



## ANALYSIS OF THE BIODEGRADATION OF POLYETHYLENE BY BACTERIA ISOLATED FROM DUMP SITES AT HANWA, ZARIA, KADUNA STATE

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### ABSTRACT

Polyethylene (PE) is among the most commonly used synthetic plastics, yet it poses a serious environmental challenge due to its resistance to natural degradation. This study was carried out to examine the ability of two indigenous bacterial strains, *Pseudomonas aeruginosa* and *Klebsiella quasipneumoniae*, isolated from soil samples collected at dumpsites in Hanwa, Zaria, Kaduna State, Nigeria, to degrade polyethylene under laboratory conditions. The bacteria were identified through morphological and biochemical methods, as well as molecular techniques using 16S rRNA gene sequencing. Biodegradation was assessed over a 21-day period by measuring the weight loss of polyethylene at different temperatures (37°C, 45°C, and 50°C), pH levels (6.0, 7.0, and 8.0), and polyethylene concentrations (0.2 g, 0.4 g, and 0.6 g). The results showed that *Pseudomonas aeruginosa* achieved a maximum degradation of 53.3%, while *Klebsiella quasipneumoniae* followed closely with 41.7%. Biofilm formation and increased turbidity were also observed, indicating active microbial metabolism. These findings suggest that native bacteria from waste-polluted environments have promising potential for use in the bioremediation of polyethylene waste, especially when environmental conditions are optimized.

**Keywords:** Polyethylene Biodegradation, Plastic-Degrading Bacteria, *Pseudomonas aeruginosa*, Environmental Bioremediation and Biofilm Formation

### INTRODUCTION

Environmental pollution is the most challenging problem in today's world which is increasing day by day leading to devastatingly and irreparable damage to our mother earth (Umar, 2025). Bioremediation has evolved as an effective technique to counteract the negative impacts of environmental pollution in various ways. According to the United States Environmental Protection Agency (EPA), bioremediation is a waste management technique that relies upon the use of biological activities of microorganisms to interact with the environmental factors causing change in the physical/chemical conditions of hazardous waste and finally converting it into comparably less toxic or even nontoxic products (Bunty *et al.*, 2017).

Plastic is a synthetic polymer widely used in almost every field of life and the massive use of this synthetic polymer has led to its accumulation in the environment thus, polluting the environment (Angga *et al.*, 2021). The most serious concern is that most of the conventional plastics such as polyethylene, polypropylene, polystyrene, poly (ethylene terephthalate), poly (vinyl chloride) etc., are non-biodegradable and their augmentation in the nature has been a constant threat for the environment as their accumulation of plastic is hazardous to food chain, causing overall ecological imbalance leading to health impairment in humans as well (Bunty *et al.*, 2017).

Polyethylene (PE) has the highest yield amongst plastics as more than 100 million tons is produced each year globally (Danco *et al.*, 2019). PE-based materials are used in various industries, including transportation, construction, agriculture, machine building, and packaging (Geyer, 2020). However, a large proportion of PE products are not subjected to proper disposal after use. Published statistics indicate that less than 20% of PE waste is recycled each year (Biki *et al.*, 2021). The pollution caused by polyethylene includes blocking drains, water, soil, air contamination, sewage lines around the urban

areas due to non-degradability and is not beneficial to the topsoil (Dey, *et al.*, 2020).

Biodegradation of polyethylene in summary entails the following steps: Attachment of the microorganism to the surface of the polyethylene, growth of the microorganism using the polyethylene as a carbon source and lastly ultimate degradation of the polyethylene (Singh and Rawat, 2019).

Studies on diverse activities of *Pseudomonas* and *Klebsiella* have been carried out to investigate their capabilities to degrade and metabolize a variety of synthetic plastics polymers and the by-products. *Pseudomonas* species have the unique ability to degrade and metabolize the polymers with extracellular oxidative and/or hydrolytic enzyme activities, which facilitate uptake and degradation of the polymer fragments, and control interaction between biofilms and polymer surfaces (Wilkes and Aristilde, 2017).

The aim of this study is to Isolate, characterize some Bacteria and investigate their potentials in the comparative degradation of polyethylene wastes of some dump sites in Hanwa, Zaria, Kaduna State.

### MATERIALS AND METHODS

#### Study Area and Sample Collection

The study was conducted at waste dumpsites located in Hanwa, a community within Zaria Local Government Area of Kaduna State, Nigeria, positioned at latitude 11.1186°N and longitude 7.7019°E. Zaria, also known as Zazzau, is a historic and industrial town with a population of approximately 736,000. The city generates large volumes of municipal solid waste daily, predominantly from household sources, with polyethylene being one of the most common waste types.

Soil samples were collected from three dumpsites at a depth of 3 cm using a sterile stainless-steel spatula. Three samples were collected from each site, spaced 20 cm apart, yielding nine samples in total. These were labelled A1, A2, A3, B1, B2, B3, C1, C2 and C3 (Gumbi *et al.*, 2019). The samples were transported in sterile, labelled, self-sealing polyethylene bags to the Department of Microbiology, Ahmadu Bello University, Zaria.

