Science World Journal Vol. 21(No 2) 2026 https://dx.doi.org/10.4314/swj.v21i2.53
www.scienceworldjournal.org
ISSN: 1597-6343 (Online), ISSN: 2756-391X (Print)
Published by Faculty of Science, Kaduna State University

Full Length Research Article

BIODEGRADATION OF EXPANDED POLYSTYRENE BY BACTERIAL ISOLATES FROM SELECTED DUMPSITES IN KADUNA SOUTH, NIGERIA

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ABSTRACT
Expanded polystyrene (EPS) is a petroleum-based plastic widely used in food packaging, insulation, and disposable products. Its resistance to natural degradation contributes significantly to environmental pollution and accumulation in terrestrial and aquatic ecosystems. This study investigated the biodegradation potential of bacterial isolates recovered from selected dumpsites in Kaduna South, Kaduna State, Nigeria. Soil samples were collected from domestic waste dumpsites, and bacterial isolates were recovered using standard microbiological techniques. The biodegradation potential of the isolates was evaluated using a weight-loss method over a 60-day incubation period. Isolates G, M, and P, which exhibited comparatively higher and consistent biodegradation efficiencies, were further characterized using biochemical tests and 16S rRNA gene sequencing. Biodegradation data were analyzed using repeated measures ANOVA at $p < 0.05$. Seventeen bacterial isolates were recovered and exhibited varying biodegradation efficiencies ranging from 6.59% to 61.52%. Isolate G, molecularly identified as *Bacillus* sp. strain GSKN, recorded the highest biodegradation efficiency (61.52%) after 60 days of incubation. Molecular characterization identified the remaining selected isolates as *Bacillota* bacterium strain MSKN and *Pseudoxanthomonas* sp. strain PSKN. The obtained nucleotide sequences were deposited in the NCBI GenBank database under accession numbers PZ345677, PZ345678, and PZ345679, respectively. The findings demonstrate that bacterial isolates from dumpsite soils can degrade EPS and highlight their potential for environmentally sustainable strategies to manage plastic-polluted environments.

Keywords: *Bacillus*; biodegradation; expanded polystyrene; indigenous bacteria; plastic pollution; *Pseudoxanthomonas*.

INTRODUCTION

Plastic pollution has become a major environmental challenge due to the extensive production, utilization, and disposal of synthetic polymers in terrestrial and aquatic ecosystems (Andrady & Neal, 2009). Among these polymers, expanded polystyrene (EPS) is widely used in food packaging, disposable containers, and insulation materials because of its lightweight, durable, and shock-absorbing properties. However, the hydrophobic nature and stable carbon backbone of EPS make it highly resistant to natural degradation, resulting in its persistence and accumulation in the environment (Ho *et al*., 2018; Gu, 2021).

The increasing consumption of plastic products, coupled with inadequate waste management practices, has led to the accumulation of plastic debris in soils, drainage systems, and water bodies, particularly in developing countries. Conventional plastic waste management methods such as landfilling and incineration are associated with several environmental concerns, including greenhouse gas emissions, release of toxic compounds, and long-term persistence of plastic residues (Hopewell *et al*., 2009).

Microbial biodegradation has emerged as a promising and environmentally sustainable approach to managing plastic pollution. Various microorganisms can colonize plastic surfaces and utilize polymeric materials as carbon and energy sources through enzymatic and oxidative processes. Bacterial genera such as *Bacillus*, *Pseudomonas*, and *Acinetobacter* have been reported to degrade hydrocarbon-based plastics under different environmental conditions (Jadaun *et al*., 2022; Wei & Zimmermann, 2017). Previous studies have demonstrated the biodegradation potential of microorganisms isolated from plastic-contaminated environments, highlighting their role in the natural attenuation of plastic wastes (Auta *et al*., 2018; Ogunbayo *et al*., 2019; Zhang *et al*., 2024).

Despite the growing interest in microbial degradation of plastics, information on bacterial isolates capable of degrading EPS in Kaduna State, Nigeria, remains limited. Therefore, this study investigated the biodegradation potential of bacterial isolates recovered from selected dumpsites in Kaduna South, Kaduna State, Nigeria, and characterized selected high-performing isolates using biochemical and molecular techniques.

