Full Length Research Paper

RKGP Journal of Environmental Microbiology and Microbial Ecology
ISSN: 1595-3335

Volume 1(2), pages 08-15, January 2026
ISSN :1595-3335
https://doi.org/101.32235/RKGP-JEMME2025.013
https://rkgpjournals.org/index.php/RJEMME/index

Valorization of poultry feather with poultry litters and evaluation of effects on the microbial biota, minerals and plant growth potential

Linda U. Obi*, Peace A. Obiefule, Victor C. Ekemezie and Frances N. Olisaka

Department of Biological Sciences, Godfrey Okoye University, Enugu, Enugu State, Nigeria.

*Corresponding author. Email: linda@gouni.edu.ng.

Received December 21, 2025; Revised January 19, 2026; Accepted January 21, 2026

The persistence and accumulation of keratin-rich poultry feathers contribute to environmental pollution and inefficient waste disposal due to their resilient structure. Poultry litter, however, may serve as a co-substrate to enhance microbial biodegradation of feathers, thereby reducing greenhouse gas emissions and improving nutrient recovery. This study evaluated microbial and biochemical interactions during the co-degradation of feathers and poultry litter. Microbial counts (bacteria and fungi), mineral composition, and optimal substrate ratios were determined. Controlled degradation experiments in different ratios of poultry feathers to litters revealed that weight of feathers (5 g) and litter (5 g) supported the highest microbial activity. Bacterial counts increased from 1.3 × 10^3 to 3.1 × 10^4 CFU/ml, while fungal counts rose from 1.6 × 10^2 to 2.0 × 10^5 CFU/ml. Mineral analyses showed significant variations before and after degradation. The feather–litter mixture produced the highest phosphorus concentration post-degradation (14.710 mg/L), while feather-only treatments retained the most nitrogen (27.58 g/L) and potassium (12.760 mg/L). These results demonstrated that feathers delivered consistent nitrogen, while litter supplied phosphorus, potassium and organic carbon to the substrate, establishing a balanced setting that promoted microbial growth. By transforming feathers and litter into nutrient-rich hydrolysates, this strategy provides a sustainable alternative for soil amendment, reduces environmental pollution, and promotes circular bioeconomy practices.

Keywords: Poultry feathers, keratin degradation, biofertilizer potential, soil fertility, plant growth.

INTRODUCTION

Keratin is a structural protein found in feathers, wool, hair, nails, and skin. Its high cysteine content forms strong disulfide bonds, giving keratin exceptional stability and resistance to microbial degradation (Reddy *et al.,* 2021). While this durability is biologically advantageous, it poses challenges in waste management, as keratin-rich residues persist in natural environments (Verma *et al.,* 2021).

Keratin exists in two forms: α-keratin, present in mammalian hair and wool, which has a flexible helical structure; and β-keratin, found in bird feathers and reptilian scales, characterized by a rigid pleated-sheet structure (Sharma and Gupta, 2022). The persistence of β-keratin, in particular, makes feather waste from poultry farming a pressing environmental issue. Globally, poultry processing generates an estimated 40 million tons of chicken feathers annually, much of which is discarded (Gupta *et al.,* 2023). Similarly, wool processing, hair waste from salons, and domestic grooming activities add to the global keratin waste burden (Thompson *et al.,* 2023; Ali *et al.,* 2022).

Conventional disposal methods such as land filling and incineration have significant drawbacks. Land-filled keratin remains largely undegraded, consuming space and risking

Table 1. Experimental set-up of degradation of poultry feathers and litters.

Treatment ID	Poultry Feathers (% w/v)	Poultry Litter (% w/v)	Water Volume (ml)
T1	0.25 (1.25 g)	1 (5 g)	500
T2	1 (5 g)	0.25 (1.25 g)	500
T3	1 (5 g)	1 (5 g)	500
T4	1 (5 g)	0	500
T5	0	1 (5 g)	500

leachate contamination (Verma *et al.,* 2021). Incineration, though volume-reducing, releases sulfur oxides and carbon dioxide, contributing to acid rain and climate change (Zoccola *et al.,* 2023). Inappropriate disposal in natural environments can further disrupt ecosystems and wildlife (Reddy *et al.,* 2021).

Given these challenges, keratin valorization has emerged as a sustainable waste management approach. By converting keratin waste into valuable products such as biodegradable films, biofertilizers, biofuels, and cosmetic ingredients, valorization supports both environmental protection and resource efficiency (Ali *et al.,* 2022; Reddy *et al.,* 2021). For example, feather-derived hydrolysates provide nitrogen-rich fertilizers that improve soil fertility, while keratin peptides enhance cosmetic formulations (Thompson *et al.,* 2023).

