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Microbiological Assessment and Public Health Risk Potential of Fresh Cow Dung from Selected Locations in Gwagwalada, Abuja, Nigeria

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Abstract

Fresh cow dung is widely used as an organic fertilizer because of its high nutrient content and beneficial effects on soil fertility. However, it may also harbour microorganisms of environmental and public health importance. This study investigated the Microbiological Assessment and Public Health Risk Potential of Fresh Cow Dung collected from four locations (Old Kutunku Abattoir, University of Abuja environment, Gwako and Giri) in Gwagwalada, Abuja, Nigeria. Fresh cow dung samples were collected aseptically and analysed using standard microbiological techniques. Serially diluted samples were cultured on Nutrient Agar, MacConkey Agar and Potato Dextrose Agar using the spread plate technique, with the 10^{-3} dilution used for plating. Bacterial isolates were identified based on cultural characteristics, Gram staining and biochemical tests, while fungal isolates were identified using colony morphology and lactophenol cotton blue microscopy. Total viable bacterial counts on Nutrient Agar ranged from 3.50×10^4 to 6.10×10^5 CFU/mL, while total enteric bacterial counts on MacConkey Agar ranged from 4.50×10^4 to 7.00×10^5 CFU/mL. The lowest counts were recorded at Giri, with 3.50×10^4 CFU/mL on Nutrient Agar and 4.50×10^4 CFU/mL on MacConkey Agar, whereas the highest counts were recorded at the University of Abuja environment, with 6.10×10^5 and 7.00×10^5 CFU/mL, respectively. Six bacterial taxa (*Staphylococcus aureus*, *Streptococcus* sp., *Bacillus* sp., *Escherichia coli*, *Proteus mirabilis* and *Salmonella* spp.) and three fungal taxa (*Aspergillus* sp, *Mucor* sp. and *Rhizopus* sp.) were identified. Although bacterial counts varied among locations, the differences were not statistically significant ($p > 0.05$). The findings demonstrate that fresh cow dung contains diverse microorganisms, including organisms of public health significance. Proper handling and treatment before agricultural application are recommended to minimize environmental contamination and potential health risks.

Introduction

Cow dung is one of the most abundant livestock wastes generated worldwide and is widely used as an organic fertilizer because of its high nutrient content and ability to improve soil fertility, aeration and water-holding capacity. It contains appreciable quantities of nitrogen, phosphorus, potassium and several micronutrients that enhance plant growth

and support soil microbial activity. Consequently, cow dung is an important component of sustainable agricultural practices, particularly in developing countries where organic manure remains a major alternative to inorganic fertilizers, with additional applications in crop production, biogas generation and environmental management (Food and Agriculture Organization [FAO], 2001; Sharma et al., 2021). In Gwagwalada, where agricultural activities, livestock production and expanding urban settlements occur in close proximity, the use and handling of cow dung may facilitate the dissemination of potentially harmful microorganisms within the local environment, making its microbiological assessment relevant to public health in Abuja.

Beyond its agronomic benefits, cow dung serves as a natural habitat for a diverse microbial community comprising bacteria, fungi, protozoa and other microorganisms. Many of these microorganisms contribute positively to the decomposition of organic matter and nutrient recycling, thereby maintaining soil productivity. However, fresh cow dung may also harbour microorganisms of public health importance, including enteric and opportunistic pathogens capable of contaminating agricultural soils, irrigation water, crops and surrounding environments when manure is improperly handled or applied without adequate treatment (World Health Organization [WHO], 2022; Jauregi et al., 2021). The microbial composition of cow dung is influenced by several factors, including animal diet, age, environmental conditions, geographical location and manure management practices (Gurmessa et al., 2021; Zalewska et al., 2024; Neupane et al., 2021).

Several bacterial genera frequently associated with cattle manure include *Escherichia*, *Salmonella*, *Staphylococcus*, *Streptococcus*, *Proteus*, and *Bacillus*, while common fungal genera include *Aspergillus*, *Mucor* and *Rhizopus*. Although many of these microorganisms perform beneficial ecological functions, some species have been implicated in foodborne infections, environmental contamination and opportunistic diseases in humans and animals (WHO, 2022). Their presence in untreated manure therefore raises concerns regarding the microbiological safety of using fresh cow dung in agriculture and the potential dissemination of pathogens into the food chain (Jauregi et al., 2021; Staley et al., 2021; Sukhum et al., 2021).

