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ISOLATION AND CHARACTERIZATION OF A PLASTIC DEGRADING MICROBE FROM INSECT GUT

Swathi Lakshmi, Vinita Balasubramanya*
Department of PG Biotechnology, NMKRV College, Bengaluru – 560011
***Corresponding author email address**: vinita.balasubramanya@gmail.com

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Abstract
Microbial degradation of plastics has been traditionally studied in soil microbes. In this study, plastic-degrading microbes were isolated from the midgut and hindgut of cockroach (Periplaneta americana) using minimal media containing polyethylene glycol (PEG) and polyvinyl pyrrolidone (PVP). These microbes could also survive in polyethylene and polyvinyl chloride (PVC) containing media, as confirmed by decrease in weight, thin layer chromatography and FTIR analysis. Identified as strains of Enterobacter cloacae and Klebsiella pneumoniae, these microbes show promising potential for sustainable plastic biodegradation and mitigation of plastic pollution.

Keywords: Plastic degradation, insect gut microbes, Enterobacter cloacae, Klebsiella pneumoniae

1. INTRODUCTION

Global plastic production has exceeded 413 million tons, 40% of which was single-use packaging (Plastics Europe, 2020). Plastics now pollute oceans, soils, and drains, while microplastics threaten health. Only 9-14% of plastic waste is recycled; most ends up in landfills, causing pollution and hazardous emissions (Sumathi *et al*., 2016).

A safer alternative is the biodegradation of plastic which involves the adhering of microbes to the surface and formation of biofilms that enable enzymatic cleavage of polymers into smaller molecules. These fragments are then metabolized into water, carbon dioxide, and biomass. Pretreatments like photo-oxidation enhance degradation for microbial consortia and enzymes such as hydrolases and laccases hasten the breakdown of plastics (Tokiwa *et al*., 2009).

In this study, fluid from cockroach (*Periplaneta americana*) midgut and hindgut was enriched for plastic-degrading microbes using minimal media with PEG or PVP as the sole carbon source. These bacterial cultures were then tested for growth in pretreated polyethylene and PVC. Microbes were characterized, identified by 16S rDNA sequencing and tested for their ability to degrade common plastics.

2. MATERIALS AND METHODS

2.1 Insect selection and dissection

Adult specimens of the common cockroach (*Periplaneta americana*) were collected from local habitats. The cockroach was anesthetised with chloroform, and dissected to expose the digestive system. Fluids from the midgut and hindgut (Fig 1) were withdrawn using a sterile hypodermic needle and transferred into sterile 1.5 ml Eppendorf tubes containing 100µL of sterile saline.

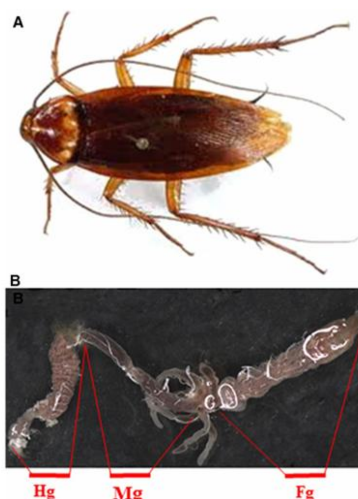


Fig 1. Adult cockroach (*Periplaneta americana*) (A) and the digestive system (B) showing the Foregut (Fg), Midgut (Mg) and Hindgut (Hg) (Adapted from Bertino-Grimaldi *et al*., 2013).

2.2 Gut microbiome isolation

50µL of the saline suspensions of midgut and hindgut fluid were inoculated into 25 mL nutrient broth and cultured overnight at 37ºC. 100 µL of this culture was then spread on nutrient agar plates and further incubated at 37ºC overnight. Colonies were counted and characterised based on size, shape, colour, texture, margin regularity, and elevation. Bacteria were characterised by Gram staining.

2.3 Isolation of potential plastic degrading insect gut microbes

Potential plastic degrading microbes were enriched in a minimal salts medium which contained 1% polyethylene glycol (PEG) or 1% polyvinylpyrrolidone (PVP) as the sole carbon source. The composition of the minimal salt medium is given in Table 1.

Table 1. Composition of minimal salts medium.

MINIMAL SALT	WEIGHT (in grams)
KH_2PO_4	0.454 g
Na_2HPO_4	1.194 g
NH_4Cl	0.1 g
$MgSO_4$	0.05 g
$CaCl_2$	0.0005 g
$FeSO_4$	0.002 g
$MnSO_4$	0.0005 g
$ZnSO_4$	0.0002 g

50µL of the saline suspension of midgut and hindgut microbes was spread on minimal salts medium agar plates which contained 1% PEG or 1% PVP. The plates were incubated at 37ºC till colonies were observed. These colonies were

subsequently transferred into liquid minimal salts media enriched with 1% PEG or 1% PVP to promote the growth of plastic-degrading microorganisms.

2.4 Time course of PEG and PVP degradation

The degradation of PEG and PVP was analysed by thin layer chromatography (TLC) on Silica gel 60F254 sheets (Merck) using the solvent systems given in Table 2.

Table 2. Solvent systems used for the TLC analysis of degradation products of PEG and PVP

Solvent system	Ratio
Ethyl acetate: Methanol: Water	1:1:1
Chloroform: Methanol: Water	1:1:1
Dichloromethane: Methanol: Water	1:1:1
Isopropanol: Methanol: Water	1:1:1
Isopropanol: Liquor ammonia	3:2

Spent medium from the midgut and hindgut cultures grown in minimal salts medium with PEG and PVP was spotted on the TLC sheet and introduced into the solvent systems given in Table 2. After the run, the sheet was dried and stained with iodine vapours. PEG, PVP and their degradation products were identified as dark brown spots.
A time course of PEG and PVP degradation was carried out using the optimum solvent system. Four liquid cultures viz. Hindgut (HG) + 1% PEG, Midgut (MG) + 1% PEG, Hindgut (HG) + 1% PVP and Midgut (MG) + 1% PVP were used for the time course. 1 mL aliquots of culture were aseptically withdrawn from each sample into Eppendorf tubes and frozen at -20ºC, every day for a period of 6 days. On the 7th day, the aliquots were thawed and analysed by TLC.