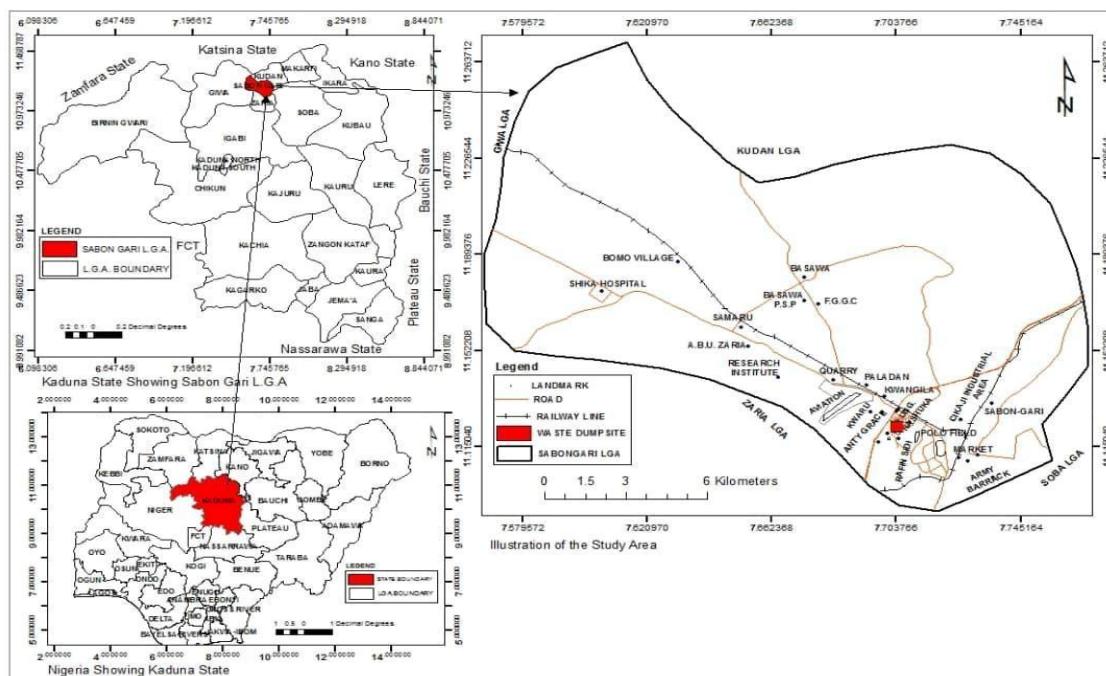


Figure 1: A Map Showing the Study Area  
Source: KASU GIS UNIT (2023)

### Physiochemical Analysis of Soil Samples

#### Determination of Particle Size (Sand, Silt, and Clay)

Soil particle size distribution was determined using the hydrometer method as described by IITA (1979). A blank was prepared by mixing 100 ml of 5% sodium hexametaphosphate with 880 ml of deionized water in a 1000 ml cylinder. For analysis, 50 g of air-dried, sieved soil (<2 mm) was mixed with 50 ml of dispersing solution and 100 ml of distilled water. The mixture was allowed to stand for 30 minutes, then shaken mechanically for 1 hour and transferred into a 1000 ml measuring cylinder, topped to volume with distilled water, and left to equilibrate overnight. Before readings, the suspension was stirred with a plunger for 30 seconds. A hydrometer was inserted, and the first reading (silt + clay) were recorded at 40 seconds. A second reading was taken after 2 hours to measure clay content. Sand percentage was determined by difference, and textural class was assigned using the USDA soil texture triangle.

#### Determination of Soil pH

The determination of soil pH was done using standard procedure as reported by Estefan *et al.* (2013). Twenty grams (20g) of soil sample was taken into a 100ml beaker to which 40ml of distilled water was added. The suspension was stirred at regular interval for 30 minutes to ensure effective dispersal and dissolution of all soluble compounds. The pH meter was calibrated with two buffers, one on the acidic side and other alkaline. The pH was then recorded using a pH meter. The electrodes were rinsed with distilled water after each use.

#### Determination of Organic Carbon

Organic carbon content was determined using the Walkley-Black wet oxidation method (Luilo and Othman, 2010). One gram (1 g) of sieved, air-dried soil (<0.5 mm) was transferred into a 500 ml Erlenmeyer conical flask. Ten millilitres (10 ml) of 0.167 M potassium dichromate ( $K_2Cr_2O_7$ ) solution and 20 ml of concentrated sulfuric acid ( $H_2SO_4$ ) were added. The mixture was swirled and allowed to stand for 30 minutes. It was then diluted with 200 ml of distilled water, followed by

the addition of 10 ml of 85% phosphoric acid ( $H_3PO_4$ ), 0.2 g of sodium fluoride (NaF), and 10 drops of ferroin indicator. The solution was titrated with 0.5 M ferrous sulfate ( $Fe^{2+}$ ) until a colour change from yellow-orange to green-gray was observed. A blank titration was also conducted without soil to standardize the  $Fe^{2+}$  solution.

#### Determination of Organic Matter

Organic matter content (%) was estimated by multiplying the measured organic carbon value by the Van Bemmelen factor of 1.724 (Jackson, 1964):

$$\% \text{ Organic Matter} = \% \text{ Organic Carbon} \times 1.724 \quad (1)$$

#### Determination of Total Nitrogen

Total nitrogen was determined using the Kjeldahl digestion method as described by Malgwi, (2013). One gram (1 g) of soil was digested with concentrated sulfuric acid and a catalyst mixture of copper sulfate and potassium sulfate. The digested sample was distilled, and the released ammonia was trapped in boric acid, followed by titration with standardized hydrochloric acid. Total nitrogen (%) was calculated from the volume of titrant used.

#### Soil Moisture Content

Moisture content was determined gravimetrically following the method described by Gardner (1986). Ten grams (10 g) of fresh soil were weighed into a pre-weighed crucible, oven-dried at 105°C for 24 hours, cooled in a desiccator, and reweighed. Moisture content (%) was calculated as:

$$\text{Moisture (\%)} = [(Wet \text{ weight} - Dry \text{ weight}) \div Wet \text{ weight}] \times 100 \quad (2)$$

#### Isolation and Identification of Bacteria

Bacteria were isolated from the soil using Plate Count Agar and purified through repeated sub-culturing. The cultures were incubated at 37°C for 24 hours. Isolates were designated A1, A2, A3, B1, B2, B3, C1, C2, and C3 for each growth medium. These pure cultures were maintained at ambient temperature and their viability was sustained through frequent

monthly sub-culturing and refrigeration at 4°C. Colony morphology, Gram staining, and a range of biochemical tests (Catalase, Oxidase, Urease, Methyl Red, Voges Proskauer, Indole, Motility, Citrate, Sucrose, Maltose and Mannitol) were used for preliminary identification.

