



Research Article

Insect Gut *Microbiome* as a Frontier in Plastic Biodegradation: An In-Depth Review of Enzymatic Mechanisms and Approaches for Polymer Degradation Analysis

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Abstract | The process of breaking down synthetic polymer chains into smaller molecules or fully mineralized end products like CO₂ and H₂O through physical, chemical, or biological mechanisms is known as plastic degradation. Most commercial plastics are extremely resistant to degradation in natural environments because they have a high molecular weight, are not susceptible to enzymatic degradation and lack enzymatic recognition sites. Mechanical recycling, incineration, and landfilling represent the conventional approaches to dispose plastic waste. Given the extent of present plastic pollution, these approaches have shown to be insufficient as they produce secondary pollutants and do not tackle the worldwide buildup of synthetic polymers in ecosystems. This has led to the increasing potential of biological approaches based on biodegradation by insects. *Zophobas atratus*, *Galleria mellonella*, and *Tenebrio molitor* larvae have specialized gut microbes that use intricate enzymatic cascades to start the depolymerization of synthetic polymers that are chemically inert, such as polyethylene (PE) and polystyrene (PS). *Enterobacter*, *Pseudomonas*, *Citrobacter*, and *Serratia* are important microbial genera that target resistant polymer backbones by producing oxidases, monooxygenases, and hydrolases. In addition to discussing biotechnological applications for sustainable plastic waste management, this review summarizes the current understanding of how insect gut microbiomes break down plastics, including the enzymatic mechanisms, metabolic pathways, and analytical evidence of degradation.

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Introduction

Synthetic plastics are produced using polymerization reactions, which link together short units called monomers in order to build up long

chains of polymers from a range of feedstocks, the primary ones being petroleum chemicals. The most widely manufactured plastics are polyethylene (PE), polypropylene (PP), polystyrene (PS), polyethylene terephthalate (PET) and polyvinyl chloride (PVC).

These materials have many commercial applications due to their high molecular weight, hydrophobicity, mechanical strength, and resistance to chemical and enzymatic attack. The global production of plastics has also increased significantly over the last few years and is expected to continue to rise over time (Yang *et al.*, 2024a). The attributes that make plastics useful to commerce also make them very persistent in natural environments. Physical, chemical, or biological processes that tend to reduce the polymers to shorter chains are called plastic degradation. For instance, polyethylene and polystyrene have a lifespan of hundreds to thousands of years (Pivato *et al.*, 2022), and there is still significant underperformance in recycling rates worldwide (PlasticsEurope, 2023). As a sustainable biological alternative, biodegradation which is defined as the enzymatic breakdown of polymers by living organisms (Zhang *et al.*, 2022) has drawn Plastics such as polyethylene and polystyrene remain in the environment for hundreds of years before gradually breaking down into micro- and nanoplastics, which are now found in all ecosystems, including the human body, and are receiving significant scientific attention as potential solutions.(Peng *et al.*, 2024).

The first major study into insect-mediated plastic biodegradation came in 2015 when researchers discovered that bacteria from the guts of the plastic-eating waxworms could biodegrade polyethylene (Yang *et al.*, 2015). Over the years three insect species have become important model organisms: *Zophobas atratus*, *Galleria mellonella* (greater wax moth larva) and *Tenebrio molitor* (yellow mealworm). These insects have gut microbial consortiums that carry out enzymatic depolymerization and physically break up plastics by mastication. *Enterobacter*, *Pseudomonas*, *Citrobacter*, *Serratia*, and *Dysgonomonas* are important gut microbial genera that have been shown to degrade plastic. These microbes attack chemically inert polymer backbones by using cascades of hydrolytic and oxidative enzymes. Understanding of these processes has been significantly increased by developments in metagenomics, enzyme biochemistry, and analytical chemistry (Yang *et al.*, 2024a; Ding *et al.*, 2023).

Key insect species as plastic-degrading systems

The main biological model systems for researching plastic biodegradation are three insect larval species. Each has been shown to physically fragment and biochemically alter synthetic polymer substrates, and each has a unique gut microbiome community

influenced by diet and type of plastic.

Tenebrio molitor, Yellow mealworm

The most researched insect for plastic biodegradation is *Tenebrio molitor*, also known as the yellow mealworm (Yang *et al.*, 2024a; Brandon *et al.*, 2021). *Enterobacter* and *Citrobacter* species, which are enriched during plastic feeding and directly linked to PS and PE depolymerization, predominate in its gut microbiome. It has been demonstrated that bran-to-plastic co-diets significantly increase the rates of PS and LDPE degradation and change the composition of the core gut microbiome (Lou *et al.*, 2021; Peng *et al.*, 2022b). Specifically in *T. molitor* larvae fed plastic, functional metatranscriptomics has revealed upregulation of the oxidoreductase and serine-hydrolase gene families (Lou *et al.*, 2021).

