Journal of Pharmacology, Genetics and Molecular Biology (JPGMB)
ISSN: 3049-3757 | Vol. 02, Issue-02, March-April, 2026

Metagenomic Exploration of Landfill Microbiota for Novel Plastic-Degrading Enzymes

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Abstract:

Plastic waste has become one of the most pressing environmental challenges worldwide, primarily because synthetic polymers do not easily break down under natural conditions. As a result, large quantities of plastic accumulate in landfills, where they persist for long periods. Interestingly, these landfill environments are not just waste storage sites but also complex ecosystems that host diverse microbial communities. Over time, some of these microorganisms have adapted to survive by interacting with and even utilizing resistant plastic materials. Recent advancements in metagenomics have made it possible to study these microbial communities without the need for traditional culturing techniques. This has opened new avenues for discovering previously unknown plastic-degrading enzymes. In this review, we explore how landfill microbiota act as valuable sources of biodegradation potential and discuss various metagenomic approaches used to identify such enzymes. Special attention is given to key enzyme groups, including PETases, cutinases, lipases, and esterases, which play crucial roles in breaking down synthetic polymers. This review also outlines these limitations and discusses future directions for developing sustainable and effective plastic waste management strategies.

Keywords: Plastic pollution; Metagenomics; Landfill microbiota; Plastic-degrading enzymes; PETase; Cutinase; Biodegradation; Microbial consortia; Bioinformatics; Sustainable waste management**.**

Received: Jan. 15, 2026 **Revised: Feb. 28, 2026** **Accepted: March. 22, 2026** **Published: April 22, 2026**

DOI: **https://doi.org/10.64062/JPGMB.Vol2.Issue2.8**

https://jpgmb.com/1/issue/archive

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1. Introduction

The exponential increase in plastic production since the mid-20th century has resulted in the widespread accumulation of plastic waste across terrestrial and aquatic ecosystems. Global plastic production has surpassed hundreds of millions of tons annually, with a substantial proportion ultimately accumulating in landfills or leaking into the environment[1]. Commonly used polymers such as polyethylene (PE), polypropylene (PP), polystyrene (PS), and polyethylene terephthalate (PET), along with biodegradable alternatives like polylactic acid (PLA), are favoured due to their durability, lightweight properties, and economic feasibility. However, these same characteristics contribute to their resistance to natural degradation, leading to their persistence for extended periods and resulting in severe ecological consequences[2]. The continuous accumulation of plastic waste has further led to the formation of microplastics, posing risks to soil health, aquatic systems, and food chains.

Landfills represent the primary disposal sites for a significant fraction of global plastic waste, particularly in regions with limited recycling infrastructure. These environments are highly heterogeneous and dynamic, characterized by fluctuating physicochemical conditions such as temperature gradients, moisture levels, oxygen availability, and organic matter composition. Such conditions create selective pressures that drive microbial adaptation and evolution[3]. Recent studies have demonstrated that landfill ecosystems harbour complex microbial communities capable of interacting with plastic materials and potentially utilizing them as carbon sources[4]. The coexistence of bacteria and fungi within these environments further enhances biodegradation potential through synergistic interactions and metabolic cooperation. Traditional microbiological methods have long relied on culturable organisms, which represent only a small fraction of total microbial diversity, thereby limiting the discovery of efficient plastic-degrading microorganisms. The advent of metagenomics has revolutionized this field by enabling the direct extraction and analysis of environmental DNA without the need for cultivation[5].

This culture-independent approach allows researchers to explore the vast genetic reservoir present within environmental microbiomes and identify novel enzymes with potential applications in biodegradation. Recent advancements in high-throughput sequencing and computational tools have further expanded the scope of metagenomic analysis, enabling large-scale identification of functional genes and metabolic pathways. Recent studies have highlighted the immense potential of metagenomics combined with machine learning in uncovering plastic-degrading enzymes. For instance, large-scale analyses of landfill microbiomes have identified tens of thousands of potential plastic-degrading enzymes, demonstrating the extensive enzymatic diversity present in such environments[6]. Similarly, computational approaches have enabled the identification of numerous novel enzyme candidates from environmental microbiomes, significantly accelerating the discovery pipeline[7].