For molecular identification, genomic DNA was extracted, and the 16S rRNA gene was amplified using PCR. The amplicons were sequenced and analysed using the NCBI BLAST database to confirm the bacterial species.

### Preparation of Polyethylene

The general grade polyethylene waste was obtained from the waste disposal sites. It was initially washed with 70% ethanol until all visible particles adhered to it are washed up completely. It was then rinsed with distilled water for an hour and dried in hot air oven for 1 hour 30 minutes. Afterward, the large pieces were crushed by grinding with a mortar and pestle along with sufficient amount of crystalline NaCl to make grinding easier. It was grinded to a fine rupture thread form. Rupturing the polyethylene with salt solution enabled washing away of all impurities and organic matter adhering to it. The mixture was transferred into a conical flask with distilled water and was mixed well in a shaker for 1 hour. The solution was then filtered using Whatman no.41 filter paper. Polyethylene particles recovered from the filter paper was dried in the oven for an hour before use in the experiments (Sonil and Smiti, 2010).

### Experimental Set Up and Treatment of Polyethylene

The 0.5 Mcfarland standard concentration of different isolated suspected Bacteria was inoculated individually into 100ml of nutrient broth in respective conical flask except the control.

0.2g of polyethylene were amended to each flask except the blank. The following were the experimental designs for treatments:

$$PEA_2 = (\text{Polyethylene} + \text{Pseudomonas A}_2) \quad (3)$$

$$PEC_3 = (\text{Polyethylene} + \text{Klebsiella C}_3) \quad (4)$$

So on in that manner, all the treatments were incubated in incubator shaker at (180rpm) for 3 weeks. All samples were incubated at 37-50°C and pH6-8. Negative control and Blanks were used to examine viability of the bacteria (Gumbi et al., 2019).

### Assessment of Degradation

The weight loss in the reaction mixture and in the polyethylene, weight was calculated using the formula:

$$[(I-F) \div I] \times 100 \quad (5)$$

Where;

I=Initial weight,

F=Final weight

Visible changes in the culture media (e.g., turbidity, biofilm formation) were also recorded as indicators of microbial activity and interaction with the polymer.

## RESULTS AND DISCUSSION

### Physicochemical Analysis of Soil Samples

The physicochemical analysis of the soil samples from the dumpsites (Table 1) revealed a predominantly sandy loam and loamy sand texture. The pH ranged from 5.80 to 6.30, with moisture content between 19.6% and 21.4%. Organic carbon content was highest in sample C (3.71%), followed by A (3.47%) and B (1.56%). This suggests a moderately acidic environment with sufficient organic matter to support microbial growth.

**Table 1: Physicochemical Analysis of Soil Samples**

Sample	% Clay	%Silt	%Sand	Textural Class	
A	9	14	77	Sandy Loam	
B	7	16	77	Sandy Loam	
C	7	12	81	Loamy Sand	
Sample	% Moisture Content	% Organic Carbon	% Organic Matter	% Nitrogen	pH
A	19.6	3.4713	5.9815	0.4339	5.80
B	20.4	1.5561	2.6827	0.2223	6.30
C	21.4	3.7107	6.3967	0.4638	5.92

### Morphological Identification of Bacterial Isolates

Twenty-six bacterial isolates were identified based on colony morphology (Table 2), Gram staining, and cell shape. The majority were Gram-positive rods, with some cocci and Gram-negative rods. Among these, isolates A<sub>21</sub> and C<sub>32</sub> were selected and later identified through molecular analysis as *Pseudomonas aeruginosa* and *Klebsiella quasipneumoniae*, respectively.

### Biochemical Characterization of Bacterial Isolates

The biochemical profiles confirmed the identity of the selected isolates (Table 3). *Pseudomonas aeruginosa* (A<sub>21</sub>) was catalase-positive, oxidase-positive, urease-positive, and citrate-positive. *Klebsiella quasipneumoniae* (C<sub>32</sub>) showed

positive results for catalase, urease, citrate, and hydrogen sulphide production, among other tests. These biochemical traits support their metabolic capability to utilize synthetic substrates like polyethylene.

### Molecular Identification and Phylogeny

The 16S rRNA gene sequences of the isolates were analysed and compared using NCBI BLAST. Phylogenetic analysis confirmed that isolate A<sub>21</sub> is *Pseudomonas aeruginosa*, and isolate C<sub>32</sub> is *Klebsiella quasipneumoniae* (Figure 3 and 4). These identifications align with the morphological and biochemical findings and validate their selection for biodegradation studies.

**Table 2: Morphological Identification of Bacterial Isolates**

Sample No.	Sample Code	Gram Reaction	Cell Morphology
1	A11	+	Rod
2	A12	+	Rod
3	A13	+	Long Rod
4	A14	+	Rod

Sample No.	Sample Code	Gram Reaction	Cell Morphology
5	A21	-	Short Rod
6	A22	+	Rod
7	A31	+	Rod
8	A32	+	Long Rod
9	B11	+	Cocci
10	B12	+	Rod
11	B13	+	Long Rod
12	B21	+	Rod
13	B22	+	Rod
14	B23	+	Rod
15	B31	+	Cocci
16	B32	-	Short Rod
17	B33	+	Rod
18	C11	-	Short Rod
19	C12	+	Rod
20	C13	+	Rod
21	C21	+	Rod
22	C22	+	Rod
23	C23	+	Rod
24	C31	+	Cocci
25	C32	-	Long Rod
26	C33	+	Long Rod