2.5 Fourier transform infrared spectroscopy (FTIR) analysis of degradation products

Samples were submitted to the Department of Chemistry at NMKRV College for Fourier Transform Infrared Spectroscopy (FTIR) analysis, on a BRUKER 100 62427 FTIR analyzer. Interpretation of the FTIR spectra was done by assigning the correct functional group to the peaks corresponding to the wave numbers.

2.6 Analysis of plastic degradation of plastics from MG and HG isolates

Single use polyethylene (PE) bags were cut into small pieces, weighed and pretreated by exposure to direct sunlight for 14 days, after which they were thoroughly washed, dried, and weighed again. The pretreated PE pieces were transferred into liquid minimal salts media inoculated with both midgut (MG) and hindgut (HG) microbial isolates. The cultures were grown for 25 days.
Polyvinyl chloride (PVC) pieces were cut into small fragments, pre-weighed, and pretreated by 7 days of exposure to direct sunlight. The fragments were then washed, dried, and weighed and inoculated into liquid minimal salts media containing hindgut isolates and incubated for 30 days.
Post incubation, 1 mL of culture media was transferred into an Eppendorf tube for FTIR analysis.
For both PE and PVC, the medium was analysed by FTIR and the plastic fragments recovered, washed, dried, and weighed again to assess any further reduction in weight.

2.7 Identification of bacterial isolate(s)

Selected isolates were identified by 16S rDNA sequencing, outsourced to Sakhala Enterprises, Bengaluru. The bacteria were identified using a BLAST analysis against the available sequences in the NCBI database.

3. RESULTS AND DISCUSSION

The common cockroach (*Periplaneta americana*) was selected for the current study because of its well-established

ability to harbour diverse, rich and synergistic microbial communities in the gut, known to degrade complex organic compounds, including plastics (Bertino-Grimaldi *et al*., 2013).

3.1 Gut microbiome of *Periplaneta americana*

Bacterial colonies isolated from the hindgut and midgut fluid were characterised by their size, shape, margin, elevation, opacity, and pigmentation. About 20-25 colonies of the midgut included mucoid, orange pigmented colonies. The colony characteristics of microflora found in the midgut fluid are given in Table 3.

Table 3. Colony characters of *P. americana* midgut microflora.

Colonies	Size	Edge/ Shape	Elevation	Colour	Mucoid/ Non Mucoid	Texture	Submerged / Surface
1.	Pinpoint (In the form of a group)	Round & smooth	Raised	White	Non Mucoid	Powdery	Surface
2.	Same as the first colony	Round & smooth	Raised	White	Non Mucoid	Powdery	Surface
3.	Moderate	Irregular & spreading	Flat	Orange	Mucoid	Smooth but slightly wrinkled	Surface
4.	Small	Wrinkled & Lobate	Umbonate	Translu cent	Mucoid	Wrinkled	Surface
5.	Small	Round with scalloped margin	Hilly	White	Mucoid	Wavy, Wrinkled	Surface
6.	Small	Round	Flat	Translu cent	Non Mucoid	Smooth	Submerged
7A.	Small	Round & wrinkled	Craterifor m	White	Non Mucoid	Wrinkled	Surface
7B.	Pinpoint	Round	Convex	White	Mucoid	Smooth	Surface
9.	Same Characteristics as seen in colony 3						
10.	Same Characteristics as seen in colony 1						
11.	Same Characteristics as seen in colony 7B						
12.	Same Characteristics as seen in colony 3						
13.	Moderate in size	Irregular, Wavy	Flat	Yellow	Mucoid	Smooth	Surface
14.	Moderate	Irregular, Wavy	Flat	Yellow	Mucoid	Smooth	Surface
15.	Same as 13 However multiple colonies are seen						

The 25-30 colonies of the hindgut included large orange-pigmented colonies and some minute pigmented colonies. The colony characters of hindgut microflora are listed in Table 4.

Table 4. Colony characters of *P. americana* hindgut microflora.

Colonies	Size	Edge/ Shape	Elevation	Colour	Mucoid /Non Mucoid	Texture	Submerged / Surface
1.	Big, Large	Rhizoid	Flat	Brown	Non Mucoid	Wooly	Surface
2.	Moderate	Irregular & spreading	Flat	Orange	Mucoid	Smooth but slightly wrinkled	Surface
3, 4, 5, 6	are same as colonies seen in1						
8.	Moderate	Wavy and irregular	Raised	White	Non Mucoid	Wrinkled	Surface
9.	Moderate	Irregular & spreading	Flat	Orange	Mucoid	Smooth but slightly wrinkled	Surface
10.	String length	Long, elongated and irregular	Raised	White	Non Mucoid	Wrinkled	Surface
11.	Same as seen in 9 colonies						
12.	Moderate	Irregular and spreading	Flat	White	Mucoid	Smooth	Surface
13.	Pinpoint	Regular	flat	Translu	Non	Smooth	Submerged
				cent	mucoid		
14.	Same as seen in 9 & 12th colonies						
15.	Small	Round	Convex	White	Mucoid	Smooth	Surface

The midgut appears to have a more diverse population than the hindgut (Fig 2). One large woolly fungal colony was observed in the hindgut fluid (Fig 2, right). Upon staining, it was identified to be a *Penicillium* spp.

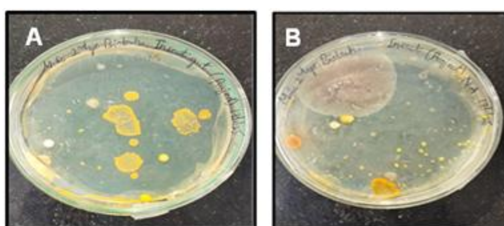


Fig 2. Microflora of *P. americana* midgut (A) and hindgut (B) fluid.