Furthermore, emerging research emphasizes the role of microbial consortia, synthetic biology, and artificial intelligence in enhancing plastic degradation efficiency and designing robust enzyme systems[8]. Collectively, these advancements underscore the importance of integrating metagenomics, bioinformatics, and biotechnology to better understand and harness the plastic-degrading potential of landfill microbiota. This integrated approach holds significant promise for developing sustainable and scalable solutions to mitigate the growing global plastic pollution crisis.

2. Landfill Microbiota: Diversity and Ecological Significance

Landfill ecosystems represent complex and dynamic habitats that harbour an extensive diversity of microorganisms, including bacteria, fungi, and archaea. These microbial communities are fundamental to the functioning of landfill environments, where they drive essential processes such as organic matter decomposition, methane generation, and nutrient recycling[9]. The heterogeneity of landfill conditions—ranging from aerobic zones near the surface to strictly anaerobic regions in deeper layers—creates diverse ecological niches that support a wide range of metabolically versatile microorganisms[10]. Bacteria form the major portion of microbial communities in landfills, with common genera such as *Pseudomonas*, *Bacillus*, *Streptomyces*, and *Actinomyces* playing an important role in breaking down complex organic materials[11]. In particular, members of the phylum Actinobacteria are highly significant because they produce extracellular enzymes that can act on resistant compounds, including certain types of synthetic plastics[12]. Alongside bacteria, fungi like *Aspergillus* and *Penicillium* also contribute to degradation processes. Their filamentous growth allows them to spread over solid surfaces, while the enzymes they secrete help in breaking down polymers[13].

In the deeper, oxygen-limited regions of landfills, archaea especially methanogenic archaea become more prominent. These microorganisms are involved in the final steps of decomposition, where they convert intermediate breakdown products into methane and carbon dioxide[14]. Although archaea do not directly degrade plastics, they play an essential supporting role by maintaining the balance of the microbial ecosystem and facilitating the overall degradation process.

The ecological importance of landfill microbiota is largely driven by their remarkable ability to adapt to harsh and changing conditions. Microorganisms in these environments are constantly exposed to stress factors such as temperature fluctuations, limited nutrients, and the presence of toxic substances like plastics and their additives. To survive, they develop adaptive strategies such as genetic changes, horizontal gene transfer, and the formation of biofilms on plastic surfaces[15]. Biofilms are especially important because they allow microbes to firmly attach to plastic materials and concentrate their enzymes in one place, making the degradation process more effective.

Recent metagenomic studies have shown that landfill microbial communities contain a vast pool of genes linked to plastic degradation, including those responsible for producing enzymes like hydrolases, esterases, and oxidoreductases[16]. These findings suggest that landfills function as natural bioreactors, where microbial communities continuously evolve and work together to break down complex and persistent materials. In addition, the presence of microbial consortia enhances this process, as different species contribute unique metabolic functions, leading to a more efficient and coordinated degradation of polymers[17].

2.1 Bacterial Communities

Bacteria form the most abundant and functionally active group of microorganisms in landfill environments. Common genera such as *Pseudomonas*, *Bacillus*, *Streptomyces*, and *Actinomyces* are frequently observed and are well known for their ability to break down complex organic materials[18]. These bacteria are highly adaptable and can utilize a wide variety of carbon sources. They often play a key role in the early stages of plastic degradation by attaching to polymer surfaces and releasing enzymes that begin the breakdown process. For example, *Pseudomonas* species are widely recognized for their efficiency in degrading hydrocarbons and plastics due to their strong enzymatic systems and ability to survive in challenging environments[19]. Similarly, *Bacillus* species produce stable enzymes that remain active even under fluctuating environmental conditions, making them particularly useful in degradation processes.