Table 3: Biochemical Characterization of Bacterial Isolates

Sample Code	Catalase	Oxidase	Urease	Methyl Red	Voges Proskauer	Indole	Motility	Citrate	Sucrose	Maltose	Mannitol
A1 <sub>1</sub>	-	+	+	-	+	-	+	-	-	-	+
A1 <sub>2</sub>	+	+	-	-	+	-	+	+	-	-	-
A1 <sub>3</sub>	+	-	-	+	+	-	+	+	-	-	-
A1 <sub>4</sub>	+	+	+	+	+	-	+	-	-	-	-
A2 <sub>1</sub>	+	+	+	-	-	-	+	+	-	-	-
A2 <sub>2</sub>	-	-	+	-	-	-	+	-	-	-	+
A3 <sub>1</sub>	+	+	-	+	+	-	-	-	-	+	+
B1 <sub>1</sub>	+	-	+	+	+	-	+	+	-	-	-
B1 <sub>2</sub>	+	-	+	+	-	-	-	+	+	+	-
B1 <sub>3</sub>	+	-	+	+	-	-	-	+	+	+	-
B2 <sub>1</sub>	-	+	+	-	+	-	+	-	-	+	+
B2 <sub>2</sub>	+	+	+	+	+	-	-	+	-	-	+
C1 <sub>1</sub>	+	-	+	-	+	-	-	-	+	-	-
C1 <sub>2</sub>	-	+	-	+	-	-	-	-	+	+	-
C1 <sub>3</sub>	+	+	-	-	+	-	+	-	+	-	+
C2 <sub>1</sub>	-	-	-	+	+	-	+	+	+	+	+
C2 <sub>2</sub>	+	-	+	-	+	-	-	+	+	+	+
C2 <sub>3</sub>	+	-	-	+	-	-	+H <sub>2</sub> S	-	-	+	+
C3 <sub>2</sub>	+	-	-	-	+	-	-	+	+	+	+
C3 <sub>3</sub>	+	-	+	+	-	-	+H <sub>2</sub> S	+	+	+	-

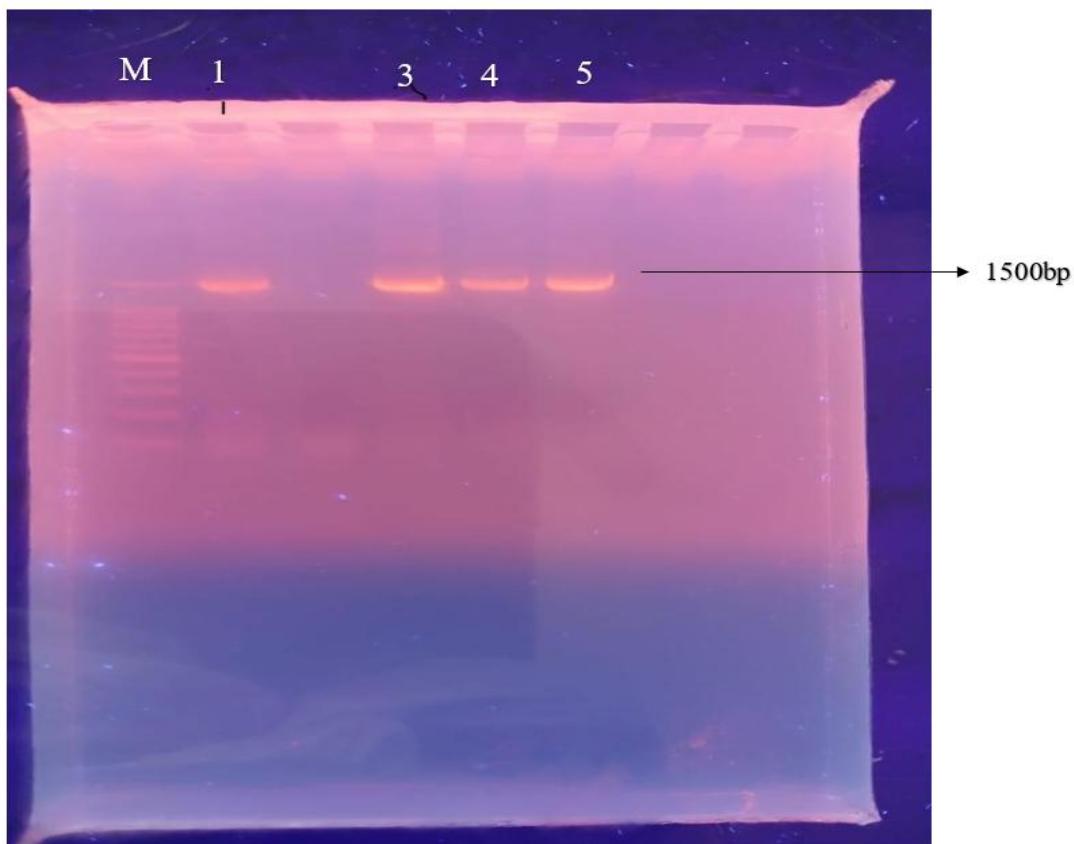


Plate 1: Agarose gel Electropherogram After PCR Amplification of 16S rRNA Gene of the Bacterial Isolates. (M) Molecular Marker of 100bp; *Pseudomonas aeruginosa* and *Klebsiella quasipneumoniae* Lane 1= Sample A2<sub>1</sub>, Lane 3= Sample A2<sub>1</sub>, Lane 4= Sample C3<sub>2</sub>, Lane 5= Sample C3<sub>2</sub>

