of surface erosion observed via scanning electron microscopy [12]. FTIR analysis confirmed cleavage of ester linkages, and biosurfactants like rhamnolipids were found to enhance polymer accessibility by reducing the surface tension.

Polyethylene (PE), composed of a highly inert C–C backbone, is among the most resistant plastics to microbial attack. Nonetheless, *P. aeruginosa* has demonstrated the ability to adhere to PE surfaces and initiate minor degradation, probably through surface erosion. Studies report surface pitting, reduced hydrophobicity, and slight weight loss (approximately 20–25%) after prolonged incubation [26, 27]. Notably, low-density polyethylene (LDPE) exhibited pronounced surface pitting, decreased hydrophobicity, and around 20% weight loss, which increased to questionable 50.5% after 2 months

of incubation [28]. In contrast, high-density polyethylene (HDPE) showed greater resistance, with a maximum weight loss reported of up to 20% [29]. FTIR spectroscopy has revealed the emergence of polar functional groups, such as hydroxyl and carbonyl moieties, indicating oxidative surface modification rather than deep polymer breakdown. Despite the growing number of these reports regarding PE biodegradation, the evidence for true mineralization remains largely inconclusive. As critically emphasized by Jendrossek [30], most reports rely on indirect indicators, such as weight loss, surface oxidation, or fragmentation, without demonstrating complete assimilation of polymer-derived carbon into biomass or its conversion to CO_2 by isotope-labeling techniques.

Polyvinyl chloride (PVC), composed of a C–C backbone with pendant chlorine atoms, also underwent notable changes upon exposure to *P. aeruginosa*. Biofilm formation was observed on PVC surfaces, accompanied by surface erosion and structural alterations within the polymer matrix. These modifications were associated with approximately 30% weight loss [31], suggesting that despite its halogenated structure, PVC remains susceptible to microbial degradation under prolonged incubation.

Polypropylene (PP) is one of the least degradable polymers, with a saturated C–C backbone. While *P. aeruginosa* can form biofilms on these surfaces, degradation is minimal and limited to superficial modifications [32].

Polylactic acid (PLA) is a biodegradable polyester derived from renewable resources such as corn and sugarcane. Despite its eco-friendly profile, PLA exhibits limited degradability under natural conditions, often requiring industrial composting for effective breakdown. *P. aeruginosa* has emerged as a promising candidate for PLA degradation, particularly strain S3 [33], which demonstrates esterolytic activity at ambient temperatures. Studies have confirmed surface erosion, weight loss, and the release of lactic acid oligomers following microbial treatment, with scanning electron microscopy revealing cracks and biofilm formation on PLA surfaces. Enzymes such as esterases, lipases, proteases, and cutinases are central to this process, targeting ester bonds within the polymer matrix and facilitating depolymerization [34, 35]. Genomic analysis of PLA-degrading strains, including *P. aeruginosa* S3, *Sphingobacterium* sp. S2, and *Geobacillus* sp. EC-3, has identified key genes involved in xenobiotic metabolism, biofilm regulation, and lactate utilization, supporting their role in PLA biodegradation under mesophilic and thermophilic conditions [33].

P. aeruginosa was shown to biodegrade the bio-based plastic poly(butylene succinate-co-butylene adipate) (PBSA), mineralizing approximately 78% of the polymer into CO_2 within 40 days [36]. This high mineralization rate underscores the remarkable biodegradation capacity of *P. aeruginosa*, positioning it as a promising candidate for bio-based plastic waste treatment.

In addition to PBSA, *P. aeruginosa* has demonstrated the ability to degrade polyhydroxyalkanoates (PHA), with molecular weight reductions ranging from 7 to 17% and up to 29% weight loss [37]. Clear zone formation during incubation with polyhydroxybutyrate (PHB) further confirmed active biodegradation within 15 days [38].

PAZy-based enzymatic profiling of *P. aeruginosa*

Number of genetic traits and enzymatic activities underline the ability of *P. aeruginosa* to efficiently interact and degrade polymeric substrates. *P. aeruginosa* PAO1 genes involved in plastic degradation were identified by blasting (query coverage > 80% and > 60% identity) against the PlasticsDB [39] and the Plastics-Active Enzymes Database (PAZy) (Table 1) [40]. Notably, high query coverage and identity scores were observed for PET-degrading esterases such as PpEst (tesA) from *Pseudomonas pseudoalcaligenes* and other environmental *Pseudomonas* strains, suggesting conserved catalytic domains within the genus. The detection of homologs to PU-degrading enzymes from *Agrobacterium tumefaciens* and bioplastic-targeting depolymerases from *Pseudomonas chlororaphis*