Within the framework of the circular economy, keratin valorization offers dual benefits: reducing environmental pollution and creating economic opportunities. This study investigates the biodegradation of poultry feathers with poultry litter as a co-substrate, with emphasis on optimizing degradation conditions and evaluating the resulting hydrolysate for soil amendment.

MATERIALS AND METHODS

Study area and sample collection

Samples were obtained from a poultry farm and waste dumpsite at Amaechi, Enugu South, Enugu State, Nigeria. Using sterile gloves, feathers and litters were collected into zip-lock plastic bags, maintained under aseptic conditions, and stored at 4°C until analysis.

Experimental design

Five treatments (in triplicates) were set up using 500 mL of water each (Table 1): The treatments were incubated at ambient temperature for four weeks with frequent agitation. Samples were collected before and after incubation for microbial and chemical analysis.

Microbial analysis

Isolation and enumeration: Serial dilutions were plated on Nutrient Agar (for bacteria, incubated at 37°C for 24–72 h) and Potato Dextrose Agar (for fungi, incubated at 28°C for 24–72 h). Colony counts were expressed as CFU/ml (Collins *et al.,* 1989).

Identification: Representative colonies were purified and preserved as stock cultures at 4°C. Isolates were characterized using gram staining and biochemical tests including catalase, coagulase, oxidase, citrate utilization, indole, and methyl red (Meena *et al.,* 2015).

Mineral analysis

Nitrogen content was determined using the Kjeldahl method. Results were expressed as %N using the formula:

$$\%N = (V \times N \times 1.4)/W$$

Where, V = acid volume difference, N = acid/NaOH molarity, W = sample weight.

Phosphorus analysis was done by the Murphy–Riley method with absorbance measured at 700 nm while Potassium, Zinc, and Iron were measured using Atomic Absorption Spectrophotometry (AAS).

Molecular characterization of plant-growth promoting genes

PCR amplification targeted **NifH** (nitrogen fixation) and **PhoD** (phosphate solubilization) genes was performed using specific primer pairs PoL-F GC (5′- TGCGAYCCSAARGCBGACTC-3′) and Pol-R (5′- ATSGCCATCATYTCRCCGGA-3′), (Tsipinana *et al.,* 2025), and ALPS-F730 (5' CAG TGG GAC GAC CAC GAG GT-3') and primers ALPS-R1101 (5'-GAG GCC GAT CGG CAT GTC G-3') (Tsipinana *et al.,* 2025; Sakurai *et al.,* 2024; Fraser *et al.,* 2011). Amplified products were visualized on 1% agarose gels stained with ethidium bromide.

Data analysis

Data were analyzed using one-way ANOVA at a 5% significance level. Shapiro–Wilk test (α = 0.05) confirmed normality. Significant differences among treatments were further analyzed using Tukey's HSD test.

RESULTS

Total viable bacterial counts

The initial and final bacterial counts (CFU/ml) across treatments combining feather (F) and litter (L) in different proportions is presented in Table 2. The treatment with 5 g feather and 5 g litter (T1) showed a marked increase in bacterial load, rising from 1.3×10^3 to 3.1×10^4 CFU/ml. Feather-only treatments (T2) exhibited a moderate increase from 1.1×10^3 to 4.1×10^3 CFU/ml. In contrast,

Table 2. Total viable bacterial counts (CFU/ml) for different treatments.

Treatment ID	Initial Mean Bacterial Count (CFU/ml)	Final Mean Bacterial Count (CFU/ml)
T1	1.3×10^3	3.1×10^4
T2	1.1×10^3	4.1×10^3
T3	2.3×10^3	5.0×10^5
T4	1.6×10^3	2.4×10^4
T5	1.6×10^2	2.6×10^3

Table 3. Total viable fungal counts (CFU/ml) for different treatments.

Treatment ID	Initial Mean Fungal Count (CFU/ml)	Final Mean Fungal Count (CFU/ml)
T1	1.6×10^2	2.0×10^5
T2	No growth	1.8×10^3
T3	No growth	1.2×10^2
T4	No growth	1.5×10^2
T5	1.2×10^2	1.7×10^5

litter-only treatment (T3) demonstrated the highest increase, from 2.3×10^3 to 5.0×10^5 CFU/ml. Treatments with mixed ratios (T4 and T5) also showed growth, with T4 increasing from 1.6×10^3 to 2.4×10^4 CFU/ml and T5 from 1.6×10^2 to 2.6×10^3 CFU/ml.

Total viable fungal counts

Fungal growth in the different treatments is summarized in Table 3. T1 exhibited the highest fungal increase, rising from 1.6×10^2 to 2.0×10^5 CFU/ml. T2 showed no initial growth but reached 1.8×10^3 CFU/ml at the end. Similarly, T3 and T4 exhibited no initial growth but later recorded 1.2×10^2 and 1.5×10^2 CFU/ml, respectively. T5 grew from 1.2×10^2 to 1.7×10^5 CFU/ml.