MATERIALS AND METHODS

Materials

The materials used in this study included Expanded polystyrene (EPS) foam takeaway containers obtained from Central Market, Kaduna. Microbiological culture media consisted of nutrient agar and nutrient broth, along with other analytical-grade microbiological reagents. Molecular biology components included the AccuPrep Genomic DNA Extraction Kit (Bioneer, South Korea), the Ribose-1 forward primer (5'-GGACTACAGGGTATCTAAT-3') and the Ribose-2 reverse primer (5'-AGAGTTTGATCCTGG-3')

METHODS

Study Area and Sample Collection

Soil samples were collected aseptically from domestic waste dumpsites located at Kurmin Mashi, Tudun Wada, and Ungwan Muazu in Kaduna South Local Government Area, Kaduna State, Nigeria. Samples were obtained from 10 randomly selected points at a depth of 0–15 cm and transported to the Biotechnology Laboratory at the Nigerian Defence Academy, Kaduna, for analysis.

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Preparation of Expanded Polystyrene Fragments
Expanded polystyrene foam takeaway containers were washed thoroughly with distilled water, air-dried, and cut into fragments measuring approximately 1 × 1 cm prior to use.

Physicochemical Analysis of Soil Samples
The physicochemical properties of the soil samples were analyzed to determine environmental conditions influencing microbial activity and the biodegradation of polystyrene. The parameters assessed included soil pH, electrical conductivity (EC), water holding capacity, and moisture content.

Determination of soil pH
Soil pH was determined using a calibrated digital pH meter. Ten grams (10 g) of air-dried soil sample was weighed into a clean beaker, and 25 mL of distilled water was added to form a soil-water suspension (1:2.5 w/v). The mixture was stirred thoroughly and allowed to stand for 30 minutes. The pH meter was calibrated using standard buffer solutions (pH 4.0 and 7.0). The electrode was immersed in the supernatant, and the pH value was recorded (AOAC, 2016).

Determination of electrical conductivity (EC)
Electrical conductivity was measured using a conductivity meter. Ten grams (10 g) of soil sample was mixed with distilled water to form a soil extract, which was allowed to settle. The conductivity probe was inserted into the supernatant, and the reading was recorded. Electrical conductivity values were expressed in deciSiemens per meter (dS/m) as an indicator of the soil's ionic strength (Rhoades, 1996).

Determination of water holding capacity
Water-holding capacity was determined using a 30 g air-dried soil sample placed in a suitable container. A measured volume of 100 cm^3 of distilled water was added to saturate the soil sample. The mixture was left to stand to maximize water absorption, after which excess water was drained. The wet soil was weighed and then dried in an oven at 105 °C to constant weight. Water-holding capacity was calculated as the percentage of water retained relative to the soil's dry weight (Klute, 1986).

Determination of moisture content
Moisture content was determined using the oven-drying method. A clean, dry crucible was first weighed (W_1), after which 5 g of a fresh soil sample was added and weighed to obtain W_2. The sample was then dried in a hot-air oven at 105 °C for 24 hours until a constant weight was reached. After drying, the crucible containing the dried soil was cooled in a desiccator and reweighed to obtain W_3. The percentage moisture content was calculated using the formula:
Moisture content (%) = (W2 - W3) / (W2 - W1) × 100
(AOAC, 2016).

Isolation of Bacteria
One gram of each soil sample was suspended in 9 mL of sterile distilled water and serially diluted up to 10^{-6}. Aliquots (0.1 mL) from the 10^{-4}, 10^{-5}, and 10^{-6} dilutions were spread onto nutrient agar plates and incubated at 37°C for 24 h. Following incubation, colonies were counted and expressed as colony-forming units per gram (CFU/g) of soil. Distinct bacterial colonies were purified by repeated streaking on nutrient agar plates and stored at 4 °C for further biochemical and molecular characterization.

Characterization of Bacterial Isolates
Bacterial isolates were characterized based on their morphological and biochemical properties. Standard microbiological procedures were employed to identify isolates.