Table 1 Comparative PAZy-based homology analysis of plastic-degrading enzymes in the *P. aeruginosa* genome

Plastic type	Query coverage	Identity	Microorganism (enzyme)	Reference
Synthetic plastic-petroleum based				
PET	100	72.14	*Pseudomonas pseudoalcaligenes* (PpEst (tesA))	[41, 42]
PET	100	66.82	*Pseudomonas* sp. strain 9.2 (EstB)	[43]
PU	99	62.14	*Agrobacterium tumefaciens* (amidase)	[44]
Bio-based plastic				
PLA	98	86.38	*Pseudomonas chloroaphis* PA23 (PHA depolimerase)	[45]
PCL	98	85.66	*Pseudomonas putida* KT2442 (PHA depolimerase)	[46]
PHA	94	65.43	*Pseudomonas chlororaphis* PA23 (lipase)	[47]

and *P. putida* KT2442 further supports the hypothesis that *P. aeruginosa* may possess latent or inducible enzymatic functions relevant to both synthetic and bio-based plastic degradation.

This genomic evidence complements earlier functional predictions and reinforces the notion that *P. aeruginosa*, despite not being traditionally classified as a plastic degrader, may serve as a reservoir of biocatalytic potential. The presence of lipase and depolymerase homologs associated with PHA and PLA degradation is of particular interest, given the increasing industrial relevance of bioplastics and bio-based plastic and the need for microbial systems capable of closing the loop in biopolymer life cycles. Moreover, the cross-species homology observed here demonstrates the evolutionary conservation of "plastic-active" enzymes and highlights the importance of domain-level annotation in uncovering hidden biodegradation capabilities. Additionally, oxidative enzymes such as monooxygenases and peroxidases may initiate polymer oxidation, introducing functional groups that facilitate subsequent enzymatic attack. According to KEGG annotations [48] for *P. aeruginosa* PAO1, the genome encodes at least 54 monooxygenases, 19 peroxidases, and 45 dioxygenases, highlighting its oxidative versatility.

Taken together, these results provide a strong case for further experimental validation, including transcriptomic profiling under polymer exposure and heterologous expression of candidate genes. They also offer a foundation for future synthetic biology approaches aimed at enhancing plastic degradation through targeted enzyme and pathway engineering.

P. aeruginosa auxiliary pathways in plastic degradation

P. aeruginosa produces a range of biosurfactants, among which rhamnolipids are considered particularly significant [49]. They reduce surface tension and emulsify hydrophobic compounds, improving microbial access to plastics. Rhamnolipids also influence biofilm architecture and dispersion, affecting colonization and degradation dynamics. Rhamnolipids, as well-characterized biosurfactants produced by *P. aeruginosa*, have gained increasing attention due to their multifunctional roles in bioremediation, emulsification, and microbial adhesion [49]. Their amphiphilic nature facilitates the solubilization of hydrophobic compounds, including hydrocarbons and synthetic polymers, thereby enhancing microbial access and enzymatic degradation. In addition to their environmental relevance, rhamnolipids are being explored for industrial applications such as bio-based detergents, agrochemical formulations, and biolubricants.

Biofilm formation plays a synergistic role in plastic degradation (Fig. 2). *P. aeruginosa* forms robust biofilms on hydrophobic plastic surfaces, concentrating enzymes and metabolites that enhance degradation. A recently published study showed that exposure to PCL significantly increased biofilm formation, which in turn boosted antibiotic resistance and plastic breakdown efficiency [50]. In the biofilm form, bacteria produce higher amounts of rhamnolipids [49], which emulsify hydrophobic substrates and promote microbial colonization. Clinical isolates have demonstrated increased biofilm density and resilience on polymer surfaces, suggesting that degradation intermediates may act as signaling molecules or nutrient sources [25]. This dual functionality, biodegradation coupled with surface colonization, could be strategically exploited to improve enzyme delivery and retention on plastic waste.

The study by Guzik et al. [51] presents a promising alternative strategy: the chemical pretreatment of PE via pyrolysis to generate low molecular weight paraffins, which can then serve as substrates for microbial synthesis of biodegradable PHAs. This two-step chemo-biotechnological approach circumvents the inherent recalcitrance of high crystallinity, hydrophobic polymers