Galleria mellonella, Greater wax moth larva

In *Galleria mellonella*, greater wax moth larva, PE-fed larvae exhibited the same lipid content as those fed normally, indicating that PE was metabolically assimilated not merely passed through (LeMoine *et al.*, 2020; Cassone *et al.*, 2020). *Enterobacter* and *Pseudomonas* are dominant plastic associated genera in the gut microbiome of *G. mellonella*. Importantly, the larvae of this species have been demonstrated to be able to digest PS microplastics completely in vivo, and both microbiota-dependent and microbiota-independent pathways of degradation have been identified, indicating the insect host is providing some enzymatic capacity to the degradation process (Wang *et al.*, 2022).

Zophobas atratus, Superworm

Zophobas atratus, the superworm, is capable of degrading PS, PE, and polyurethane foam (PU) and has a wide substrate preference for plastics. It has an enriched gut microbiome for *Enterococcus* and *Citrobacter* species when fed plastic; and the composition changes depending on the type of plastic fed (Luo *et al.*, 2021; Wang *et al.*, 2022a). Researching on *Z. atratus* has yielded particularly important enzyme discoveries: cytochrome P450 monooxygenases (CYP) and alkane hydroxylases (AlkB) have been identified in gut metagenomes and confirmed in isolated *Pseudomonas aeruginosa* strains (PDB-1 and PDB-2) that can degrade LDPE, LLDPE, and EPS in pure culture (Zaman *et al.*, 2024).

Comparing the three model systems, *Zophobas atratus* presents the widest range of PS, PE, and PU degradation substrates, provides the most convincing mechanistic evidence through the isolation and culture of *P. aeruginosa*, and the results are the most experimentally robust. Although *Galleria mellonella* provides the clearest evidence for host-level metabolic assimilation and microbiota-independent degradation pathways, this reduces its usefulness as a model for microbiome-mediated biocatalyst discovery. *Tenebrio molitor* remains the most widely studied system at the gene expression level, but its degradation is almost entirely microbiome dependent and slow. However, for all three species, degradation is confirmed primarily by surface-level spectroscopic changes and changes in molecular weight rather than by complete mineralization, so the strength of the evidence for genuine, industrially significant depolymerization is still limited.

Table 1: Key insect species involved in plastic biodegradation, associated gut microbiome genera, and main findings.

Insect species	Common name	Plastics degraded	Key gut microbiome genera	Reference
Tenebrio molitor	Yellow Mealworm	PS, PE, PP, PVC, PU	<i>Enterobacter</i> , <i>Citrobacter</i> , <i>Serratia</i> , <i>dysgonomonas</i>	Yang <i>et al.</i> , 2024; Lou <i>et al.</i> , 2021; He <i>et al.</i> , 2023
Galleria mellonella	Greater wax moth	PE, PS	<i>Enterobacter</i> , <i>Pseudomonas</i>	LeMoine <i>et al.</i> , 2020; Wang <i>et al.</i> , 2022;
Zo-phobas atratus	Superworm	PS, PE, PU	<i>Enterococcus</i> , <i>Citrobacter</i> , <i>Pseudomonas aeruginosa</i>	Luo <i>et al.</i> , 2021; Zaman <i>et al.</i> , 2024

Plastic substrates and chemical recalcitrance

Polyolefins (PE, PP) and vinyl polymers (PS) are the most studied plastics in terms of biodegradation mediated by insect gut microbiota. Polyolefins (PE, PP) and vinyl polymers (PS) are the most studied plastics with respect to biodegradation mediated by the insect gut microbiota, as they share structural features that confer extreme chemical inertness (Yang *et al.*, 2024a; Yang *et al.*, 2021; Jiang *et al.*, 2021; Zhang *et al.*, 2022). The ester, amide, or ether linkages that the majority of known hydrolytic enzymes need as recognition sites are absent from their non-polar polymer backbones (An *et al.*, 2023). These materials' extremely hydrophobic surfaces also keep water out

and hinder the access of aqueous enzymes (Zhang *et al.*, 2022). Because of its aromatic pendant rings, which require oxidative attack for ring cleavage before backbone fragmentation can proceed, PS poses an additional challenge (Przemieniecki *et al.*, 2020). Since PE and PP are purely aliphatic polymers, their degradation depends instead on monooxygenase-mediated hydroxylation of the carbon skeleton. These plastics can persist in the environment for decades to thousands of years, during which time they gradually disperse polymer-derived material throughout all environmental compartments through fragmentation into microplastics and nanoplastics.