Identification of bacterial isolates

Bacterial isolates were identified based on colony morphology, gram staining, and biochemical tests. Eight organisms were identified: *Escherichia coli*, *Citrobacter* spp., *Enterobacter*, *Staphylococcus* sp., *Yersinia* sp., *Bacillus* spp., *Klebsiella pneumoniae*, and *Proteus mirabilis* (Table 4). Gram-negative bacteria predominated, while Gram-positive bacteria were also present. Colony morphology, along with results from catalase, oxidase, coagulase, methyl red, and indole tests, confirmed their identity.

Morphology of fungal isolates

Three fungal genera were identified based on physical and microscopic features. *Aspergillus* sp. exhibited grayish colonies with septate hyphae, *Fusarium* sp. showed fluffy white colonies with septate hyaline hyphae, while *Penicillium* spp. displayed greenish, powdery colonies with septate hyphae and conidiophores bearing conidia (Table 5).

Prevalence of bacterial isolates

Prevalence of bacterial isolates varied across treatments. *Citrobacter* spp. (67%) and *Proteus mirabilis* (60%) were the most frequent, while *Staphylococcus* spp. (40%) and *Yersinia* sp. (33.2%) were less common (Table 6). Mixed feather-litter samples (especially T1) showed the highest diversity.

Prevalence of fungal isolates

Fungal prevalence was highest for *Aspergillus* sp. (60%), followed by *Penicillium* spp. (40%) and *Fusarium* sp. (30%) (Table 7). Feather-litter ratios (T1) supported the greatest diversity, while feather-only samples showed reduced fungal growth.

Table 4. Identification of bacterial isolates.

Isolate ID	Colony Morphology	Gram Reaction	Cat	Oxi	Coa	MR	Ind	Probable Organism
1	Grayish-white, smooth, mucoid colonies (NA)	–ve rods	+	–	–	+	+	*E. coli*
2	Round, flat, colorless colonies (MAC)	–ve rods	+	–	–	+	+	*Citrobacter* spp.
3	Large yellow colonies (NA)	–ve rods	+	–	–	+	+	*Enterobacter*
4	Yellow, mucoid colonies (NA)	+ve cocci	+	–	+	+	+	*Staphylococcus* sp.
5	Very large whitish cottony colonies (NA)	+ve rods	+	–	–	+	+	*Yersinia* sp.
6	Small whitish mucoid colonies (NA)	–ve rods	+	–	–	+	+	*Bacillus* spp.
7	Pink, raised mucoid colonies (MAC)	–ve rods	+	–	+	–	–	*Klebsiella pneumoniae*
8	Raised whitish mucoid colonies (NA)	–ve rods	+	–	+	–	+	*Proteus mirabilis*

Key: *Cat = Catalase; Oxi = Oxidase; Coa = Coagulase; MR = Methyl Red; Ind = Indole; NA = Nutrient agar; MAC = MacConkey agar; + = positive; – = negative.*

Table 5. Morphological and microscopic features of fungal isolates.

Isolate ID	Colony Morphology	Microscopic Features	Probable Organism
A	Grayish colonies with white background	Septate hyphae	*Aspergillus* sp.
B	White fluffy hyphae	Septate hyaline hyphae	*Fusarium* sp.
C	Greenish/blue/white powdery colonies	Septate hyphae with conidiophores	*Penicillium* spp.

Table 6. Prevalence of bacterial isolates across treatments.

Treatment ID	Total no. of samples	*E. coli*	*Citrobacter spp*	*Proteus mirabilis*	*Klebsiella pneumoniae*	*Staphylococcus spp*	*Bacillus spp*	*Enterobacter*	*Yersinia sp.*
T1	2	1 (50%)	2 (100%)	2 (100%)	2 (100%)	1 (50%)	2 (100%)	1 (50%)	1 (50%)
T2	2	1 (50%)	1 (50%)	2 (100%)	1 (50%)	0	1 (50%)	1 (50%)	1 (50%)
T3	2	2 (100%)	1 (50%)	1 (50%)	2 (100%)	2 (100%)	0	1 (50%)	0
T4	2	2 (100%)	2 (100%)	1 (50%)	0	1 (50%)	0	1 (50%)	1 (50%)
T5	2	1 (50%)	2 (100%)	2 (100%)	1 (50%)	1 (50%)	2 (100%)	0	2 (100%)
Total	10	7 (47%)	8 (67%)	8 (60%)	6 (53.4%)	5 (40%)	5 (67%)	4 (33%)	5 (33.2%)

Table 7. Prevalence of fungal isolates across treatments.