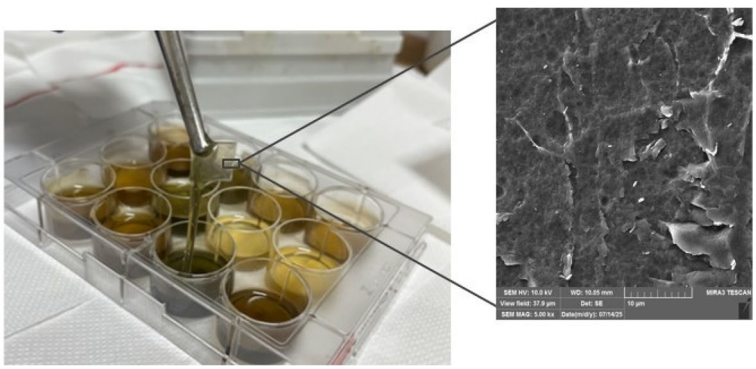


Fig. 2 PET plastic in a *P. aeruginosa* biofilm formation assay and SEM micrograph of PET plastic surface after prolonged exposure to biofilm

by transforming them into metabolically accessible intermediates, thereby efficiently upcycling postconsumer PE into PHAs. Several studies suggest that *Pseudomonas aeruginosa* can channel such degradation intermediates into central metabolic pathways, enabling the biosynthesis of compounds like PHAs. Notably, *P. aeruginosa* PAO1 has been shown to accumulate up to ~25% of its cell dry weight as PHA when supplied with polyethylene pyrolysis wax in the presence of rhamnolipids [51]. Beyond this example, broader strategies for plastic waste valorization have been reported, including the use of engineered microbial strains, individual bacteria, and mixed consortia to convert PET monomers, PE pyrolysis oils, and oxidized plastic fragments into PHAs, thereby establishing diverse and scalable routes for bio-based plastic production from waste substrates [52, 53]. In addition, *P. aeruginosa* is well known for rhamnolipid biosynthesis, and valorization of plastic-derived intermediates into biosurfactants such as rhamnolipids has also been explored [54].

Challenges and biosafety risks associate with *P. aeruginosa*

P. aeruginosa's enzymatic activity is highly sensitive to environmental fluctuations in temperature, pH, and nutrient availability, which can limit degradation efficiency. While biofilms facilitate surface attachment, they may also impede nutrient diffusion and slow metabolic rates. Most reports describe superficial erosion rather than complete mineralization, often leaving behind microplastic residues [55]. As an opportunistic pathogen commonly linked to hospital-acquired infections, especially in immunocompromised individuals, *P. aeruginosa* deployment in environmental or industrial settings requires caution. To address these limitations, researchers are exploring non-pathogenic strains or transferring degradative gene clusters into safer hosts like *Pseudomonas putida*. Alternatively, enzyme-based strategies such as purification and immobilization allow direct application to plastic substrates, avoiding the risks of live microbial release. Together, these approaches mark a shift from passive biodegradation to precision-engineered bioremediation, positioning *P. aeruginosa* as a genetically adaptable platform for next-generation plastic degradation, provided its safety profile is rigorously managed.

Future outlook

While *P. aeruginosa* possess intriguing possibilities for microbial plastic degradation, its role remains complex and conditional. Its metabolic adaptability and ability to form biofilms on hydrophobic surfaces suggest a natural predisposition for interacting with synthetic polymers, particularly those with ester linkages. Despite its potential, *P. aeruginosa*'s limited degradation efficiency and pathogenic nature raise concerns regarding its suitability for direct environmental use. The evidence points to a bacterium that is biologically equipped to initiate degradation but not necessarily to complete it in a way that is scalable or environmentally safe. However, the emergence of novel enzymes within clinical isolates and the potential for synthetic enhancement open new avenues for biotechnological innovation. Rather than seeing *P. aeruginosa* as a standalone solution, it is more accurate to consider it a modular component within a broader, engineered strategy. Its future utility will depend not only on its biology but on how thoughtfully it is integrated into systems designed to address the multifaceted challenge of plastic pollution.

Abbreviations

PE	Polyethylene
PP	Polypropylene
PET	Polyethylene terephthalate
PU	Polyurethane
PVC	Polyvinyl chloride
PCL	Polycaprolactone
PHB	Poly(3-hydroxybutyrate)
PHA	Polyhydroxyalkanoates
PLA	Polylactic acid
PBSA	Poly(butylene succinate-co-butylene adipate)
ROS	Reactive oxygen species
FTIR	Fourier-transform infrared spectroscopy
LCC	Leaf-branch compost cutinase
PAZy	Plastics-Active Enzymes Database

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Authors' contributions

IA and DM contributed equally to the conceptualization, literature review, and writing (original draft and review & editing) of this manuscript. Both authors read and approved the final version.

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Data availability

Data sharing is not applicable to this article as no datasets were generated or analysed during the current study.

Declarations

Ethics approval and consent to participate

Not applicable.

Consent for publication

Not applicable.

Competing interests

The authors declare no competing interests.

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