3.2 Isolation of potential plastic degrading microbes

PEG and PVP are water soluble long chain polymers that resemble plastics like polyethylene (PE) and polyvinyl chloride (PVC) (Ahmed *et al*., 2018). Their structures are given in Fig 2.

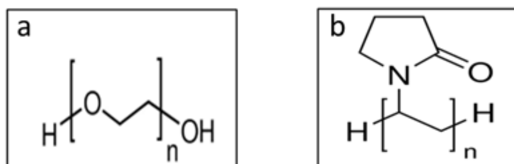


Fig 2. Structures of polyethylene glycol (PEG) (a) and polyvinylpyrrolidone (PVP) (b).
(Source: www.sigmaaldrich.com)

Potential plastic degrading microbes were enriched from the midgut and hindgut fluids, by introducing an aliquot into minimal salt medium with 1% polyethylene glycol (PEG) or 1% polyvinylpyrrolidone (PVP) as the exclusive carbon source. Both midgut and hindgut contained microbes that survived and grew in the minimal salts medium with PEG or PVP (Fig 3).

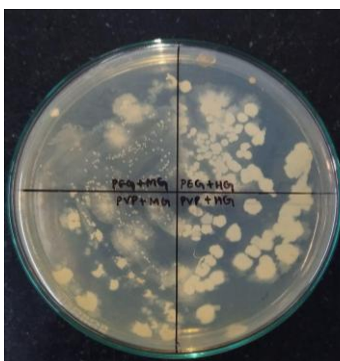


Fig 3. Quadrant streak of midgut and hindgut fluid grown on 1% PEG and 1% PVP containing minimal salts media.

Cultures developed in the minimal salts liquid media with 1% PEG or 1% PVP showed clustering or aggregation of bacterial cells (Fig 4).

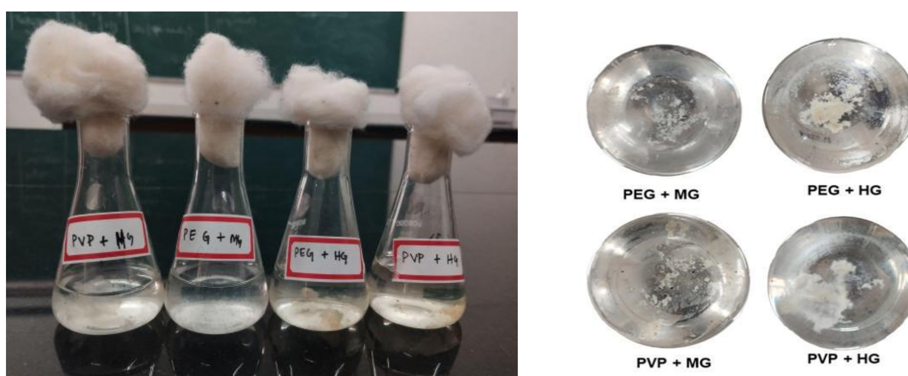


Fig 4. Formation of aggregates by midgut and hindgut microbes in liquid culture with 1% PEG or PVP. Left: Front view of flasks, Right: View from below.

This emergence of microbial consortium indicates a synergistic relationship among several bacterial species, suggesting that plastic degradation might be a collaborative effort involving a community of microorganisms rather than relying on a single bacterial strain. Such consortia are recognized for improving biodegradation efficiency due to their complementary metabolic pathways, cross-feeding interactions, and shared enzyme production.

All isolates from the hindgut and midgut, grown in media containing 1% PEG or 1% PVP were Gram-negative coccobacilli (Fig 5).

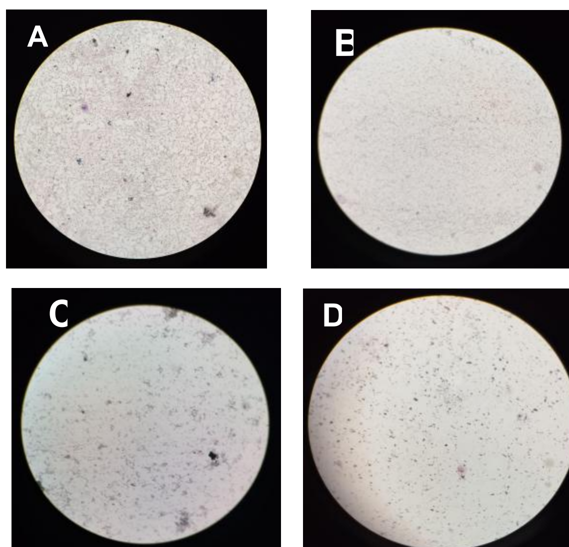


Fig 5. Gram stains of the PEG and PVP enriched cultures from *P. americana.* A: PEG + midgut B: PEG + hindgut C: PVP + midgut D: PVP +hindgut.

3.3 Analysis of PEG and PVP Degradation – Thin layer chromatography

Confirmation of the degradation of PEG and PVP was done by thin layer chromatography (TLC) using isopropanol: methanol: water (1:1:1) for PEG and isopropanol: liquor ammonia (3:2) for PVP separation (Fig 6).

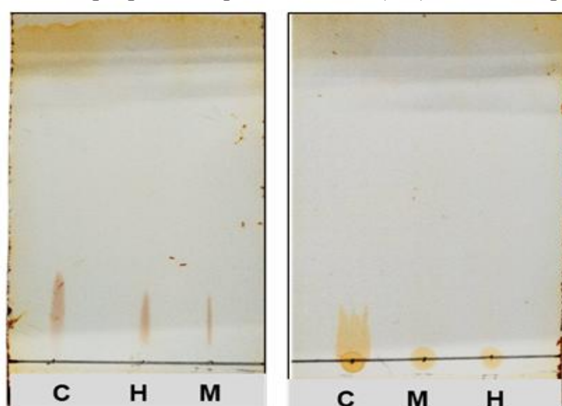


Fig 6. TLC of PEG (left) and PVP (right) degradation by midgut (M) and hindgut (H) microbes. C is the control with just 1% PEG (left) and 1% PVP (right).