Treatment identity	Total no. of samples	*Aspergillus sp*	*Fusarium sp.*	*Penicillium spp.*
T1	2	1 (50%)	1 (50%)	2 (100%)
T2	2	1 (50%)	1 (50%)	0
T3	2	2 (100%)	1 (50%)	0
T4	2	1 (50%)	0	1 (50%)
T5	2	1 (50%)	0	1 (50%)
Total	10	6	3	4

Mineral characterization

The mineral contents varied widely before and after biodegradation. The analysis revealed reductions in nitrogen (N), phosphorus (P), and potassium (K) after degradation, with varying significance across treatments with p-value ranged from 0.00002369 to 0.00856. For example, phosphorus decreased significantly in T1, T4, and T5 (p-value = 0.00002369, $p < 0.05$) (Figure 1a), while nitrogen and potassium reductions were significant in T2 and T4 (p-value = 0.00006163, p-value = 0.0114) respectively (Figures 1b and 1c). Iron increased in most treatments, whereas zinc reduced across the treatments (Figures 1d and 1e).

Detection of plant-growth promoting genes

PCR amplification confirmed the presence of plant-growth promoting genes: *nifH* gene (~360 bp) present in all treatments (Plate 1), indicating nitrogen-fixing potential and *phoD* gene (~380 bp), also present in all treatments (Plate 2) suggesting phosphate-solubilizing potential. These findings demonstrate that feather-litter hydrolysates harbor microbes with genes beneficial for plant growth.

DISCUSSION

Results from this study indicate that bacterial proliferation was most pronounced in treatments containing poultry litter, especially when combined with feathers. The higher counts observed in these treatments suggest that litter provides a nutrient-rich substrate particularly nitrogen and organic carbon that supports microbial growth. This observation aligns with studies reporting enhanced microbial activity in litter-rich environments (Rivera *et al.,* 2023; Chen *et al.,* 2022). In contrast, feather-only treatments supported lower bacterial counts, implying that feathers alone, being rich in keratin but low in readily available nutrients, are insufficient for robust microbial growth. These findings emphasize the importance of nutrient balance in promoting microbial activity and highlight the potential of feather–litter combinations in bioremediation and biofertilizer production (Li *et al.,* 2022; Zhou *et al.,* 2020; Smith *et al.,* 2019).