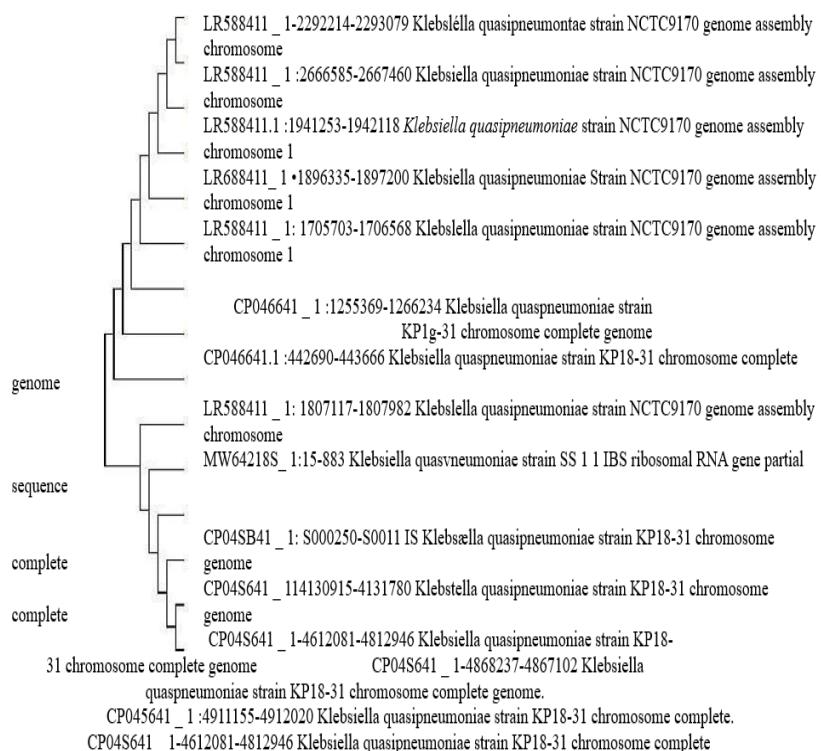
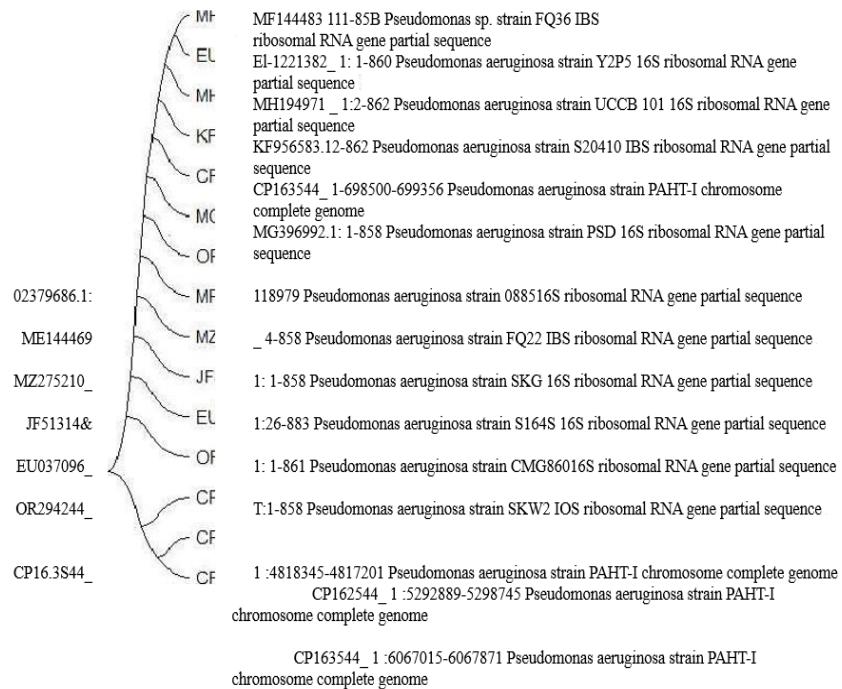


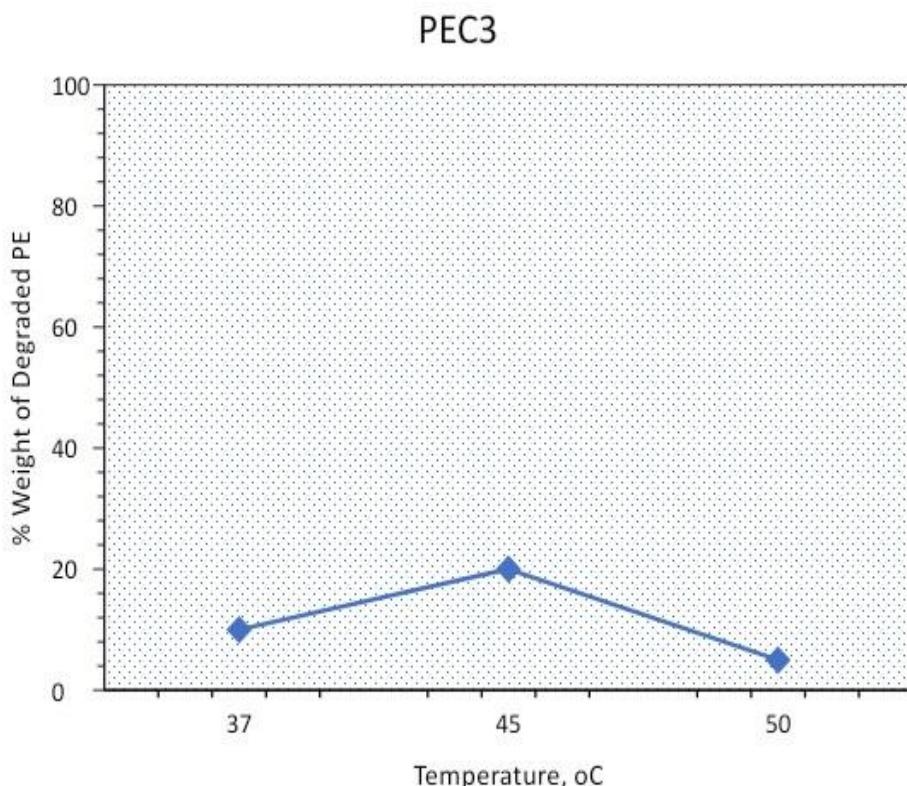
Figure 3: Phylogeny Tree of *Klebsiella quasipneumoniae*

Figure 4: Phylogeny Tree of *Pseudomonas aeruginosa*

#### Effect of Temperature on Polyethylene Degradation

The rate of biodegradation of polyethylene at 45°C showed a similar trend to that at 37°C, with the percentage of degradation being slightly higher at 45°C for both bacterial strains. A 20% degradation of polyethylene was achieved by *Klebsiella quasipneumoniae* (Figure 5). *Pseudomonas aeruginosa* did not show any growth at 50°C (Figure 6), and

thus no polyethylene degradation was achieved at this temperature. However, a 5% degradation of polyethylene was achieved by *Klebsiella quasipneumoniae* at 50°C. The decrease in biodegradation rate may be attributed to the high temperature making it difficult for the organisms to adapt to changes in nutrient availability and toxin concentration as they approached the stationary phase.