In Nigeria, fresh cow dung is frequently deposited around abattoirs, grazing fields, livestock markets and rural communities, where it is commonly used as organic manure with little or no prior treatment. In Gwagwalada Area Council, livestock production and agricultural activities occur alongside expanding residential settlements, abattoir operations and local food-marketing activities, creating opportunities for contact between untreated animal manure, agricultural soils, water sources and food-handling environments. This urban–rural interface makes Gwagwalada particularly relevant for assessing the microbial quality of fresh cow dung and its potential implications for environmental and public health in Abuja. Despite the widespread use of cow dung in the area, information on the occurrence and distribution of culturable bacteria and fungi associated with fresh cow dung remains limited for Gwagwalada and other parts of the Federal Capital Territory. Establishing a baseline of the culturable microorganisms present in fresh cow dung from different locations within Gwagwalada is therefore important for understanding its agricultural value and identifying potential microbial risks associated with its handling, disposal and application to agricultural land (Zalewska et al., 2024; Staley et al., 2021; Nwanta et al., 2010).

This study was undertaken to isolate and identify bacteria and fungi associated with fresh cow dung collected from selected locations within Gwagwalada Area Council, Abuja, Nigeria. Specifically, the study determined the total viable bacterial counts of the samples and identified the bacterial and fungal isolates using standard cultural, morphological, biochemical and microscopic techniques. The findings provide baseline information on the microbiological quality of fresh cow dung and contribute to existing knowledge regarding its safe handling and utilization in agricultural and environmental applications.

Materials and Methods

Study Area and Sample Collection

Fresh cow dung samples were collected from four locations within Gwagwalada Area Council, Federal Capital Territory, Nigeria, namely Old Kutunku Abattoir, the University of Abuja environment, Gwako, and Giri. Two fresh cow dung samples were collected independently from each location, giving a total of eight samples (n = 2 per location). The samples were aseptically collected into sterile universal containers, placed in an icebox maintained at approximately 4°C, and transported to the Microbiology Laboratory, Department of Microbiology, University of Abuja, for analysis within 1 h of collection.

Preparation of Culture Media

All microbiological media were prepared according to the manufacturers' instructions and sterilized by autoclaving at 121°C for 15 min. Nutrient Agar (NA), MacConkey Agar (MAC), and Potato Dextrose Agar (PDA) were used for primary enumeration and isolation of bacteria and fungi, respectively. Distinct bacterial colonies obtained from NA and MAC were subsequently subcultured onto Mannitol Salt Agar (MSA), Eosin Methylene Blue Agar (EMB), and Salmonella-Shigella Agar (SSA) for secondary differentiation and characterization. Glassware was sterilized using a hot-air oven at 170°C for 2 h, while media and distilled water were sterilized by autoclaving before use following standard microbiological laboratory procedures (Cheesbrough, 2006).

Preparation of Sample Suspension and Serial Dilution

One gram (1 g) of each cow dung sample was aseptically weighed and transferred into 9 mL of sterile distilled water and thoroughly mixed to obtain the initial 10^{-1} suspension. Serial ten-fold dilutions were subsequently prepared by transferring 1 mL of the suspension into 9 mL of sterile distilled water in the next tube to obtain 10^{-2}, followed by successive dilution up to 10^{-5}. The 10^{-3} dilution was used for bacterial enumeration by the spread plate technique (Cheesbrough, 2006; American Public Health Association [APHA], 2017).

Isolation and Enumeration of Bacteria

Aliquots (0.1 mL) from the 10^{-3} dilution were inoculated onto Nutrient Agar and MacConkey Agar plates using the spread plate technique. The inoculated bacterial plates were incubated aerobically at 37°C for 24 h, while PDA plates were incubated at room temperature for 72 h for fungal growth. After incubation, colonies were counted using a colony counter, and the bacterial counts were expressed as colony-forming units per millilitre (CFU/mL) following standard microbiological procedures (APHA, 2017). Counts obtained on Nutrient Agar were reported as total viable bacterial counts, while counts obtained on MacConkey Agar were reported as total enteric bacterial counts.