Among these groups, Actinobacteria are especially important because of their strong ability to degrade tough and resistant materials, including synthetic polymers. Genera like *Streptomyces* and *Actinomyces* produce a variety of extracellular enzymes—such as hydrolases, esterases, and oxidases—that help break down complex polymer structures[20]. Their filament-like growth also allows them to spread efficiently over solid surfaces like plastics, improving contact between enzymes and substrates. In addition, these bacteria are well adapted to nutrient-poor environments, which makes them particularly effective in long-term degradation processes within landfills.

Recent metagenomic studies have further shown that landfill bacterial communities contain a wide range of genes linked to plastic degradation, indicating a vast and largely untapped potential for biotechnological applications[21]. Overall, bacterial populations not only initiate the breakdown of plastics but also work together within microbial communities to support further degradation, making them essential players in the natural recycling processes occurring in landfill ecosystems.

2.2 Fungal Contributions

Fungi play an important and often complementary role in the degradation of plastics within landfill environments. Common fungal genera such as *Aspergillus* and *Penicillium* are widely reported for their ability to break down complex polymeric materials through the secretion of extracellular enzymes[22]. These fungi produce a variety of oxidative and hydrolytic enzymes, including laccases, peroxidases, cutinases, and esterases, which are capable of attacking the chemical bonds present in synthetic polymers. This enzymatic activity helps in weakening the polymer structure, making it more accessible for further microbial degradation[23]. One of the key advantages of fungi in plastic degradation is their filamentous mode of growth. Unlike bacteria, fungi grow as long, thread-like structures called hyphae, which collectively form a mycelial network. This structure allows them to effectively colonize and penetrate solid substrates such as plastic surfaces, increasing the contact area between enzymes and the polymer[24]. As a result, fungi are particularly efficient in initiating the surface erosion and fragmentation of plastics, especially in environments where nutrients are limited.

Fungi are also highly adaptable to harsh environmental conditions commonly found in landfills, including variations in temperature, pH, and moisture levels. Their ability to survive under such stress conditions enables them to persist and remain active over long periods[25] in addition, fungal species often work in association with bacterial communities, forming synergistic relationships where fungi initiate polymer breakdown and bacteria further metabolize the resulting degradation products[26]. Emerging studies highlight that fungi are becoming increasingly important as sources of new plastic-degrading enzymes. When they work together with bacteria, the overall degradation process becomes much more efficient[27].

2.3 Archaeal Populations

Archaea, particularly methanogenic archaea, are key members of microbial communities in landfill environments, especially in deeper layers where oxygen is absent. These microorganisms thrive under anaerobic conditions and play a crucial role in the final stages of organic matter degradation. Methanogens convert intermediate products such as acetate, hydrogen, and carbon dioxide generated during the breakdown of complex materials into methane and carbon dioxide[28]. Although archaea are not directly involved in the initial breakdown of plastic polymers, their metabolic activities are essential for maintaining the overall efficiency of the degradation process. In landfill ecosystems, plastic degradation often occurs through a series of interconnected microbial processes. Bacteria and fungi initiate the breakdown of polymers into smaller compounds, which are then further metabolized into simpler molecules. Methanogenic archaea utilize these intermediates, preventing their accumulation and ensuring the smooth continuation of degradation pathways[29]. This cooperative interaction between different microbial groups highlights the importance of archaea in supporting the overall biodegradation system.

Archaea are also highly adapted to extreme and nutrient-limited environments, allowing them to survive under the harsh conditions commonly found in landfills, such as high pressure, variable temperatures, and low oxygen availability[30]. Their presence contributes not only to waste stabilization but also to biogas production, which has potential applications as a renewable energy source. Recent metagenomic studies have further revealed the diversity and functional importance of archaeal communities in landfill microbiomes, emphasizing their indirect yet vital role in the degradation of complex and persistent materials, including plastics [31].