Figure 5: Temperature and % Weight Degradation of Polyethylene by *Klebsiella quasipneumoniae*

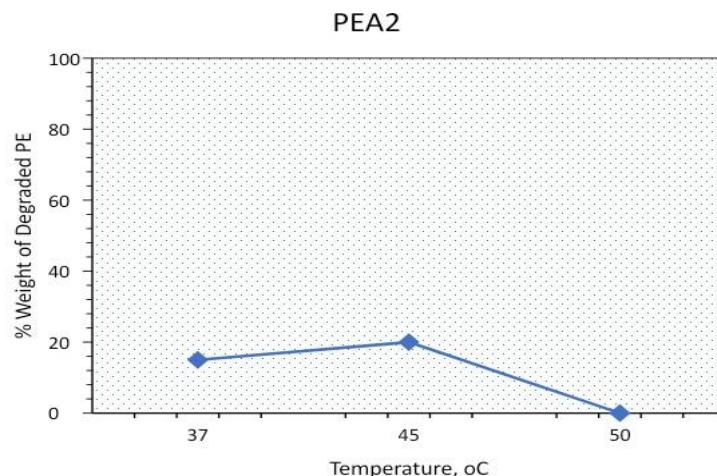


Figure 6: Temperature and % weight Degradation of Polyethylene by *Pseudomonas aeruginosa*

#### Effect of pH on Polyethylene Degradation

The maximum degradation of polyethylene by *Pseudomonas aeruginosa* and *Klebsiella quasipneumoniae* occurred at pH 6

and 7 at 37°C (Figure 7 and Figure 8), achieving a 20–40% degradation rate. Both strains showed diminished activity at pH 8, with degradation rates falling to around 20%.

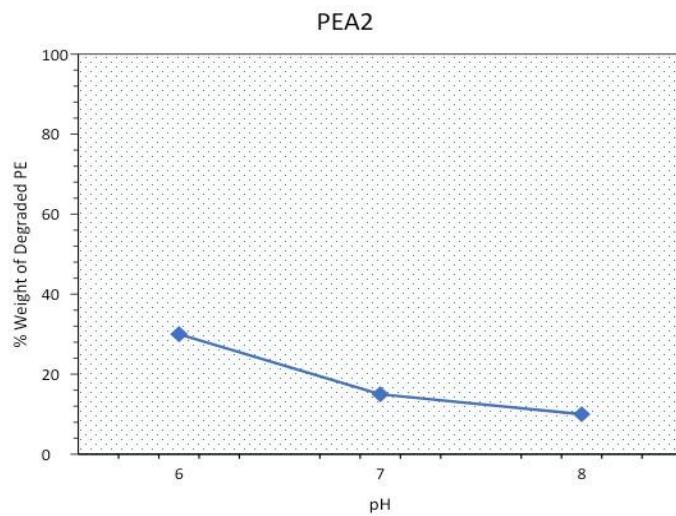


Figure 7: pH and % Weight Degradation of Polyethylene by *Pseudomonas aeruginosa*

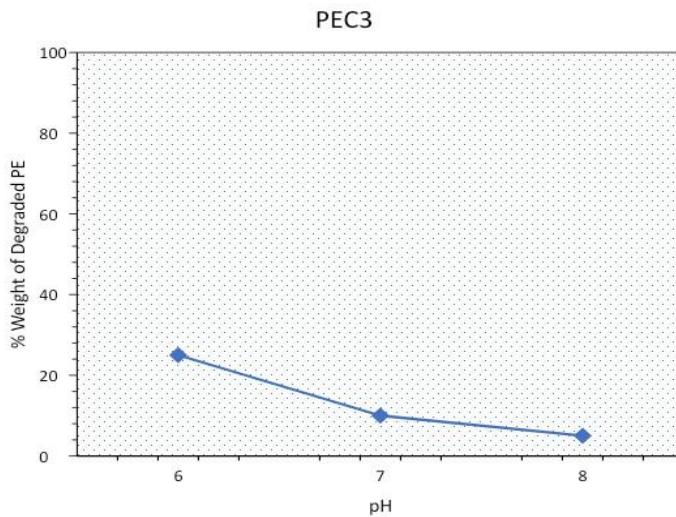


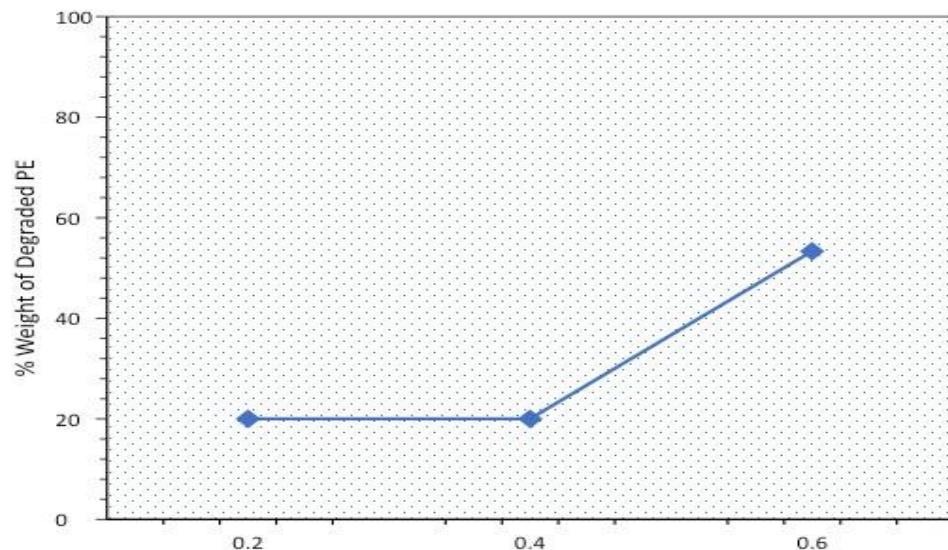
Figure 8: pH and % Weight Degradation of Polyethylene by *Klebsiella quasipneumoniae*