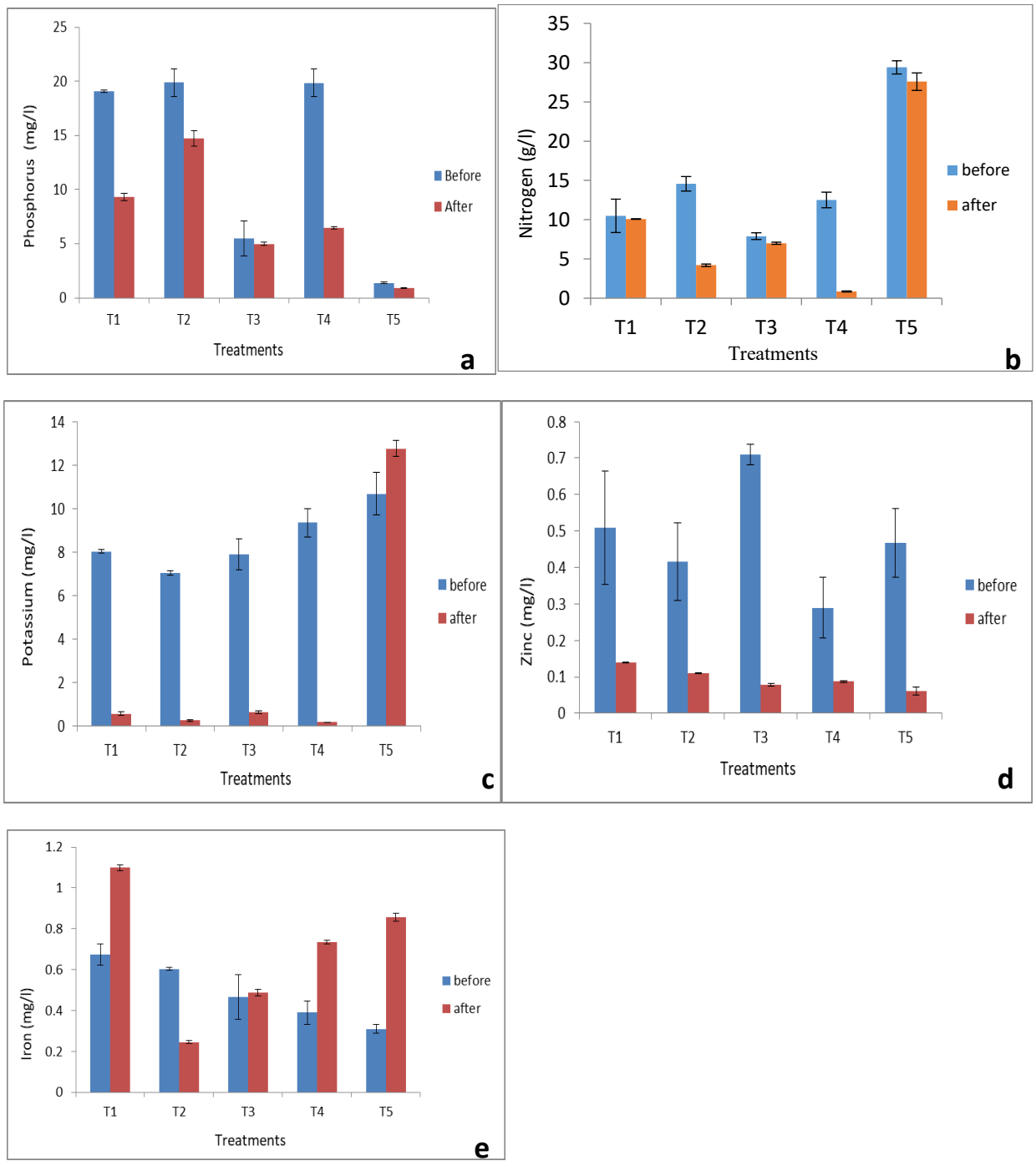

Figure 1. **a-e** shows the trends in phosphorus, nitrogen, potassium, zinc, and iron before and after degradation.

Fungal counts followed a similar pattern, with the highest growth observed in feather–litter mixtures. Treatments with litter only or small amounts of litter showed moderate fungal growth, while feather-only treatments exhibited minimal activity. These results suggest that litter supplies key nutrients required for fungal proliferation, supporting previous reports that nutrient-rich organic wastes enhance fungal colonization (Li and Wong, 2021; Smith *et al.,* 2019). Balanced feather–litter ratios appear to provide an optimal substrate for fungal activity, facilitating keratin breakdown and supporting biofertilizer potential.

Eight bacterial isolates were identified, including *E. coli*, *Citrobacter* sp., *Enterobacter*, *Staphylococcus* sp., *Yersinia* sp., *Bacillus* sp., *Klebsiella pneumoniae*, and *Proteus mirabilis*. Gram-negative species dominated, reflecting their metabolic adaptability in nutrient-rich envi-

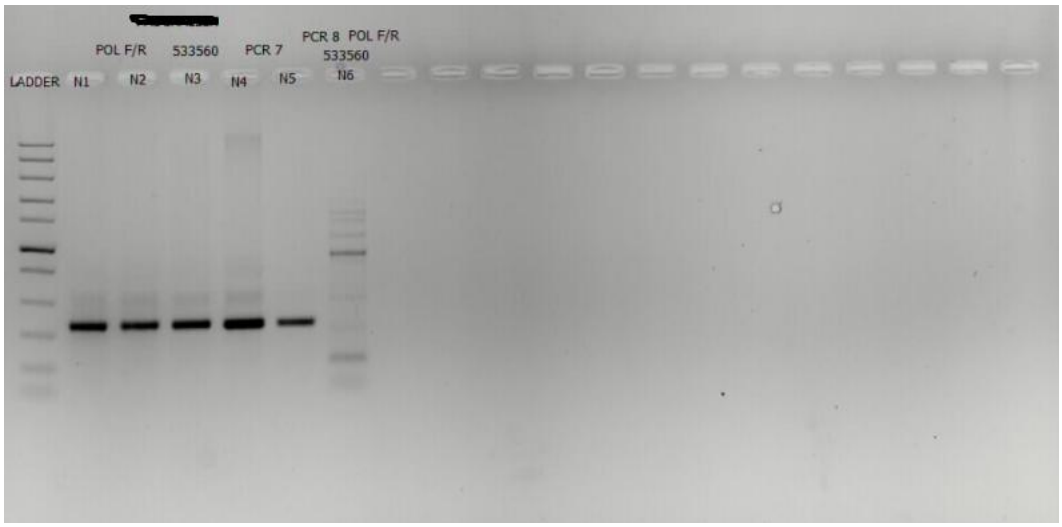

Plate 1. Agarose gel electrophoresis of *nifH* gene in the treatments. First lane = DNA ladder; Second lane, N1 = T1; Third lane, N2 = T2; Fourth lane, N3 = T3; Fifth lane, N4 = T4; Sixth lane, N5 = T5; Seventh lane = DNA Ladder.