TLC was then used to monitor polymer degradation during the incubation period. The time course analysis of PEG and PVP degradation by microbial isolates from the cockroach hindgut (H) and midgut (M) was done along with uninoculated controls (Fig 7).

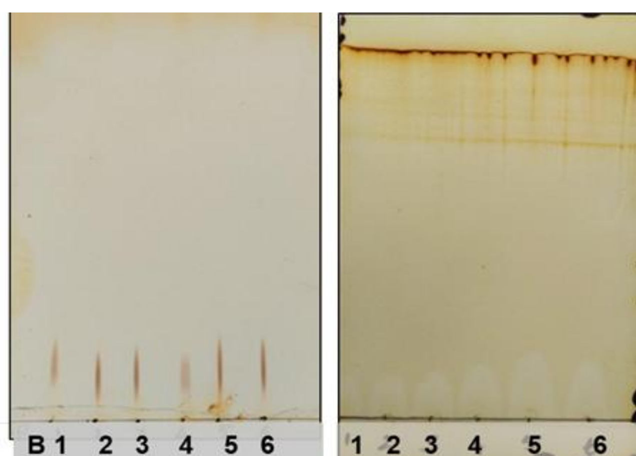


Fig 7. Time course of PEG (left) and PVP (right) degradation by *P. americana* gut microbes. The numbers indicate the days of incubation of the microbes with PEG or PVP.

For PEG (Fig 7, left) lanes 1 through 6 represent sequential days of incubation. Throughout the experiment, clear and discrete spots remain consistently visible at the baseline with only minor fluctuation in intensity, suggesting negligible degradation of PEG within the first week. The absence of new spots corresponding to higher Rf values further supports the resistance of PEG to enzymatic breakdown under the given experimental conditions.
In contrast, PVP degradation (Fig 7, right) demonstrates progressive changes in staining patterns over time relative to controls. The emergence of faint, distinct bands migrating toward the solvent front suggests the presence of smaller molecular weight fragments with increased mobility on the TLC plate. Notably, hindgut-derived isolates exhibited better activity than the midgut isolates.

3.4 Analysis of PEG and PVP degradation - FTIR analysis

FTIR was employed to identify functional groups such as hydroxyl (O–H), carbonyl (C=O), and ether (C–O) groups and assess the changes in the molecular structure of PEG and PVP within the samples. The FTIR spectra for the PEG and PVP degradation by the midgut and hindgut samples are given in Fig 8.

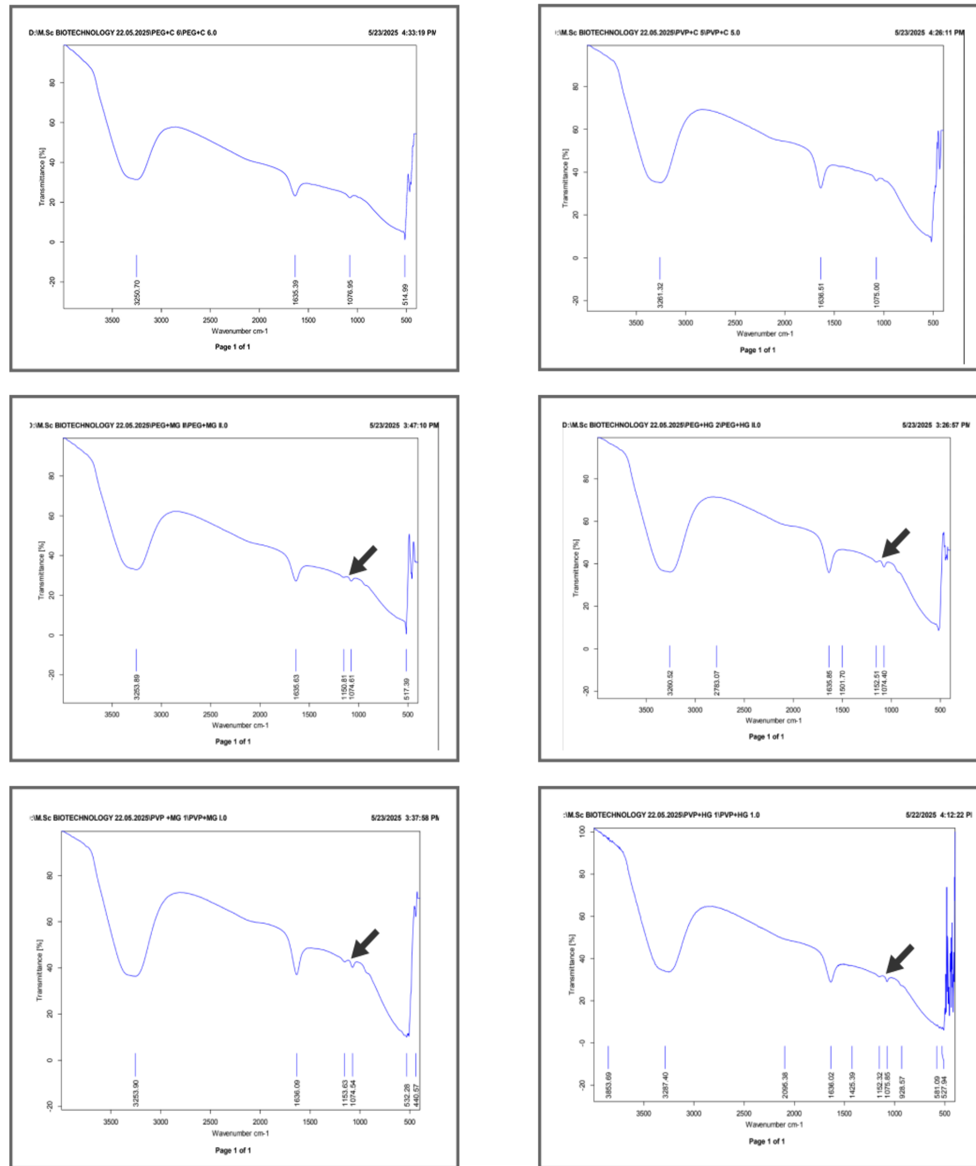


Fig 8. FTIR spectra of PEG (control), PVP (control) (top L & R), PEG (midgut and hindgut) (middle L & R) and PVP (midgut and hindgut) (bottom L & R). The unique peaks are indicated by the arrow.