Gram Staining and Microscopy
A smear of each bacterial isolate was prepared on a clean glass slide, air-dried, and heat-fixed. The smear was flooded with crystal violet for 1 minute and rinsed with distilled water. Gram's iodine was applied for 1 minute, followed by decolorization with acetone-alcohol for a few seconds. The smear was then counterstained with safranin for 1 minute, rinsed, and air-dried. The slides were observed under a light microscope (oil immersion, 100×), and the isolates were classified as Gram-positive or Gram-negative based on their staining characteristics. Gram-positive bacteria appeared purple, while Gram-negative bacteria appeared pink (Cheesbrough, 2000).

Biochemical Tests

Catalase Test
A small portion of the bacterial colony was placed on a clean glass slide, and a drop of 3% hydrogen peroxide was added. Immediate effervescence (bubble formation) indicated a positive result, while the absence of bubbles indicated a negative result (Cappuccino & Sherman, 2014).

Oxidase Test
A small amount of bacterial colony was transferred onto oxidase reagent-impregnated filter paper. A dark purple color change within 10-30 seconds indicated a positive result, while no color change indicated a negative result (Cheesbrough, 2000).

Citrate Utilization Test
Bacterial isolates were inoculated onto Simmons citrate agar slants and incubated at 30 °C for 24-48 hours. A change in color from green to blue indicated a positive result, showing the organism's ability to utilize citrate as a sole carbon source. In contrast, the absence of color change indicated a negative result (Cappuccino & Sherman, 2014).

Coagulase Test
The coagulase test was performed by emulsifying a portion of the bacterial colony in a drop of plasma on a clean slide. The formation of visible clumps within a few seconds indicated a positive result, while no clumping indicated a negative result. This test provided additional confirmation of bacterial identity, particularly in differentiating pathogenic Staphylococcus species from non-pathogenic ones (Cheesbrough, 2000).

Triple sugar iron (TSI) Test
Bacterial isolates were inoculated into Triple Sugar Iron (TSI) agar slants by stabbing the butt and streaking the slant surface. The tubes were incubated at 30 °C for 24 hours.
Changes in color of the slant and butt, gas production, and hydrogen sulfide (H_2S) formation were observed and recorded. A yellow color indicated acid production from carbohydrate fermentation, while a red color indicated alkaline reaction. A black precipitate indicated H_2S production, while gas production was indicated by cracks or bubbles in the medium (Cappuccino & Sherman, 2014).

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Biodegradation Assay of Expanded Polystyrene

Expanded polystyrene (EPS) fragments measuring approximately 1 × 1 cm were surface-sterilized using 70% ethanol, rinsed thoroughly with sterile distilled water, air-dried, and weighed using a digital analytical balance.

Nutrient broth was prepared and dispensed as 100 mL aliquots into sterile conical flasks. Bacterial inocula were standardized to 0.5 McFarland standard, corresponding to approximately 1 × 10^6 cells/mL, before inoculation into flasks containing sterilized EPS fragments. Uninoculated flasks containing EPS fragments served as controls.

The experimental setups were incubated at 37°C for 60 days and monitored at intervals of 15, 30, 45, and 60 days. At each sampling interval, EPS fragments were recovered aseptically, washed with distilled water to remove attached biomass, air-dried, and reweighed.

The percentage biodegradation of EPS was determined using the equation adapted from Ogunbayo *et al*. (2019):

Percentage biodegradation (%) = [(Initial weight − Final weight) / Initial weight] × 100

Molecular Characterization of Selected Isolates

Isolates G, M, and P were selected for molecular characterization based on their comparatively higher and more consistent biodegradation efficiencies throughout the incubation period.

Genomic DNA was extracted using the AccuPrep Genomic DNA Extraction Kit (Bioneer, South Korea) according to the manufacturer's instructions. Amplification of the 16S rRNA gene was carried out by polymerase chain reaction (PCR) using Ribose-1 forward primer (5'-GGACTACAGGGTATCTAAT-3') and Ribose-2 reverse primer (5'-AGAGTTTGATCCTGG-3') following the method described by Danjuma *et al*. (2025). The primer pair targeted conserved regions of the bacterial 16S rRNA gene and produced an expected amplicon size of approximately 789 bp.