Gut microbiome composition

The gut *microbiomes* of plastic-degrading insects are taxonomically diverse communities shaped by diet, insect species, and plastic substrate. 16S rRNA amplicon sequencing and shotgun metagenomics have consistently shown that plastic feeding enriches specific microbial lineages with catabolic potential (Yang *et al.*, 2024a; Ding *et al.*, 2023; Mamtimin *et al.*, 2023). Core plastic-associated bacterial genera identified across multiple insect hosts include *Enterobacter*, *Pseudomonas*, *Citrobacter*, *Serratia*, *Dysgonomonas*, and *Enterococcus*. Their relative abundances increase significantly during plastic feeding, suggesting a direct functional relationship between microbial enrichment and degradation activity (Lou *et al.*, 2021; Mamtimin *et al.*, 2023; Goveas *et al.*, 2023).

Degradation efficiency is largely dependent on symbiotic relationships between the insect host and its *microbiome*. A physicochemical niche that encourages microbial plastic oxidation is created by the alkaline gut environment, different pH gradients from anterior to posterior gut regions, and fluctuating redox conditions (Brandon *et al.*, 2021). Microbial diversity is greatly increased when wheat bran or other co-substrates are added to the diet.

Enzymatic mechanisms of plastic depolymerization

The physical and biochemical stages of insect-mediated plastic degradation are coordinated. Mechanical mastication is the first step in the process. Larval mandibles physically break plastic into micro- and nanoparticles, most of which are small in size (Peng *et al.*, 2023). This physical fragmentation is an essential first step that cannot be effectively replicated by a purely environmental microbial system without

the insect, and greatly increases the surface area that can be colonized by microbes and enzymes for attack.

Table 2: Gut microbiome composition in plastic-degrading insects.

Insect	Identified microbes	Method used	Function
Ten-ebrio molitor	<i>Enterobacter</i> , <i>Citrobacter</i> , <i>Serratia</i> , <i>dysgonomonas</i>	16S rRNA, metatranscriptomics	PS/PE/PP oxidation; hydrolase and oxidoreductase gene expression
Galleria mellonella	<i>Enterobacter</i> , <i>Pseudomonas</i>	16S rRNA, culture isolation	PE oxidation; active PS/PE/PU degradation via both host and microbial pathways
Zo-phobas atratus	<i>Enterococcus</i> , <i>Citrobacter</i> , <i>Pseudomonas aeruginosa</i>	16S rRNA, shotgun metagenomics	AlkB and CYP monooxygenase genes expression

Plastic particles pass through various sections of the gut where the oxygen saturation is different, the pH changes from anterior (alkaline) to posterior (acidic), and the gut contains a special redox milieu (Brandon *et al.*, 2021) that facilitates enzymatic depolymerization. Gut bacteria form biofilms on plastic surfaces, and secrete extracellular enzymes that initiate oxidative modification. Polyethylene requires oxygen functionality for it to be subjected to further enzymatic processing and the hydroxylation of aliphatic C–H bonds is a necessary first step in this procedure. Before backbone fragmentation can occur in polystyrene P450 systems oxidatively ring-open the aromatic pendant groups. According to FTIR and GPC analysis, these enzymatic processes result in detectable carbonyl groups, hydroxyl groups, and shorter oligomeric chains (Chen *et al.*, 2022a;

Brandon *et al.*, 2021). Gut microbial communities change in favor of absorbing the released carbon fragments as oxidative modification progresses.

Oxidative enzyme systems implicated in plastic depolymerization

Analytical methods for verifying polymer modification

A variety of complementary analytical techniques that differentiate true chemical modification from surface contamination or physical ingestion are necessary for rigorous verification of plastic biodegradation in insect gut systems. Fourier Transform Infrared Spectroscopy (FTIR, ATR-FTIR) is the major and most in-use verification technique. By tracking the emergence of new carbonyl (C=O) and hydroxyl (O–H) absorption peaks that are lacking in virgin plastic samples, it can identify functional group changes in plastic samples and frass residues. These new peaks are indicative of the oxidative surface modification of the polymer. For characterizing the insect biodegradation of plastic samples Wang *et al.* (2022b) showed the usefulness of ATR-FTIR, which is now the reference technique for such studies. Gel permeation chromatography (GPC) provides a quantitative measure of changes in polymer molecular weight, in which the number-average molecular weight (Mn) and the weight-average molecular weight (Mw) are calculated. A decrease of these values after gut transit will indicate depolymerization. Feed and gut passage experiments performed in the larval gut of mealworms confirmed the depolymerization of the materials via chain scission and differentiated the true depolymerization from surface erosion only, as observed by substantial loss in weight-average and number-average molecular weight (Peng *et al.*, 2023). Changes in the crystallinity, melting point and

Table 3: Key oxidative enzymes implicated in insect gut microbiome-mediated plastic degradation.