Compounds were identified based on the wavenumbers corresponding to molecular bonds and functional groups using the website https://instanano.com/all/characterization/ftir/ftir-functional-group-search/.
The compounds in the spent medium with PEG as a sole carbon source are given in Table 5.

Table 5. Identification of degradation products of PEG by gut microbes.

PEG+ CONTROL	PEG + MIDGUT	PEG + HINDGUT	PEAK TYPE	POSSIBLE BOND	POSSIBLE MOLECULE
3250.70	3253.99	3260.52	Major	O-H Stretch H Bonded Hydroxy group	Indicates presence of hydroxyl groups, potentially from water and alcohols.
		2783.07	Major	C≡N	Nitriles
1653.39	1635.63	1635.85	Minor	Alkenyl C=C Stretch	Allyl Alcohol
		1501.70	Minor	C=C-C Aromatic ring stretch	Amide
	1150.81	1152.51	Minor	Alkyl Substituted ether C-O Stretch	Diisopropyl ether
1076.95	1074.61	1074.40	Minor	C-O Stretch Cyclic Ethers Large rings	Oxepane
514.99	517.39		Minor	Aliphatic iodine compounds C-I Stretch	1-Iodobutane

For all examined compounds (PEG+C, PVP+C, PVP+HG1, PEG+MG II, PVP+MG I, PEG+HG II), prominent absorption peaks were observed around 3500 cm^{-1}, corresponding to O–H stretching vibrations; 1650–1660 cm^{-1}, associated with C=O stretching; and near 1070 cm^{-1}, indicative of C–O stretching. These peaks are characteristic of hydroxyl, carbonyl, and ether/alcohol functional groups, consistent with the polymeric nature of PEG. The presence of these functional groups suggests potential enzymatic modifications catalyzed by the microbial isolates from the hindgut (HG) and midgut (MG).
The FTIR analysis of the compounds in the spent medium with PVP as a sole carbon source are given in Table 6.

Table 6. Identification of degradation products of PVP by gut microbes.

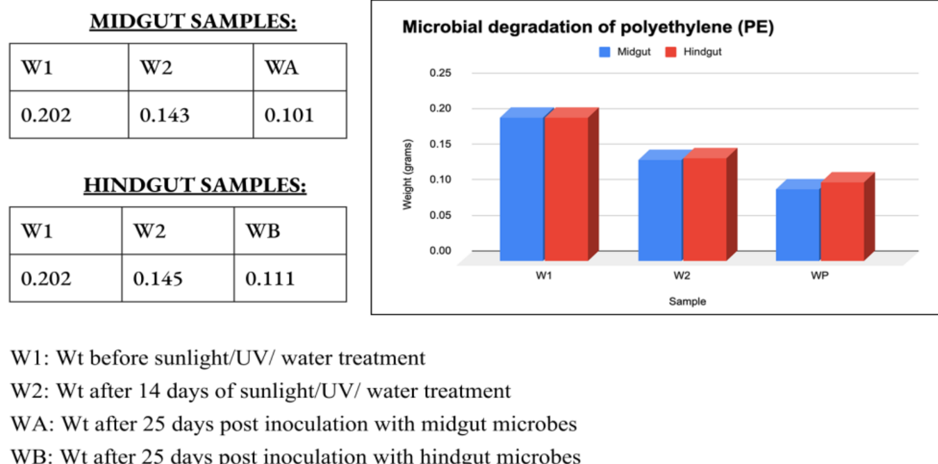
PVP + CONTROL	PVP + MIDGUT	PVP + HINDGUT	PEAK TYPE	POSSIBLE BOND	POSSIBLE MOLECULE
		3853.69	Major	X-H, where X= O, N or H	A non hydrogen bonded alcohol.
3261.32	3253.90	3287.40	Major	O-H Stretch H Bonded Hydroxy group	Indicates presence of hydroxyl groups, potentially from water and alcohols.
		2095.38	Major	C≡C	Alkynes
1636.51	1636.09	1636.02	Minor	Alkenyl C=C Stretch	Allyl Alcohol
		1425.39	Minor	C=C-C Aromatic ring stretch	
	1153.63	1152.32	Minor	Alkyl Substituted ether C-O Stretch	Diisopropyl ether
1075.00	1074.54	1075.85	Minor	C-O Stretch Cyclic Ethers Large rings	Oxepane
		928.57	Minor	Trans CH out of plane bend	Trans alkene: elaidic acid
	532.28	527.94	Minor	Aliphatic iodine	1-Iodobutane
				compounds C-I Stretch	

In the PVP degradation, the hindgut isolates showed a different pattern with peaks at 3853.69 cm^{-1}, 2095.38 cm^{-1} and 928.57 cm^{-1}. The consistent peak near 1150 cm^{-1} was detected in both midgut and hindgut, but was absent in the control samples. This peak likely corresponds to alkyl-substituted ether C–O stretching vibrations, potentially signifying the presence of di-isopropyl ether. The generation of an ether bond, together with the aerobic nature of the cultures suggests the enzymatic incorporation of oxygen in the degradation process. These changes reflect the formation of intermediate metabolites and chemical modifications driven by microbial enzymes, validating mechanisms of polymer cleavage and transformation previously described (Elahi *et al*., 2021; Silva *et al*., 2023).