The amplified PCR products were sequenced, and the resulting nucleotide sequences were analyzed using the Basic Local Alignment Search Tool (BLAST) available through the National Center for Biotechnology Information (NCBI) database to identify bacteria. The obtained sequences were subsequently deposited in the NCBI GenBank database, which assigned the accession numbers PZ345677, PZ345678, and PZ345679 for *Bacillus* sp. strain GSKN, *Bacillota* bacterium strain MSKN, and *Pseudoxanthomonas* sp. strain PSKN, respectively.

Statistical Analysis

Data obtained from the biodegradation experiment were analyzed using descriptive and inferential statistical methods. The percentage biodegradation of expanded polystyrene by the bacterial isolates was calculated from weight-loss measurements obtained during the incubation period.

Descriptive statistics were used to summarize the biodegradation data, and the results were presented in tables and graphical forms. Repeated-measures analysis of variance (ANOVA) was performed using the Statistical Package for the Social Sciences (SPSS) version 32.0 to evaluate differences in biodegradation across the incubation periods (15, 30, 45, and 60 days). Mauchly's test of sphericity was used to assess the assumption of sphericity, while multivariate tests and within-subject contrasts were used to evaluate biodegradation patterns over time. Statistical significance was set at $p < 0.05$.

RESULTS

Physicochemical Properties and Total Viable Bacterial Counts of Soil Samples

The physicochemical properties and total viable bacterial counts of soil samples obtained from the selected dumpsites are presented in Table 1. Soil pH ranged from 7.32 to 9.26, indicating neutral to slightly alkaline conditions. Electrical conductivity ranged from 1.608 to 1.614 dS/m, while moisture content ranged from 10.50% to 16.32%. Water-holding capacity ranged from 30.7% to 66.7%. Total viable bacterial counts ranged from 1.14 × 10^8 to 6.40 × 10^8 CFU/g, with Ungwan Muazu recording the highest bacterial population and Kurmin Mashi recording the lowest.

Table 1: Physicochemical properties and total viable bacterial counts of soil samples

Parameter	Kurmin Mashi	Tudun Wada	Ungwan Muazu
pH	7.32	9.13	9.26
Electrical conductivity (dS/m)	1.608	1.611	1.614
Moisture content (%)	16.32	10.50	15.92
Water holding capacity (%)	63.7	66.7	30.7
Total viable bacterial count (CFU/g)	1.14 × 10^8	1.21 × 10^8	6.40 × 10^8

Values represent the measured physicochemical properties of soil samples collected from the selected dumpsites. dS/m = deciSiemens per metre; CFU/g = Colony forming units per gram.

Characterization of Bacterial Isolates

Seventeen bacterial isolates were recovered from the dumpsite soils and exhibited variations in morphological and biochemical characteristics. Based on Gram reaction, cellular morphology, and biochemical test results, the isolates were tentatively identified as members of the genera *Staphylococcus, Bacillus, Micrococcus, Salmonella, Citrobacter, Escherichia, Pseudomonas, Acinetobacter, and Pseudoxanthomonas* (Table 2).

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Table 2: Morphological, biochemical characteristics and tentative identification of bacterial isolates

Isolate Code	Gram	Shape	Catalase	Oxidase	Citrate	TSI	Coagulase	Probable Identity
A	+	Cocci	+	−	−	K/K	−	*Staphylococcus* spp
B	+	Cocci	+	−	−	K/K	−	*Staphylococcus* spp
C	+	Cocci	+	−	+	K/K	−	*Staphylococcus* spp
D	+	Cocci	+	+	+	K/K	−	*Micrococcus* spp
E	−	Rods	+	−	+	K/A (gas, H_2S)	−	*Salmonella* spp
F	+	Cocci	+	−	−	K/A	−	*Staphylococcus* spp
G	+	Rods	+	−	−	A/A	−	*Bacillus* spp
H	+	Rods	+	−	+	K/A	−	*Bacillus* spp
I	+	Cocci	+	−	+	K/A	+	*Staphylococcus aureus*
J	+	Cocci	+	−	+	K/A	−	*Staphylococcus* spp
K	−	Rods	+	−	+	K/A	−	*Citrobacter spp*
L	−	Rods	+	−	−	A/A	−	*Escherichia coli*
M	+	Cocci	+	−	+	A/A	−	*Staphylococcus* spp
N	−	Rods	+	+	+	K/K	−	*Pseudomonas* spp
O	−	Coccobacilli	+	−	+	A/A	−	*Acinetobacter* spp
P	−	Rods	+	−	+	K/K	−	*Pseudoxanthomonas* spp
Q	+	Cocci	+	−	+	A/A	−	*Staphylococcus* spp