Enzyme	Class	Target Plastic	Mechanism	References
Laccases	(Multicopper oxidase)	Polystyrene	Single-electron oxidation of aromatic styrene pendant groups; generates radical intermediates that destabilize the polymer backbone	An <i>et al.</i> , 2023; Yang <i>et al.</i> , 2023
Alkane Hydroxylases (AlkB)	Non-haem iron monooxygenase	Polyethylene	Aliphatic polyethylene chains undergo hydroxylation, which introduces C–OH groups as a necessary initial activation step.	Zaman <i>et al.</i> , 2024
Cytochrome P450 (CYP)	Heme-containing monooxygenase	Polystyrene, Polyethylene	produces reactive oxygen species (ROS), which start the oxidative breakdown of polymer chains caused by radicals.	Sun <i>et al.</i> , 2022; Zaman <i>et al.</i> , 2024; Chen <i>et al.</i> , 2023
Serine Hydro-lases / Ary-lesterases	Hydrolase	Polystyrene, Polyethylene (oxidized intermediates)	Break down aryl and ester bonds in oxidized oligomers to finish	Yang <i>et al.</i> , 2024a; Lou <i>et al.</i> , 2021

thermal stability of polymers are measured by thermal analysis techniques such as Differential Scanning Calorimetry (DSC) and Thermogravimetric Analysis (TGA) and are correlated to structural degradation. Gas chromatography-mass spectrometry (GC-MS) is additionally used to identify and quantify the low-molecular-weight breakdown products and volatile metabolites released during biodegradation.

Factors affecting degradation efficiency

Advantages and limitations

This section provides a critical evaluation of the insect gut microbiome approach in comparison to standard criteria for assessing a bioremediation technology, based on [Yang et al. \(2024a\)](#), [An et al. \(2023\)](#), and [Vital-Vilchis and Karunakaran \(2025\)](#). The ability of insect gut *microbiome* systems to store new biocatalysts is one of their greatest benefits. Plastic-active enzymes that are not available from traditional environmental sources such as soil or water microbial communities are encoded by gut metagenomes ([Sun et al., 2022](#); [Liu et al., 2024](#)). In order to create industrial-grade plastic-degrading biocatalysts, these sequences serve as starting points for directed evolution and enzyme engineering initiatives. The biological value of this resource has been demonstrated by numerous metagenomic studies of the superworm gut, which identified entire functional gene families with the ability to break down plastic. The production of mealworms, superworms, and wax moth larvae is cost-effective and can be done with organic waste streams such as food industry byproducts and agricultural residues, potentially integrating with

existing waste management practices ([Vital-Vilchis and Karunakaran, 2025](#)). Degradation is a natural, spontaneous biological process which is driven by a renewable biological system. The enzymatic reactions themselves do not need any external energy input.

Environmental impact

Unlike the persistent organic pollutants produced by incineration, the insect gut microbiome approach avoids the hazardous chemical inputs associated with chemical recycling and produces mostly benign byproducts such as CO₂, H₂O, and microbial biomass. Insect frass that is left over after using plastic has the potential to be used as a soil amendment and retains its organic matter value, indicating co-benefits for the circular economy. Nevertheless, little research has been done on how plastic additives, especially flame retardants and UV stabilizers, affect the composition of the gut microbiome and its ability to degrade. Before large-scale deployment can be responsibly pursued, systematic research is also needed to determine the ecological fate of any toxic intermediate metabolites and the long-term stability of gut microbiome function under variable industrial conditions.

Several additional limitations limit short-term industrial use. Scalability remains a major challenge. Insect breeding and processing of gut extracts have not demonstrated the throughput needed to treat plastic waste streams at urban scale. The degradation observed so far is also often incomplete, producing microplastic and nano-plastic debris rather than

Table 4: Factors affecting insect gut microbiome-mediated plastic degradation efficiency.