3.5 Microbial degradation of polythene (PE) and polyvinyl chloride (PVC)

Cultures enriched in minimal salts medium with PEG and PVP were further used to test for their ability to grow on

and degrade actual plastics. The weight of pieces of low-density polythene and PVC pre-treated by exposure to sunlight, was found to decrease significantly (Fig 9 and 10). Interestingly, the growth of bacteria was slow (25-30 days) in both media. Also, the initially clear media progressively became slightly turbid.



MIDGUT SAMPLES:

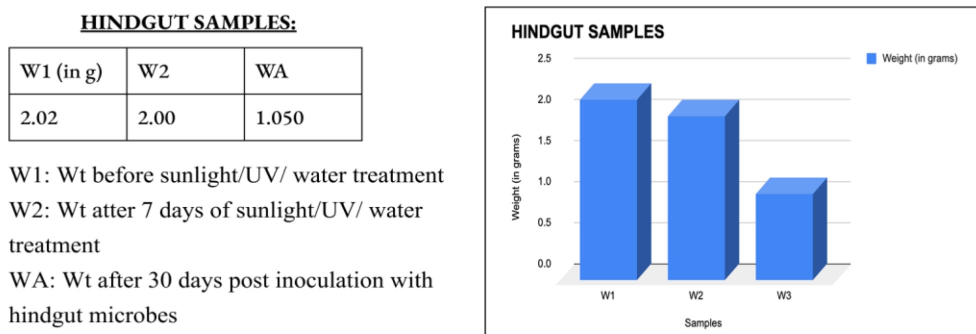
W1	W2	WA
0.202	0.143	0.101

HINDGUT SAMPLES:

W1	W2	WB
0.202	0.145	0.111

W1: Wt before sunlight/UV/ water treatment
W2: Wt after 14 days of sunlight/UV/ water treatment
WA: Wt after 25 days post inoculation with midgut microbes
WB: Wt after 25 days post inoculation with hindgut microbes

Fig 9. Weight of polythene pieces before (W1) and after weathering (W2) and after incubation with midgut (WA) and hindgut (WB) microbes.



HINDGUT SAMPLES:

W1 (in g)	W2	WA
2.02	2.00	1.050

W1: Wt before sunlight/UV/ water treatment
W2: Wt atter 7 days of sunlight/UV/ water treatment
WA: Wt after 30 days post inoculation with hindgut microbes

Fig 10. Weight of PVC pieces before (W1) and after weathering (W2) and after incubation with hindgut (WA) microbes.

Both midgut and hindgut microbial isolates demonstrated measurable degradation of polyethylene (PE) samples. In the case of midgut-derived cultures, the initial weight of the PE sample (0.202 g) progressively decreased to 0.143 g following UV/sunlight pretreatment, and further declined to 0.101 g after 25 days of microbial inoculation. Similarly, the hindgut isolates exhibited a weight reduction from an initial 0.202 g to 0.145 g after UV treatment, culminating at 0.111 g post microbial incubation.

PVC degradation was tested only with hindgut isolates due to insufficient microbial growth in midgut cultures. The PVC samples initially weighing 2.02 g exhibited minimal abiotic degradation following UV/sunlight exposure, with weight decreasing marginally to 2.00 g.

It is known that inclusion of abiotic pretreatment via sunlight and ultraviolet (UV) exposure facilitates microbial degradation. The observed modest weight reductions following UV treatment alone align with the known photo-oxidative degradation pathway where UV-generated reactive groups and chain scission increase the susceptibility of polymers to enzymatic attack (Sen and Raut, 2015; Cheng *et al*., 2021).

3.6 Analysis of plastic degradation by FTIR

To assess the changes in the polythene and polyvinylchloride pieces, FTIR analysis of the medium was carried out

(Fig 11).

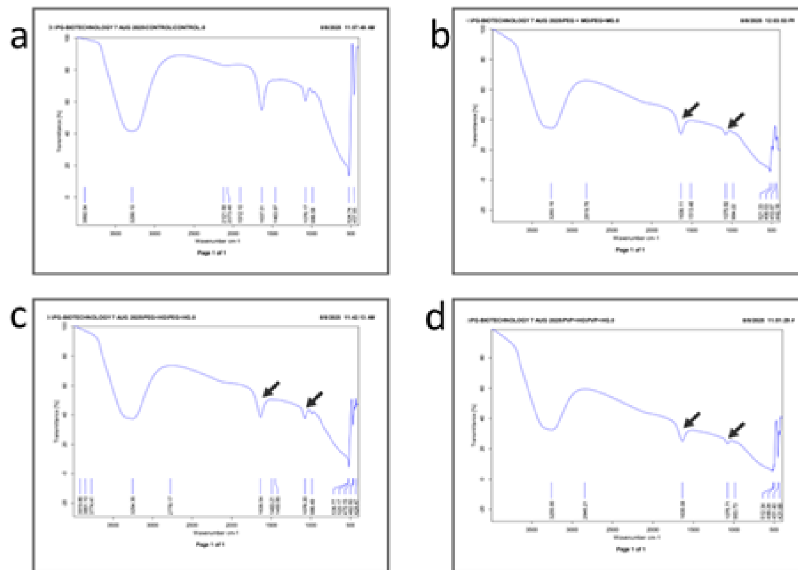


Fig 11. FTIR spectra of Control (a), PE (midgut) (b), PE (hindgut) (c) and PVC (hindgut) (d).

The wave numbers of the different peaks and their corresponding bonds are given in Table 7.

Table 7. Identification of degradation products of PE and PVC by gut microbes.