Biodegradation of Expanded Polystyrene

The percentage biodegradation of expanded polystyrene (EPS) by the bacterial isolates during the 60-day incubation period is presented in Table 3. Biodegradation efficiency varied among the isolates throughout the study period. Isolate G recorded the highest biodegradation efficiency after 60 days of incubation (61.52%), followed by isolate Q (56.73%) and isolate M (49.35%).

Although several isolates demonstrated fluctuating biodegradation patterns during the incubation period, progressive increases in biodegradation were observed in isolates G, M, and P, which were subsequently selected for molecular characterization.

Table 3: Percentage biodegradation of expanded polystyrene by bacterial isolates

Isolate Code	Biodegradation efficiency			
	Day 15 (%)	Day 30 (%)	Day 45 (%)	Day 60 (%)
A	22.73	30.00	10.76	30.91
B	6.59	38.52	7.84	33.86
C	28.64	16.21	37.88	9.85
D	21.36	23.94	34.09	14.55
E	27.42	23.48	18.48	17.42
F	25.61	17.27	58.94	19.85
G	23.33	28.94	46.82	61.52
H	40.15	13.48	37.88	39.24
I	51.43	40.65	20.52	39.87
J	41.04	20.26	64.42	32.08
K	32.86	10.52	45.84	19.35
L	45.84	45.45	50.00	29.87
M	21.43	32.86	39.74	49.35
N	36.10	31.43	46.10	18.44
O	25.27	21.09	38.18	31.27
P	7.09	10.36	34.36	38.91
Q	30.36	-9.64	25.45	56.73
Control	-0.34	-25.00	16.36	-3.75

The biodegradation trends of selected isolates G, M, and P are

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ISSN: 1597-6343 (Online), ISSN: 2756-391X (Print)
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presented in Figure 1.

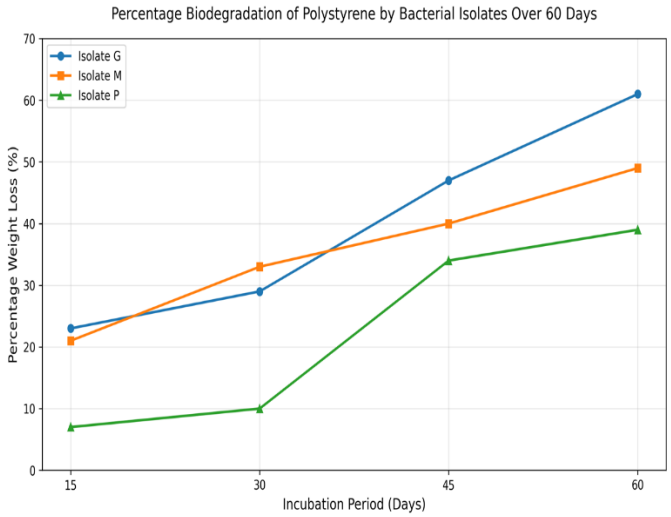

Figure 1: Percentage biodegradation of expanded polystyrene by selected bacterial isolates during a 60-day incubation period.

Figure 1 illustrates the biodegradation trends of selected isolates G, M, and P throughout the incubation period. Isolate G exhibited the highest biodegradation activity, increasing from 23.33% on Day 15 to 61.52% on Day 60. Isolate M demonstrated a gradual increase from 21.43% to 49.35%, while isolate P increased from 7.09% to 38.91% during the same period.

Statistical Analysis of Biodegradation Data

Repeated measures ANOVA was performed to evaluate differences in biodegradation across the incubation periods (15, 30, 45, and 60 days). Mauchly's test of sphericity indicated that the assumption of sphericity was met ($p = 0.606$); therefore, no correction was applied to the degrees of freedom.