Factor	Effect on Degradation	Reference
Plastic surface area and particle size	Mandibular fragmentation increases surface area; because smaller particles are more accessible to enzymes, they decompose more quickly.	Yang et al., 2024 ; Pivato et al., 2022 Peng et al., 2023
Gut pH and redox environment	pH and redox environment of the gut Different pH gradients and redox conditions are produced by the acidic posterior gut and alkaline anterior gut, which encourage the activity of oxidative enzymes.	Brandon et al., 2021 ; Lou et al., 2021
Co-diet and nutrient supplementation	When wheat bran or other organic co-substrates are added to plastic diets, microbial diversity is greatly increased and oxidoreductase gene expression is upregulated.	Lou et al., 2021 ; Ding et al., 2023
Plastic type and polymer structure	Degradation rates are significantly influenced by the molecular weight, crystallinity, and chemical structure of polymers.	Yang et al., 2021 ; Przemieniecki et al., 2020 ; Zhang et al., 2022
Gut microbial community composition	The abundance and diversity of plastic-associated genera (<i>Enterobacter</i> , <i>Pseudomonas</i> , <i>Citrobacter</i> , <i>Serratia</i> , <i>Dysgonomonas</i>) directly determine degradation capacity	Mamtimin et al., 2023 ; Goveas et al., 2023 ; Lou et al., 2021
Insect species and host physiology	Due to variations in mandibular strength, gut anatomy, and host-derived enzymatic contributions, different insect species have different degradation efficiencies.	Wang et al., 2022a ; Jiang et al., 2021 ; LeMoine et al., 2020

complete petrification to CO₂ and H₂O, with the risk of redistribution of smaller plastic particles into the environment. Actual plastic waste also contains additives such as flame retardants, plasticizers, and UV stabilizers, which influence the composition and decomposition of the gut microbiota effectiveness is poorly characterized. Biosecurity is another concern, as the expansion of insect farming and the release of consortia of modified or enriched gut microbes raise questions about containment and unintended environmental consequences.

Future perspectives

A feasible route toward the industrial-scale use of insect gut microbiome-derived plastic degradation systems is provided by the convergence of metagenomics, synthetic biology, directed enzyme evolution, and bioprocess engineering. Novel plastic-active biocatalysts from insect gut communities are being found more quickly thanks to high-yield enzyme discovery pipelines that combine shotgun metagenomics, machine learning-based protein function prediction, and functional heterologous expression screening (Sun *et al.*, 2022). Degradation rates that are compatible with industrial waste treatment targets may be made possible by directed evolution of key oxidases, which can enhance catalytic efficiency, thermostability, and substrate range beyond natural limits.

Conclusions and Recommendations

Tenebrio molitor, *Galleria mellonella*, and *Zophobas atratus* gut microbiomes are promising, biologically active systems for depolymerizing chemically resistant plastics, such as PS, PE, PP, PVC, and PU, though current degradation rates remain well below what industrial-scale waste treatment requires. Through coordinated cascades of laccases, alkane hydroxylases, cytochrome P450 monooxygenases, and serine hydrolases, core gut bacterial genera such as *Citrobacter*, *Serratia*, *Pseudomonas*, *Enterococcus*, and *Dysgonomonas* perform enzymatic degradation. Although the degradation rates of these insects are still much lower than the industrial requirements, novel biocatalysts can be unearthed from their gut metagenomes, which remains an unmatched source of new biocatalysts, and there are still large gaps in knowledge to be filled in terms of characterization of enzymes and large-scale feasibility. These biological solutions offer a scientifically sound path

to a microbiome-based approach to plastic waste management via enzyme engineering, synthetic microbial consortia, and bioreactor integration.

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Novelty Statement

While conventional disposal fails against persistent synthetic polymers, this review highlights the gut microbiomes and enzymatic cascades of plastic-degrading insect larvae. By linking metabolic pathways to biotechnological applications, it provides a focused framework for sustainable waste management.

Author's Contribution

Zahid Ali: Data Curation and Visualization.

Umm E Habiba Saeed: Data Curation, Formal Analysis.

Ahsan Munir: Literature Search, Writing Original Draft.

Mariyam Khan: Conceptualization, Supervision, Writing.

Naira Yaseen: Data Curation, Writing Review & Editing.

Rukhma Waris: Data Curation, Writing Review & Editing.

Syeda Quratulain Gillani: Conceptualization, Methodology, Writing Original Draft, Administration, and Supervision.

Generative AI and AI-assisted technology statement

The authors declare that no generative AI and AI assisted technology was used in the creation of this manuscript.

Conflict of interest

The authors have declared no conflict of interest.

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