CONTROL	PE + MIDGUT	PE + HINDGUT	PV + HINDGUT	PEAK TYPE	POSSIBLE BOND	POSSIBLE MOLECULE
3892.04		3851.10				
3290.10	3260.16	3254.35	3255.90	Major	O-H Stretch H Bonded Hydroxy group	Indicates presence of hydroxyl groups, potentially from water and alcohols.
2121.58	2819.76	2778.17	2845.21	Major	C-H asymmetric stretch	Hydrocarbon chain in lipid of midgut
1637.01	1636.11	1636.54	1635.08	Minor	C=O stretch	Amide I or C=O in ester
	1513.46			Minor	Alkyl Substituted ether C-O Stretch	Diisopropyl ether
1463.97		1493.21		Minor	C-H bend	Aliphatic CH_2
1076.17	1075.50	1076.20	1075.71	Minor	C-O stretch Cyclic Ethers Large rings	Oxepane
986.58	984.22	986.49	983.73	Minor	Trans CH out of plane bend	Trans alkene: elaidic acid
524.74	521.33	536.77		Minor	C-I Stretch	Aliphatic Iodine

The FTIR spectra revealed wave numbers corresponding to ether linkages, hydroxyl (-OH), and carbonyl (-C=O) groups in the samples cultured with both midgut and hindgut bacteria (Table 7). As these bacteria are aerobic, this indicates that oxygen plays a role in the partial degradation of the polymer. Comparable metabolic pathways have been reported for Klebsiella spp., which employ enzymes such as peroxidases and laccases to biodegrade polyethylene (Zhang *et al*., 2023).

3.7 Identification of the plastic-degrading microbes

The 16S rDNA sequences of two midgut and two hindgut isolates were then used in a BLAST search for the closest neighbour for identification. The closest match was found to *Enterobacter cloacae* and *Klebsiella pneumoniae* (Fig 12, 13, 14). This is not surprising since both *Klebsiella* and *Enterobacter cloacae* have been shown to feed on plastics (Sarker *et al*., 2020; Zhang *et al*., 2023; Mohamed and Narayanan, 2024; Hu *et al*., 2025). While Klebsiella is mostly a soil microbe, it appears that some strains could colonise cockroach gut.

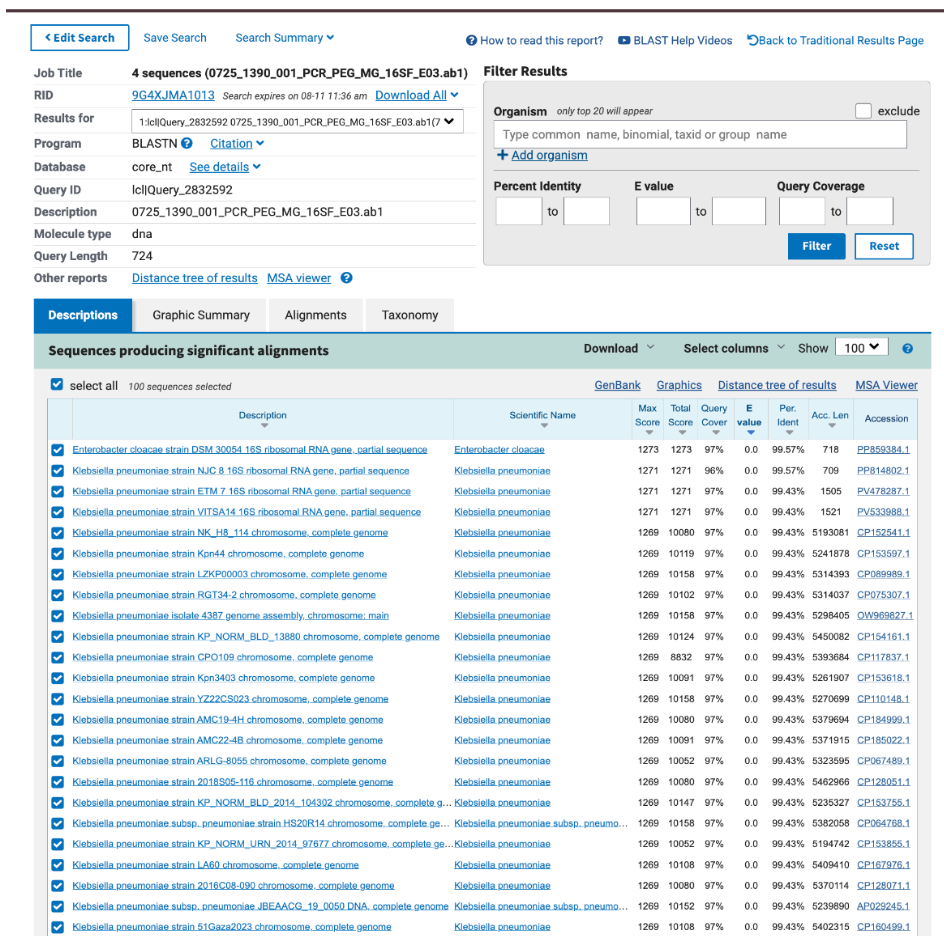


Fig 12. BLAST Analysis of the 16S rDNA sequence of the midgut and hindgut isolates.

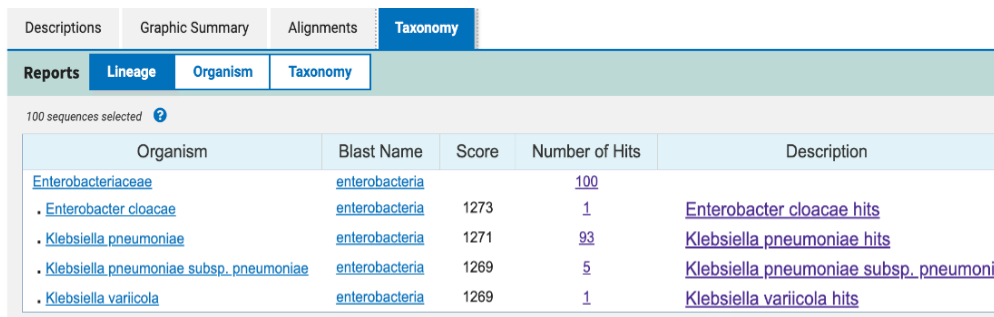


Fig 13. Establishment of the closest neighbour of the midgut and hindgut isolates by linkage.