2.4 Adaptive Strategies

Microorganisms in landfill environments are constantly exposed to harsh and fluctuating conditions, including limited nutrients, toxic compounds, and the presence of persistent plastics. To survive and function under these stresses, they develop several adaptive strategies that enhance their ability to utilize complex substrates such as synthetic polymers.

2.4.1. Horizontal Gene Transfer (HGT)

Horizontal gene transfer is one of the most important mechanisms that enables microorganisms to rapidly acquire new genetic traits. Instead of relying only on slow evolutionary changes, microbes can exchange genetic material such as plasmids or transposons with neighbouring cells. This process allows the spread of genes encoding plastic-degrading enzymes across different microbial species[32]. In landfill environments, where diverse microbial communities coexist in close proximity, HGT accelerates the development of metabolic pathways required for the breakdown of recalcitrant compounds. As a result, even microorganisms that originally lacked degradation capabilities can adapt and participate in plastic biodegradation.

2.4.2. Biofilm Formation on Plastic Surfaces

Biofilms are structured communities of microorganisms embedded within a self-produced extracellular matrix. This matrix helps microbes attach firmly to plastic surfaces and protects them from environmental stress[33]. Within these biofilms, microbial cells can communicate and coordinate their activities, leading to more efficient degradation processes. The close proximity of cells in a biofilm also enhances the localized concentration of enzymes, which improves the breakdown of polymer chains[34]. In landfill settings, biofilm formation is particularly important as it allows microorganisms to colonize otherwise inert plastic surfaces and initiate degradation.

2.4.3. Secretion of Extracellular Depolymerizing Enzymes

Microorganisms degrade plastics primarily through the production of extracellular depolymerizing enzymes. These enzymes, such as hydrolases, esterases, cutinases, and oxidoreductases, are secreted outside the cell and act directly on polymer surfaces[35]. Since most plastic polymers are too large to be taken up by microbial cells, they must first be broken down into smaller molecules. These enzymes cleave the chemical bonds within the polymer structure, converting them into oligomers and monomers that can be transported into the cell and further metabolized. The efficiency of this process depends on enzyme specificity, environmental conditions, and the physical properties of the plastic. In landfill environments, the continuous secretion of such enzymes plays a crucial role in initiating and sustaining the degradation of persistent plastic waste.

3. Metagenomic Approaches for Enzyme Discovery

Metagenomics is a powerful culture-independent approach that enables the direct study of microbial communities from environmental samples. Unlike traditional methods that rely on laboratory cultivation, it allows researchers to access the vast majority of microorganisms that are not easily culturable, particularly in complex environments like landfills. By analysing total microbial DNA, metagenomics provides valuable insights into both the diversity and functional potential of microbial communities[36].

One of the key advantages of metagenomics is its ability to uncover novel enzymes involved in the degradation of complex substrates such as plastics. By sequencing environmental DNA and analysing gene content, researchers can identify genes encoding enzymes like esterases, lipases, cutinases, and depolymerases that are potentially involved in polymer breakdown These genes can then be further studied through bioinformatics tools to predict their structure and function, even before laboratory validation. This significantly accelerates the discovery of new biocatalysts with industrial and environmental applications.

Metagenomic approaches are broadly classified into two main strategies: sequence-based and function-based screening. Sequence-based metagenomics involves high-throughput DNA sequencing followed by computational analysis to identify genes of interest based on known conserved regions or motifs. In contrast, function-based metagenomics focuses on cloning environmental DNA into suitable host organisms and screening for specific enzymatic activities, allowing the identification of completely novel enzymes that may not share similarity with known genes.