The multivariate test based on Wilks' Lambda showed no statistically significant difference in biodegradation across the incubation periods ($F(3,14) = 2.049$, $p = 0.153$). Similarly, within-subject contrasts revealed no significant linear ($p = 0.137$) or quadratic ($p = 0.861$) trends in biodegradation over time. However, the cubic trend approached significance ($p = 0.051$), suggesting possible variation in biodegradation patterns during the incubation period.

Molecular Characterization of Selected Isolates

Selected isolates G, M, and P, which showed relatively consistent increases in biodegradation throughout the incubation period, were subjected to molecular characterization by 16S rRNA gene sequencing. PCR amplification of the 16S rRNA gene produced distinct amplicons of approximately 789 bp in all selected isolates (Figure 2).

Sequence analysis using BLAST identified isolate G as *Bacillus* sp. strain GSKN, isolate M as *Bacillota* bacterium strain MSKN, and isolate P as *Pseudoxanthomonas* sp. strain PSKN. The nucleotide sequences were subsequently deposited in the NCBI GenBank database and assigned accession numbers PZ345677, PZ345678, and PZ345679, respectively (Table 4). Molecular characterization revealed that isolate M, tentatively identified as *Staphylococcus* spp. Based on biochemical characteristics, it was identified as *Bacillota* bacterium strain MSKN following 16S rRNA gene sequencing, highlighting the greater discriminatory power of molecular techniques.

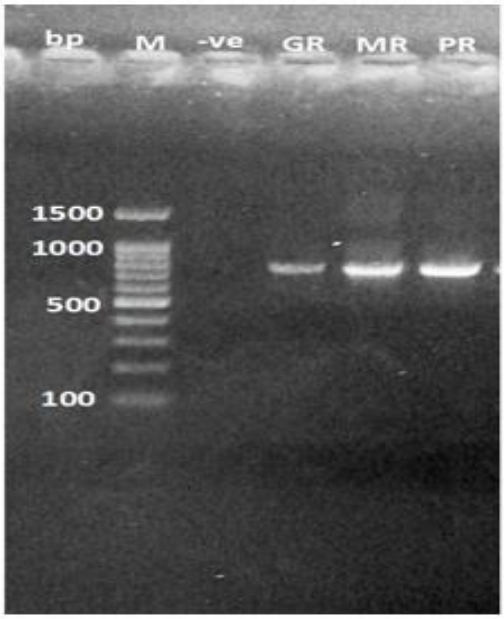

Figure 2: Agarose gel electrophoresis of PCR-amplified 16S rRNA gene fragments of selected bacterial isolates.
Lane M = DNA marker; Lane –ve = negative control; Lane GR = isolate G; Lane MR = isolate M; Lane PR = isolate P.

Table 4: Molecular identification and GenBank accession numbers of selected bacterial isolates

Isolate Code	Molecular Identification	Accession Number
G	*Bacillus* sp. strain GSKN	PZ345677
M	*Bacillota* bacterium strain MSKN	PZ345678
P	*Pseudoxanthomonas* sp. strain PSKN	PZ345679

DISCUSSION

The physicochemical properties of the dumpsite soils observed in this study suggest that the sampled environments provided favourable conditions for microbial growth and metabolic activity. The neutral-to-alkaline pH values and relatively high bacterial populations recorded across the dumpsites indicate that these environments support diverse microbial communities capable of adapting to waste-contaminated conditions. Similar observations have been reported for plastic-contaminated environments, where prolonged exposure to pollutants promotes the development of microbial populations with enhanced biodegradation potential (Gu, 2021).

The high total viable bacterial counts obtained in this study further demonstrate the suitability of dumpsite soils as reservoirs of metabolically diverse microorganisms. Polluted environments have been recognized as important sources of plastic-degrading bacteria due to continuous exposure to synthetic polymers and other organic pollutants. Miloloža *et al*. (2022) similarly isolated polystyrene-degrading *Bacillus* and *Pseudomonas* species from contaminated environmental samples, highlighting the importance of such environments in the search for plastic-degrading

microorganisms.

The morphological and biochemical characterization of the isolates revealed the presence of diverse bacterial groups, including members of the genera *Bacillus*, *Staphylococcus*, *Pseudomonas*, *Acinetobacter*, and *Pseudoxanthomonas*. The occurrence of these bacterial groups in waste-contaminated soils reflects their ecological adaptability and metabolic versatility. *Bacillus* species were among the predominant bacterial groups recovered, likely due to their ability to form endospores and survive under environmentally stressful conditions, as previously reported by Auta *et al*. (2018).