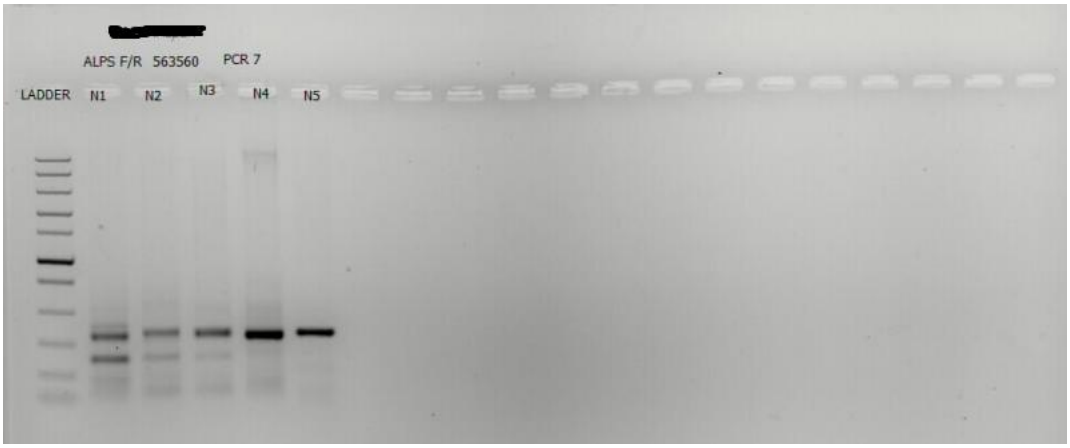

Plate 2. Agarose gel electrophoresis of *phoD* gene in the treatments. First lane = DNA ladder; Second lane, N1 = T1; Third lane, N2 = T2; Fourth lane, N3 = T3; Fifth lane, N4 = T4; Sixth lane, N5 = T5; Seventh lane = DNA Ladder.

ronments (Janda and Abbott, 2020). The presence of Bacillus spp., known producers of keratinases, highlights their role in feather degradation (Gupta and Ramnani, 2006). However, isolates such as *E. coli* and *K. pneumoniae* indicated potential pathogenic risks, underscoring the need for controlled composting systems to ensure biosafety. The observed diversity parallels findings from compost studies, which emphasize the coexistence of both degradative and opportunistic microbes (Ryckeboer *et al.,* 2003; Insam and de Bertoldi, 2007).

Three fungal genera were identified: *Aspergillus*, *Fusarium*, and *Penicillium*. Their morphological traits matched literature descriptions (Bennett and Klich, 2022; Frisvad *et al.,* 2019). *Aspergillus* and *Penicillium* are recognized for keratinolytic enzyme production, making them valuable in waste bioconversion and industrial enzyme applications (Ali *et al.,* 2020; Sharma *et al.,* 2020). While *Fusarium* sp. plays a role in nutrient cycling, its pathogenic potential requires caution. Overall, the fungal isolates reinforce the role of fungi as key contributors to organic waste degradation and soil enrichment.

Bacterial prevalence analysis showed dominance of *Citrobacter* spp. (67%) and *Proteus mirabilis* (60%), with *E. coli* also widely represented. This reflects the adaptability of these organisms to nitrogen-rich litter–feather environments. Conversely, inconsistent detection of *Staphylococcus* sp. and *Yersinia* sp. Suggests they require more specific substrates (Alori *et al.,* 2017; Sharma *et al.,* 2021). Similarly, fungal prevalence was highest for

Penicillium spp., especially in feather–litter mixtures, while *Aspergillus* dominated in litter-only samples. These findings highlight the role of litter in shaping microbial communities and confirm that balanced substrates enhance diversity (Chen *et al.,* 2020; Goyal *et al.,* 2021).

Mineral characterization revealed notable changes post-degradation. Phosphorus and nitrogen generally declined, reflecting microbial uptake during metabolism (Li*,* 2022; Sharma *et al.,* 2017). Iron levels increased in some treatments, likely due to microbial mobilization from organic matter, while zinc consistently decreased, supporting previous reports of its limited availability in keratinous substrates (Tiwari *et al.,* 2021). Potassium patterns were mixed: feather-only treatments retained or increased potassium, suggesting feathers act as a slow-release source (Xu *et al.,* 2019). These nutrient shifts confirm the complementary roles of feathers (as nitrogen reservoirs) and litter (as phosphorus and potassium contributors) in nutrient recycling, offering potential for tailored organic amendments.

Identification of plant growth promoting genes in the resulting hydrolysate is genetic evidence that feather-litter hydrolysate can be a potent microbial inoculant to support plant growth and development. This suggests that the hydrolysate can improve soil health over the long term by establishing microbes that could continuously fix atmospheric nitrogen and solubilize locked-up phosphorus, thus, reducing the need for synthetic fertilizers.