3.1. Shotgun Metagenomics

Shotgun metagenomics is a comprehensive approach that involves sequencing the total DNA extracted directly from environmental samples, without the need for prior cultivation. This method provides a detailed and unbiased view of the microbial community, capturing both abundant and rare organisms present in complex ecosystems such as landfills. By analysing the entire genetic content, researchers can identify a wide range of functional genes, including those involved in the degradation of complex polymers like plastics One of the key advantages of shotgun metagenomics is its ability to reconstruct metabolic pathways by linking genes to specific biochemical functions. This helps in understanding how different microorganisms contribute to interconnected degradation processes within microbial consortia. In addition, this approach has greatly facilitated the discovery of novel enzyme families, including hydrolases, esterases, and oxidoreductases, which play crucial roles in polymer breakdown

3.2 Functional Metagenomics

Functional metagenomics focuses on identifying microbial activities rather than relying solely on genetic sequences. In this approach, environmental DNA is extracted, fragmented, and cloned into suitable host organisms—commonly *Escherichia coli*. These recombinant hosts are then screened for specific traits, such as the ability to degrade polymers or produce particular enzymes. This activity-based screening allows researchers to directly observe functional properties, making it a highly practical method for enzyme discovery. One of the major strengths of functional metagenomics is its ability to uncover entirely new enzymes that may not share sequence similarity with previously known genes. Since it does not depend on existing database information, this method can reveal novel biocatalysts with unique structures and functions, including enzymes capable of breaking down complex and recalcitrant materials like plastics . Additionally, this method provides useful insights into enzyme expression, efficiency, and stability under near-real conditions, which is important for industrial and environmental applications. By linking genetic material with actual biochemical activity, functional metagenomics effectively complements sequence-based approaches and plays a crucial role in advancing plastic biodegradation research.

3.3 Amplicon Sequencing (16S rRNA)

Amplicon sequencing, particularly targeting the 16S rRNA gene, is widely used to explore microbial diversity in complex environments such as landfills. This method focuses on amplifying and sequencing conserved regions of the 16S rRNA gene, which is present in all bacteria and archaea but contains variable regions that allow differentiation between species. Because of this, it serves as a reliable and efficient tool for identifying a wide range of microorganisms without the need for culturing . Using this approach, researchers can **identify** microbial diversity by detecting both dominant and rare microbial taxa present in landfill ecosystems. It helps uncover the richness and evenness of microbial populations, including previously uncharacterized or uncultivable organisms that may play roles in plastic degradation .

16S rRNA sequencing is essential for understanding community structure. It provides insights into how microbial populations are organized, how they interact, and how their composition changes under different environmental conditions such as pH, temperature, and waste composition . This information is particularly useful in identifying key microbial groups that may contribute to biodegradation processes.

4. Plastic-Degrading Enzymes: Classification and Mechanisms

4.1 Polyester Hydrolases

Polyester hydrolases are a key group of enzymes involved in the biodegradation of synthetic plastics, particularly polymers such as polyethylene terephthalate (PET) and polylactic acid (PLA). These enzymes function by catalyzing the hydrolysis of ester bonds, which are the main chemical linkages holding these polymers together. By breaking these bonds, polyester hydrolases convert long polymer chains into smaller molecules such as oligomers, monomers, and eventually into metabolizable compounds like terephthalic acid and lactic acid (Wei and . The effectiveness of polyester hydrolases depends on several factors, including enzyme structure, substrate accessibility, crystallinity of the polymer, and environmental conditions such as temperature and ph. In landfill ecosystems, where plastics are exposed to microbial consortia and varying conditions, these enzymes often work synergistically to enhance degradation efficiency .

4.2. PETase and MHETase System

The discovery of PETase-producing bacteria represented a major milestone in the field of plastic biodegradation. In particular, the identification of *Ideonella sakaiensis* demonstrated, for the first time, that certain microorganisms can efficiently utilize polyethylene terephthalate (PET) as a carbon and energy source under natural conditions. This finding opened new possibilities for biologically driven plastic recycling and waste management. The degradation process involves a two-enzyme system. First, PETase initiates the breakdown of PET by hydrolyzing its ester bonds, converting the polymer into smaller intermediates, primarily mono-(2-hydroxyethyl) terephthalate (MHET). This step is crucial because it reduces the complex, high-molecular-weight polymer into a form that can be further processed. Subsequently, MHETase acts on MHET, hydrolyzing it into its basic monomers terephthalic acid (TPA) and ethylene glycol (EG) which can then be taken up and metabolized by microbial cells .