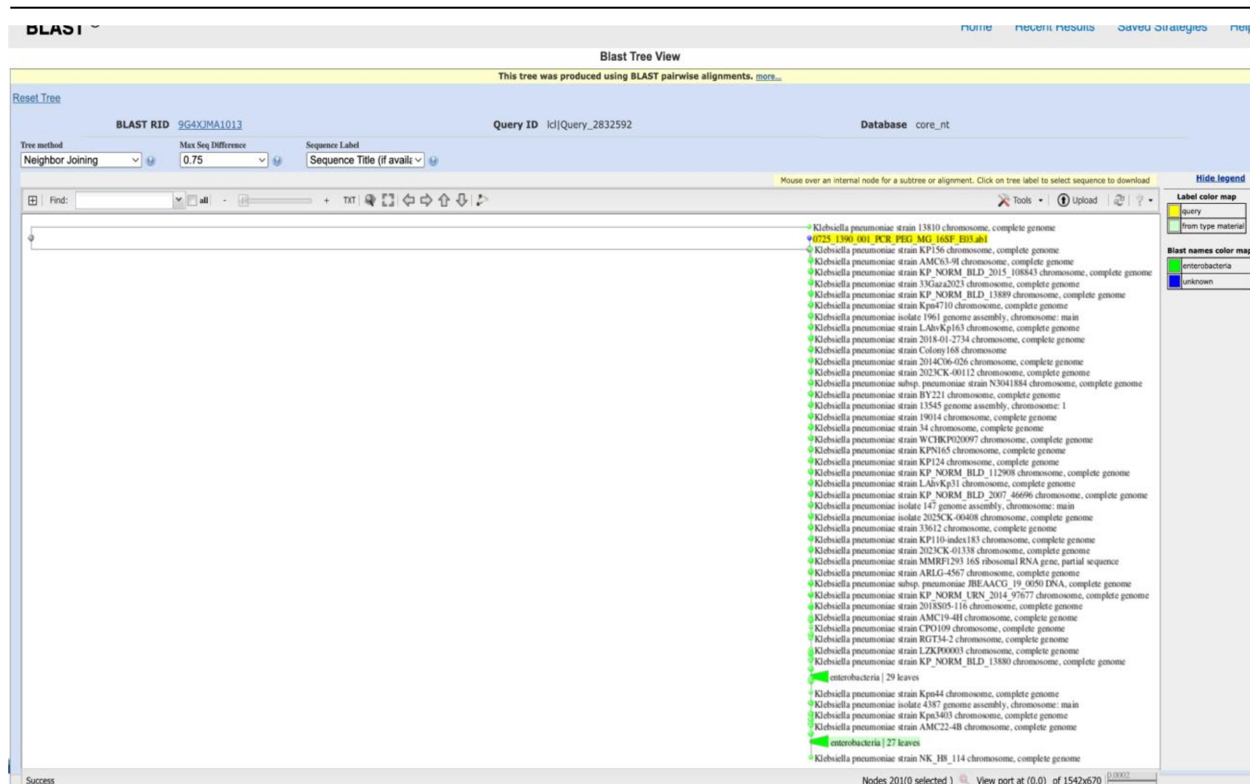


Fig 14. Establishment of the phylogenetic tree to confirm the closest possible identity of the isolates.

The four bacterial isolates obtained from the cockroach gut—two from the midgut and two from the hindgut—showed close genetic affiliation with *Enterobacter cloacae, Klebsiella pneumoniae, Klebsiella pneumoniae subspecies,* and *Klebsiella variicola* based on sequence analysis. *Klebsiella pneumoniae* has been previously documented to possess the ability to degrade low-density polyethylene (LDPE) (Sarker *et al*., 2020; Hu *et al*, 2025). Strains of this species have been demonstrated to colonize LDPE surfaces, thereby inducing physicochemical changes such as decreased crystallinity, reduced hardness, and enhanced surface roughness, all indicative of active biodegradation processes (Mohamed and Narayanan, 2024; Jacquin *et al*., 2019).

Cultures grown in minimal nutrient media supplemented with 1% polyvinylpyrrolidone (PVP) and 1% polyethylene glycol (PEG) demonstrated the formation of microbial consortia. This consortium formation serves as robust evidence that plastic degradation is a cooperative activity involving multiple bacterial strains acting synergistically. Such microbial interactions can enhance degradation efficiency by facilitating complementary enzymatic activities and metabolic cross-feeding mechanisms. The microbial diversity of the cockroach gut supports the concept of complex microbial consortia as potent plastic degraders, with biofilm-forming capacity facilitating metabolic cooperation and enzyme sharing, thereby amplifying degradation kinetics and substrate versatility (Ganesh Kumar *et al*., 2020; Cao *et al*., 2022).

Molecular identification via 16S rRNA gene sequencing and BLAST analysis linked isolates predominantly to *Enterobacter cloacae* and *Klebsiella pneumoniae* species, genera extensively documented for their environmental plastic degradation activities. These bacteria have demonstrated capabilities to colonize polymer surfaces, induce physicochemical changes such as decreased crystallinity and increased roughness, and secrete extracellular enzymes that facilitate polymer disintegration (Das and Kumar, 2015; Awasthi *et al*., 2017).

The results emphasize the ecological and biotechnological significance of insect gut microbiomes, which possess enhanced enzymatic arsenals and consortia enabling effective degradation of persistent plastic polymers. Such complex microbial assemblies may be critical for addressing the global challenge of plastic pollution through sustainable, low-energy bioremediation approaches (Cao *et al*., 2022; Khurana *et al*., 2025).

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Author contributions

VB conceptualized the project; SL executed the experiments; both SL and VB were involved in manuscript preparation.

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