Conclusion

This study demonstrates that combining poultry feathers with litter significantly enhances microbial diversity, mineral recycling, and the potential for sustainable waste valorization. Feathers provided a steady nitrogen source, while litter enriched the substrate with phosphorus, potassium, and organic carbon, creating a balanced environment for microbial proliferation. Keratin-degrading bacteria (*E. coli*, *Proteus mirabilis*, *Bacillus* spp.) and fungi (*Aspergillus*, *Penicillium*) were identified as key players in feather decomposition, emphasizing their biotechnological potential in producing biofertilizers and enzymes. However, the presence of opportunistic pathogens such as *Klebsiella pneumoniae* highlights the importance of controlled composting systems to ensure biosafety. Mineral characterization revealed active nutrient transformations, with phosphorus and zinc being depleted, nitrogen released gradually, and iron mobilized during decomposition. These findings support the integration of feather–litter mixtures into circular agriculture as sustainable organic amendments. To our knowledge, this is the first study to optimize feather degradation by identifying the optimal feather-to-litter ratio. Future studies could focus on characterizing keratinase and other degradative enzymes, and scaling up controlled bioreactors. Such approaches could maximize waste reduction, enhance soil fertility, and contribute to environmentally sustainable poultry waste management.

ACKNOWLEDGEMENT

The authors acknowledge the guidance and supervision of Dr. Linda U. Obi. We also thank colleagues in the Department of Biological Sciences, Godfrey Okoye University, Enugu, Nigeria, for their academic and technical support. The Biotechnology Laboratory, Godfrey Okoye University, is acknowledged for providing the facilities used in this study.

Conflict of Interest: The authors hereby declare that no conflicting interest exists among them.

REFERENCES

Ali, N., Dashti, N., Khanafer, M., Al-Awadhi, H., and Radwan, S. (2020). Bioremediation of soils saturated with spilled crude oil. *Scientific Report,* **10:** 1116. https://doi.org/10.1038/s41598-019-57224-x.

Ali, S., Ullah, M.A., Nawaz, A., Naz, S., Shah, A.A., Gohari, G., and Razzaq, K. (2022). Carboxymethyl cellulose coating regulates cell wall polysaccharides disassembly and delays ripening of harvested banana fruit. *Postharvest Biology and Technology,* **191(2022):** 111978.

Bennett, J.W., and Klich, M. (2003). Mycotoxins. *Clinical Microbiology Reviews*, **16(3):** 497–516.

Chen F, Ghosh A, Lin J. (2020). *5*-lipoxygenase pathway and its downstream cysteinyl leukotrienes as potential therapeutic targets for Alzheimer's disease. *Brain Behav. Immun. Retrieved from:* https://doi.org/10. 1016/j.bbi.2020.03.022

Chen, H., Gao, S., Li, Y., Xu, H.J., Li, W., Wang, J., and Zhang, Y. (2022). Valorization of livestock keratin waste: application in agricultural fields. *International Journal of Environmental Research and Public Health*, **19(11):** 6681.

Chen, H., Gao, S., Li, Y., Xu, H.J., Li, W., Wang, J., and Zhang, Y. (2022). Valorization of livestock keratin waste: application in agricultural fields. *International Journal of Environmental Research and Public Health*, **19(11):** 6681.

Collins, C.H., Lyne, P.M., Grange, J.M., and Falkinham, J.O. (1989). *Microbiological methods,* Sixth Edition. New York: Oxford University Press.

Fraser, R.D.B., and Parry D.A.D. (2011). The structural basis of the filament-matrix texture in the avian/reptilian group of hard β-keratins. *J. Struct. Biol,* **173:** 391–405. 10.1016/j.jsb.2010.09.020.

Frisvad, J.C., Hubka, V., Ezekiel, C.N., Hong, S.B., Nováková, A., Chen, A.J. (2019). Taxonomy of aspergillus section flavi and their production of aflatoxins, ochratoxins and other mycotoxins. *Stud. Mycol.* **93:** 1–63. doi:10.1016/j.simyco.2018.06.001.

Goyal, S., Chauhan, S., and Mishra, P. (2021). Circular economy research: A bibliometric analysis (2000–2019) and future research insights. *J. Clean. Prod., 287*(2021). 10.1016/j.jclepro.2020.125011.

Gupta, R., and Ramnani, P. (2006). Microbial keratinases and their prospective applications: An overview. *Appl. Microbiol. Biotechnol.* **70:** 21–33. doi: 10.1007/s00253-005-0239-8.