### Effect of Polyethylene Concentration

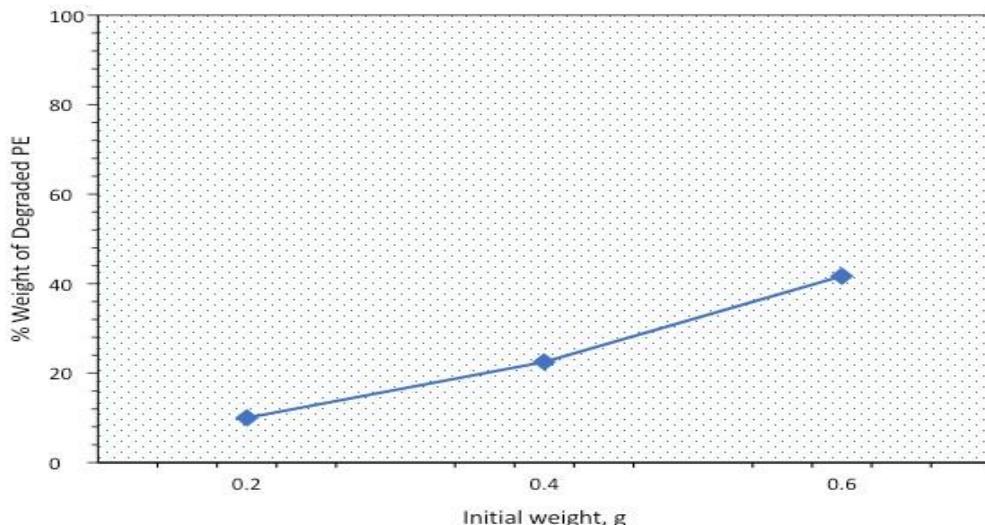
Degradation efficiency increased with rising substrate concentration. At 0.6 g, *Pseudomonas aeruginosa* and *Klebsiella quasipneumoniae* achieved their highest degradation rates, at 53.3% and 41.7%, respectively (Figure 9 and Figure 10). In contrast, lower concentrations (0.2 g and 0.4 g) yielded reduced degradation. The optimal polyethylene

concentration for bacterial growth and degradation was therefore 0.6 g, where the most significant biofilm formation and polymer breakdown were observed after three weeks. The gradual increase in polyethylene concentration was also accompanied by enhanced biofilm development and increased turbidity in the medium, reflecting elevated microbial metabolic activity.

PEA2

Figure 9: % Weight Degradation of Polyethylene by *Pseudomonas aeruginosa* at Different Concentrations

PEC3

Figure 10: % Weight Degradation of Polyethylene by *Klebsiella quasipneumoniae* at Different Concentration

### Control Observations

No significant polyethylene degradation was observed in control flasks without bacterial inoculation, confirming that weight loss was due to microbial activity.

### Discussion

Polyethylene (PE) remains one of the most ubiquitous synthetic plastics globally, posing significant environmental challenges due to its resistance to biodegradation in natural ecosystems (Shah et al., 2020). This study assessed the biodegradation ability of two bacterial isolates, *Pseudomonas*

*aeruginosa* and *Klebsiella quasipneumoniae*, from dump sites at Hanwa, Zaria, Kaduna State, under controlled laboratory conditions. One of the methods used to determine degradation in this study is the measurement of the dry weight of residual Polyethylene. The dry weight shows that there was a reduction in the weight of polyethylene across all two bacterial isolates. The initial 0.6 g of the polyethylene that was introduced to the medium inoculated with *Klebsiella quasipneumoniae* C3<sub>2</sub> was able to degrade polyethylene yielding a maximum degradation of 41.7%. However, *Pseudomonas aeruginosa* A2<sub>1</sub> yielded a maximum

degradability of 53.3% for polyethylene. This observation indicated that these Bacteria isolates utilized polyethylene as a sole carbon source resulting in partial degradation of the polymer. Such results are similar to those obtained by Gumbi et al. (2019). They reported the highest level of polyethylene degradation (weight loss) of 55% by *Pseudomonas aeruginosa* at 37°C and a concentration of 0.6% polyethylene. This was followed by a 50% degradation at 0.4% concentration of polyethylene at 37°C, and finally a 20% degradation at pH 6 all after 21 days. They observed that *Pseudomonas* can biodegrade polyethylene and the biodegradation is greatly affected by physical factors like pH, temperature and concentration of polyethylene.

During the period of incubation, it was observed that the rate at which the degradation took place was faster after the first week. This could probably mean that during this week the bacteria were utilizing the polymer as a carbon source, which led to their increase in growth (Kotova et al., 2021). However, when it approached the third week, the rate slowed down, this may be that the bacteria, due to their metabolic activities, released toxic substances into the culture medium (Braissant et al., 2020). This slowdown in the third week corresponds more closely to the stationary phase, while the lag phase would have occurred at the beginning of incubation, when cells were adjusting to the new medium before exponential growth (Nandy et al., 2020). The length of the lag phase depends directly on the previous growth condition of the organism (Bertrand et al., 2019). When the microorganism growing in a rich medium is inoculated into nutritionally poor medium, the organism will take more time to adapt with the new environment (Mahdi et al., 2018). The organism will start synthesizing the necessary proteins, co-enzymes and vitamins needed for their growth and hence there will be a subsequent increase in the lag phase (Mahdi et al., 2018). Similarly, when an organism from a nutritional poor medium is added to a nutritionally rich medium, the organism can easily adapt to the environment, it can start the cell division without any delay and therefore will have less lag phase or lag phase may even be absent (Ughy et al., 2023).