The biodegradation assay demonstrated that the bacterial isolates possessed varying capacities to degrade expanded polystyrene. The observed differences in biodegradation efficiency among the isolates may be tentatively attributed to variations in enzymatic activity, microbial attachment, biofilm formation, growth rate, and adaptation to the polymer substrate, as suggested by similar microbial systems (Amobonye *et al*., 2021; Zhang *et al*., 2022). Similar variability in polystyrene biodegradation has been reported by Seo *et al*. (2026), who observed strain-dependent differences in the biodegradation potential of bacterial isolates recovered from weathered expanded polystyrene waste.

Among the isolates investigated, isolate G, molecularly identified as *Bacillus* sp. strain GSKN, exhibited the highest biodegradation efficiency (61.52%) after 60 days of incubation. This value was considerably higher than the 13.17% degradation of polystyrene reported for *Microbacterium esteraromaticum* SW3 after 21 days by Zhang *et al*. (2024), the 6.04 ± 0.98% weight loss reported for *Flavobacterium* strain BS5 after 30 days by Seo *et al*. (2026), and the 7.73% and 7.40% degradation reported for *Gordonia* sp. and *Exiguobacterium* sp., respectively, by Kim *et al*. (2024). The comparatively higher degradation efficiency observed in the present study may be attributed to the extended incubation period, the adaptation of indigenous isolates to waste-contaminated environments, and differences in experimental conditions.

Repeated measures ANOVA revealed no statistically significant differences in biodegradation across the incubation periods. Although numerical variations in biodegradation were observed throughout the study, the absence of significant differences suggests that biodegradation did not follow a uniform time-dependent pattern across all isolates. The near-significant cubic trend observed may indicate fluctuations in microbial activity and substrate utilization during the incubation period.

Molecular characterization of selected isolates identified them as *Bacillus* sp. strain GSKN, *Bacillota* bacterium strain MSKN, and *Pseudoxanthomonas* sp. strain PSKN. The identification of *Bacillus* species as among the most efficient degraders is consistent with previous studies demonstrating their involvement in the biodegradation of hydrocarbon-based polymers (Jadaun *et al*., 2022). Likewise, the detection of *Pseudoxanthomonas* species further supports the role of environmentally adapted bacteria in the degradation of recalcitrant organic compounds. The successful recovery of these bacteria from dumpsite soils highlights the importance of indigenous microbial resources in developing sustainable biotechnological approaches to plastic waste management.

The deposition of the nucleotide sequences in the NCBI GenBank database provides molecular evidence supporting the identity of the isolates. It contributes valuable sequence information for future studies on microbial degradation of synthetic polymers.

Conclusion

This study demonstrated that bacterial isolates recovered from selected dumpsites in Kaduna South, Kaduna State, Nigeria, can biodegrade expanded polystyrene under laboratory conditions. Seventeen bacterial isolates were recovered and exhibited varying biodegradation efficiencies, with isolate G achieving the highest (61.52%) after 60 days of incubation. Molecular characterization identified selected isolates as *Bacillus* sp. strain GSKN, *Bacillota* bacterium strain MSKN, and *Pseudoxanthomonas* sp. strain PSKN, and the obtained sequences were deposited in the NCBI GenBank database.

The findings highlight the potential of indigenous bacterial isolates as environmentally sustainable agents for the biodegradation of expanded polystyrene and support their possible application in the bioremediation of plastic-polluted environments.

Further studies should investigate the enzymatic mechanisms involved in expanded polystyrene degradation and evaluate the biodegradation efficiency of microbial consortia under field conditions.

Acknowledgements

The authors acknowledge the Department of Biotechnology, Nigerian Defence Academy, Kaduna, Nigeria, for providing laboratory facilities and technical support. The authors also acknowledge DNA Labs, Kaduna, Nigeria, and Inqaba Biotechnical Industries, Ibadan, Nigeria, for molecular analysis and sequencing services.

Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Funding

This research received no specific grant from funding agencies in the public, commercial, or not-for-profit sectors.

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