4.3. Cutinases, Lipases, and Esterases

Cutinases, along with lipases and esterases, play an important role in the biodegradation of synthetic plastics, particularly aliphatic and semi-aromatic polyesters. Cutinases are versatile enzymes known for their broad substrate specificity, allowing them to act on both natural polymers like cutin and synthetic materials such as PET and PLA. Their relatively stable structure and ability to function without the need for cofactors make them especially attractive for industrial applications, including enzymatic recycling and bioprocessing. Lipases and esterases also contribute significantly to plastic degradation by initiating the breakdown of polymer chains through the cleavage of ester bonds. While lipases typically act on long-chain substrates, esterases prefer shorter-chain compounds; together, they complement each other in degrading complex polymeric materials into smaller intermediates. These smaller products can then be further metabolized by microbial communities.

In landfill environments, these enzymes often work synergistically, where cutinases may first attack the polymer surface, increasing its accessibility, followed by lipases and esterases that continue the depolymerization process. Their combined action enhances the overall efficiency of plastic degradation, especially under variable environmental conditions.

5. Environmental and Physicochemical Factors Influencing Degradation

The efficiency of plastic biodegradation in landfill environments is strongly influenced by a combination of environmental and physicochemical factors. These factors determine not only microbial activity but also the accessibility of polymers to enzymatic attack. Temperature plays a critical role in regulating enzymatic reactions. Higher temperatures generally enhance enzyme activity and increase polymer chain mobility, making plastics more susceptible to degradation. However, extremely high temperatures may denature enzymes and inhibit microbial growth, indicating the need for an optimal range. pH is another important factor that affects enzyme stability and functionality. Most plastic-degrading enzymes operate efficiently within a specific pH range, and deviations can reduce catalytic efficiency or alter enzyme structure. In landfill systems, fluctuating pH conditions can therefore influence the overall degradation process.

Moisture content is essential for microbial survival and activity. Adequate moisture facilitates the diffusion of enzymes and nutrients, promotes microbial colonization, and supports biochemical reactions involved in polymer breakdown. Dry conditions, on the other hand, can significantly limit microbial growth and slow degradation rates. Polymer properties, such as crystallinity, molecular weight, and surface area, also play a major role in determining degradation susceptibility. Highly crystalline plastics are more resistant to enzymatic attack due to their tightly packed structure, whereas amorphous regions are more accessible and degrade more readily. Similarly, polymers with lower molecular weight are generally easier for microbes to break down.

In addition to these natural factors, pre-treatment methods such as UV irradiation, thermal treatment, and chemical oxidation can significantly enhance biodegradability. These treatments introduce functional groups, create surface cracks, and reduce polymer integrity, thereby increasing microbial attachment and enzymatic accessibility.

6. Microbial Consortia and Synergistic Interactions

In natural environments such as landfills, plastic degradation is rarely carried out by a single microorganism. Most individual strains lack the complete set of enzymes required to fully break down complex polymers. Instead, microbial consortia diverse communities of interacting microorganisms work together to achieve efficient degradation. These cooperative systems are more adaptable and effective, especially when dealing with recalcitrant materials like synthetic plastics .

One of the key mechanisms behind this efficiency is the division of metabolic labour. Different microorganisms specialize in specific steps of the degradation process. For instance, some microbes initiate polymer breakdown by secreting extracellular depolymerizing enzymes, while others metabolize intermediate products into simpler compounds. This division of roles reduces metabolic burden on individual species and enhances overall system performance. Another important aspect is the presence of sequential degradation pathways, where the breakdown of plastics occurs in stages. Complex polymers are first converted into oligomers and monomers, which are then further degraded and assimilated by different members of the consortium. This stepwise process ensures more complete and efficient degradation compared to isolated microbial activity.