Gupta, S., Sharma, S., Aich, A., Verma, A.K., Bhuyar, P., Nadda, A.K., and Kalia, S. (2023). Chicken feather waste hydrolysate as a potential biofertilizer for environmental sustainability in organic agriculture management. *Waste and Biomass Valorization*, **14(9):** 2783-2799.

Insam, H., and Bertoldi, M. (2007). Chapter 3 microbiology of the composting process. *Compost Science and Technology,* **8:** 10. doi: 1016/S1478-7482(07)80006-6.

Li, Q. (2022). Perspectives on converting keratin-containing wastes into biofertilizers for sustainable agriculture. *Frontiers in microbiology*, **13:** 918262.

Li, Y., Cheng, H., Yu, M., Han, C., and Shi, H. (2022). Blends of biodegradable poly (ε-caprolactone) and sustainable poly (propylene carbonate) with enhanced mechanical and rheological properties. *Colloid Polym. Sci.,* pp. 1-10.

Meena, V.S., Maurya, B.R., and Bahadur, I. (2015). Potassium solubilization by bacterial strain in waste mica. *Bangladesh Journal of Botany*, **43(2):** 235–237. https://doi.org/10.3329/bjb.v43i2.21680.

Reddy, C.C., Mahmood, S., Mohd Safe, S.N.B., Arifn, M.A.B., Gupta, A., Sikkandar, M.Y., Begum, S.S., and Narasaiah, B. (2021). Extraction and application of keratin from natural resources: A review. *Biotech,* **11(220):** 1-12. https://doi.org/10.1007/s13205-021-02734-7

Rivera, F., Akpan, J., Prádanos, P., Hernández, A., Palacio, L., and Muñoz, R. (2023). Side-stream membrane-based NH3 extraction to improve the anaerobic digestion of poultry manure. *Journal of Water Process Engineering,* **54:** 103990. https://doi.org/10.1016/j.jwpe.2023.103990.

Ryckeboer, J., Mergaert, J., Vaes, K., Klammer, S., De Clercq, D., Coosemans, J., Insam, H., and Swings, J. (2003). A survey of bacteria and fungi occurring during composting and self-heating processes. *Annals of Microbiology,* **53:** 349-410.

Sakurai, Y.C.N., Pires, I.V., Ferreira, N.R., Moreira, S.G.C., da Silva, L.H.M., Da, A.M., and Rodrigues, C. (2024). Preparation and characterization of natural deep eutectic solvents (NADESs): Application in the extraction of phenolic compounds from Araza Pulp (Eugenia Stipitata). *Foods*, **13:** 10.3390/foods13131983.

Sharma, C., Gupta, R., and Singh, M. (2022). Chicken feather waste valorization into nutritive protein hydrolysate. *Frontiers in Microbiology,* **13:** 894512.

Sharma, C., Salem, G.E.M., Sharma, N., Gautam, P., and Singh, R. (2020). Thrombolytic potential of novel thiol-dependent fibrinolytic protease from *Bacillus cereus* RSA1. *Biomolecules.* **10:** 3. doi:10.3390/biom10010003.

Sharma, S., Gupta, A., Chik, S., Kee, C.G., Mistry, B.M., Kim, D.H., and Sharma, G. (2017). Characterization of keratin microparticles from feather biomass with potent antioxidant and anticancer activities. *Int. J. Biol. Macromol.* **104:** 189–196.

Smith, S.D., Colgan, P., Yang, F., Rieke, E.L., Soupir, M.L., Moorman, T.B., Allen, H.K., and Howe, A. (2019). Investigating the dispersal of antibiotic resistance associated genes from manure application to soil and drainage waters in simulated agricultural farmland systems. *PLOS ONE*, **14(9):** e0222470. https://doi.org/10.1371/journal.pone.0222470.

Verma, M.K., Shakya, S., Kumar, P., Madhavi, J., Murugaiyan, J., and Rao, M.V.R. (2021). Trends in packaging material for food products: Historical background, current scenario, and future prospects. *Journal of Food Science and Technology,* **58(11):** 4069-4082.

Xu, Z., Shi, L., Yang, M., and Zhu, L. (2019). Preparation and biomedical applications of silk fibroin-nanoparticles composites with enhanced properties - A review. *Materials Science and Engineering: C*, **95:** 302–311. https://doi.org/10.1016/j.msec.2018.11.010.

Zhou, Y., Li, Y., Zhang, L., Wu, Z., Huang, Y., Yan, H., Zhong, J., Wang, L. J., Abdullah, H.M., and Wang, H.H. (2020). Antibiotic administration routes and oral exposure to antibiotic resistant bacteria as key drivers for gut microbiota disruption and resistome in poultry. *Front. Microbiol.,* **11:** 1319. doi:10.3389/fmicb.2020.01319.