During the exponential phase, the bacteria are in a rapidly growing and dividing state, hence the metabolic activities are increased and the organism begin the DNA replication by binary fusion at a constant rate (Parveen et al., 2024). The growth medium is exploited at the maximal rate, the culture reaches the maximum growth rate and the number of bacteria increases logarithmically (exponentially), this could be the reason why increase was recorded in the reaction mixture during the second week. As the bacterial population continues to grow, the nutrients in the growth medium are used up by the microorganism for their rapid multiplication. This resulted in the accumulation of waste material, toxic metabolites and inhibitory compounds such as antibiotics in the medium (Wadhwa et al., 2024; Anumudu et al., 2024). This shifts the condition of the medium such as pH, temperature and concentration thereby, creating an unfavourable environment for the bacterial growth. This could be the reason for decrease in the rate of degradation in the reaction mixture. The bacterial metabolic activity likely slowed, and cell division may have ceased as the cultures entered the death phase.

Polyethylene biodegradation observed in this study is consistent with previous reports showing that, under suitable conditions, bacteria can mineralize polymer fragments through enzymatic action (Koch and Mihalyi, 2018; Ashok and Rejeesh, 2019). Furthermore, certain additives such as iron, cobalt, manganese, and calcium are known to enhance polyethylene degradability (Montazer et al., 2020), which may partly explain the breakdown observed in our isolates.

The temperature of a medium is always as one of the key factors for the enzyme activity of the microorganisms present, regardless of whether the enzymes are intracellular or extracellular. Since enzymes are biochemical catalysts, partially made up of protein, they are sensitive to heat in varying degrees. Raising temperatures of the environment generally multiplies the degree of enzyme activity. Once an optimum temperature has been reached, higher temperatures cause rapid degradation of the enzyme with concurrent and irreversible loss in activity (Zhang et al., 2018). For *P. aeruginosa*, optimal temperatures generally range from 30 °C to 44 °C (Hussein et al., 2015; Su et al., 2018). In this study, both isolates degraded polyethylene effectively at 37–45 °C, but activity declined at 50 °C, where *P. aeruginosa* did not grow and *K. quasipneumoniae* achieved only about 5% degradation. These results suggest that temperature strongly influences the metabolic efficiency of both organisms, with higher values likely inhibiting enzyme stability and overall biodegradation performance.

The results also showed that the highest degradation occurred at pH 6 and 7, while activity decreased at pH 8 (Figures 7 and 8). This implies that *Pseudomonas* and *Klebsiella* thrive best under slightly acidic to neutral conditions, whereas alkaline conditions reduce their degradation ability. This is consistent with the findings of Mouafo et al. (2021), who reported lower degradation at more extreme acidic conditions compared to near-neutral conditions.

The effects of different concentrations on biodegradation of polyethylene are expressed in Figures 9 and 10. At 0.6 g, *Pseudomonas aeruginosa* and *Klebsiella quasipneumoniae* achieved their highest degradation rates (53.3% and 41.7%, respectively), while lower concentrations (0.2 g and 0.4 g) resulted in reduced degradation. Similarly, in a study conducted by Zhang et al. (2023), a strain of *Klebsiella pneumoniae* Mk-1 degraded polyethylene films, though at a much lower rate, with a weight loss of 2.21% after 30 days. Likewise, Awasthi et al. (2017) reported that *Klebsiella pneumoniae* CH001 degraded 18.4% of thermally pretreated HDPE after 60 days.

It could be possible that both organisms may not readily degrade polyethylene under natural environmental conditions. This could be due to the fact that soil of a dumpsite is rich in methane which bacteria can readily access and utilize as its carbon source while the carbon in polyethylene is not readily available. Landfills provide ideal conditions for methanogenesis with lots of organic material and anaerobic conditions prevalent. The huge number of wastes that is buried in landfill sites can mean that methane is produced for years after the site is closed due to waste slowly decaying under the ground and hence methane is always available in the soil and to microbes present in soil. The case is slightly different in the case of laboratory as once the organism exhausts the carbon and nitrogen in the medium, it starts to tap from the polyethylene carbon backbone. This shows that degradation of polyethylene in the natural environment of the microorganisms might never be significant and huge amount will keep accumulating thus their disposal evoking a big ecological issue.

## CONCLUSION

From this study, *Pseudomonas aeruginosa* and *Klebsiella quasipneumoniae* were successfully isolated from dumpsite soils in the Hanwa area of Zaria, Kaduna State. Both strains showed capability in breaking down polyethylene under laboratory conditions. *Pseudomonas aeruginosa* recorded the highest degradation rate of 53.3%, while *K. quasipneumoniae* reached 41.7% after 21 days. It was

observed that the extent of degradation was influenced by environmental factors such as temperature, pH and polyethylene concentration. Optimal degradation occurred at temperatures between 37°C and 45°C and at slightly acidic neutral pH levels (6-7). At 50°C and under more alkaline conditions (pH), the rate of degradation dropped noticeably. The findings show that native bacteria from polluted soils can adapt to use polyethylene as a carbon source, leading to partial breakdown through their metabolic activity. Although the degradation rate was moderate, it highlights the potential of *Pseudomonas aeruginosa* and *Klebsiella quasipneumoniae* as useful agents for polyethylene bioremediation. With further optimization, these bacteria could play an important role in sustainable efforts to reduce plastic pollution.

## RECOMMENDATIONS

Some extracellular enzymes are responsible for the biodegradation of polymers. These enzymes should be characterized and the catabolic genes responsible for those enzymes with polymer utilizing ability should be identified. Also, it is recommended to understand the mechanisms responsible for the biodegradation of these polymers. Once the genes responsible for the degradation of the polymers are identified and the mechanism understood, they could be manipulated to make biodegradation more efficient. After field trials, the most efficient polymer degrading microbes should be multiplied at large scale to decompose the polymer at commercial level in order to curb the menace of polymer pollution.

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