Cross-feeding interactions also play a vital role in these communities. In this process, metabolic by-products produced by one organism serve as substrates for another, creating a tightly linked network of nutrient exchange. Such interactions not only improve resource utilization but also stabilize the microbial ecosystem, allowing sustained degradation over time

7. Applications in Waste Management and Industry

Advances in metagenomics and enzyme discovery have opened up several practical applications for managing plastic waste more sustainably. These approaches not only improve degradation efficiency but also create opportunities for recycling and industrial innovation.

7.1. Bioremediation

Bioremediation involves the use of microorganisms or their enzymes to break down pollutants directly in the environment. Metagenomics-derived enzymes, identified from landfill microbiota, can be applied for in situ degradation of plastic waste. These enzymes are often well-adapted to harsh environmental conditions, making them effective in real landfill settings. By enhancing microbial activity or introducing specific enzyme systems, it is possible to accelerate the natural breakdown of plastics, reducing their long-term environmental impact

7.2. Enzymatic Recycling

Enzymatic recycling represents a promising alternative to conventional mechanical and chemical recycling methods. In this approach, enzymes such as PETase and cutinases break down plastics into their original monomers, such as terephthalic acid and ethylene glycol. These monomers can then be purified and reused to synthesize new polymers, creating a closed-loop recycling system. Compared to traditional methods, enzymatic recycling is more environmentally friendly, as it requires lower energy input and produces fewer toxic by-products

7.3. Synthetic Biology

Synthetic biology further expands the potential of plastic biodegradation by enabling the genetic engineering of microbial strains with enhanced capabilities. Through techniques such as gene editing and pathway optimization, researchers can design microorganisms that express high levels of plastic-degrading enzymes or combine multiple degradation pathways within a single host. This not only improves degradation efficiency but also allows customization for specific types of plastics

8. Conclusion

Metagenomic exploration of landfill microbiota has emerged as a transformative and forward-looking approach in the discovery of novel plastic-degrading enzymes. As major accumulation sites for plastic waste, landfills act as dynamic and complex ecosystems where diverse microbial communities continuously adapt to harsh and fluctuating environmental conditions. This unique ecological pressure drives the evolution of specialized metabolic pathways and enzymatic systems capable of breaking down otherwise persistent synthetic polymers. Through the application of metagenomic techniques, researchers are now able to access the vast, previously hidden genetic and functional diversity of uncultivable microorganisms. This has led to the identification of key enzyme systems such as polyester hydrolases, PETase–MHETase complexes, cutinases, lipases, and esterases, all of which play critical roles in the stepwise degradation of plastics. In addition, the study of microbial consortia has highlighted the importance of synergistic interactions, where different organisms work together through division of labour, sequential pathways, and cross-feeding mechanisms to achieve more efficient degradation.

Environmental factors such as temperature, pH, moisture, and polymer characteristics further influence the efficiency of these biological processes, while pre-treatment methods can enhance polymer susceptibility to microbial attack. Importantly, the integration of metagenomics with bioinformatics, machine learning, and synthetic biology is accelerating the discovery, optimization, and application of these enzymes for real-world use. Applications in bioremediation and enzymatic recycling demonstrate the practical potential of these discoveries, offering environmentally friendly alternatives to conventional plastic waste management methods. Engineered microbial systems and enzyme-based recycling strategies, in particular, provide promising pathways toward a circular plastic economy. Overall, continued interdisciplinary research combining microbiology, molecular biology, environmental science, and engineering will be essential to fully harness the potential of landfill microbiota. Such efforts will play a crucial role in developing sustainable, efficient, and scalable solutions to mitigate the growing global challenge of plastic pollution.

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