Isolation of Pure Cultures

Distinct bacterial colonies obtained from Nutrient Agar and MacConkey Agar were subcultured onto Mannitol Salt Agar, Eosin Methylene Blue Agar, and Salmonella-Shigella Agar for secondary differentiation. Pure cultures obtained after incubation at 37°C for 24 h were maintained for subsequent characterization and identification (Cheesbrough, 2006).

Characterization and Identification of Bacterial Isolates

Bacterial isolates were characterized based on their colonial morphology, Gram reaction, cell morphology, and biochemical characteristics following standard microbiological procedures described by Cheesbrough (2006). The biochemical tests performed included catalase, coagulase, indole, urease, citrate utilization, oxidase, motility and starch hydrolysis. The combined results of these tests were used for the presumptive identification of the bacterial isolates. The identities of the isolates were interpreted with reference to standard taxonomic characteristics described in *Bergey's Manual of Determinative Bacteriology* (Holt et al., 1994).

Isolation and Identification of Fungal Isolates

Fungal isolates were obtained by inoculating the samples onto Potato Dextrose Agar (PDA) and incubating the plates at 28 ± 2°C for approximately

72 h. No antibiotic was added to the PDA. Identification was based on colony morphology, pigmentation, growth characteristics and microscopic examination using lactophenol cotton blue staining. Microscopic features, including hyphal structure, conidiophores, sporangia, rhizoids and spores, were used for the presumptive identification of the fungal isolates following standard mycological procedures (Cheesbrough, 2006; Prescott et al., 2017).

Statistical Analysis

Microbial count data were analysed using the Statistical Package for the Social Sciences (SPSS). Differences in bacterial counts among the four sampling locations were evaluated using the Kruskal–Wallis non-parametric test. Two samples were analysed from each sampling location (n = 2 per location; total N = 8). Statistical significance was accepted at $\mathbf{p < 0.05}$.

Results

Total viable bacterial and enteric bacterial counts of fresh cow dung samples

A total of six bacterial taxa were presumptively identified from fresh cow dung samples collected from the four sampling locations (Figure 1). Total viable bacterial counts on Nutrient Agar ranged from 3.50×10^4 to 6.10×10^5 CFU/mL, while total enteric bacterial counts on MacConkey Agar ranged from 4.50×10^4 to 7.00×10^5 CFU/mL. The lowest counts were recorded at Giri (3.50×10^4 CFU/mL on Nutrient Agar and 4.50×10^4 CFU/mL on MacConkey Agar), whereas the highest counts were recorded at the University of Abuja environment (6.10×10^5 CFU/mL on Nutrient Agar and 7.00×10^5 CFU/mL on MacConkey Agar). Although differences in bacterial counts were observed among the sampling locations, the Kruskal–Wallis test showed that the differences were not statistically significant for Nutrient Agar ($H(3) = 6.667$, $p = 0.083$) or MacConkey Agar ($H(3) = 4.500$, $p = 0.212$).

Statistical Analysis of Bacterial Counts

For Nutrient Agar, no statistically significant difference was observed in bacterial counts among the four sampling locations **(**$H(3) = 6.667$, $p = 0.083$). Similarly, no statistically significant difference was observed for MacConkey Agar **(**$H(3) = 4.500$, $p = 0.212$**).**

Colonial Morphology of Bacterial Isolates

Six distinct bacterial colony types were recovered from the cow dung samples, with seven bacterial isolates representing six bacterial taxa presumptively identified. The isolates differed in colony shape, pigmentation, margin, surface texture, elevation, and transparency (Table 1). The identified taxa were *Escherichia coli, Staphylococcus aureus, Streptococcus* spp., *Bacillus* spp., *Proteus mirabilis*, and *Salmonella* spp., indicating the presence of diverse bacterial populations in the samples.

Distribution of Bacterial and Fungal Isolates

A total of six bacterial taxa and three fungal taxa were recovered from the fresh cow dung samples collected across the four sampling locations (Table 2). The bacterial taxa comprised *Escherichia coli, Staphylococcus aureus, Streptococcus* sp., *Bacillus* sp., *Proteus mirabilis*, and *Salmonella* spp., while the fungal taxa comprised *Aspergillus niger, Rhizopus* spp., and *Mucor* spp. The University of Abuja environment yielded five of the six identified bacterial taxa (83.3%), while Old Kutunku Abattoir, Gwako, and Giri each yielded four bacterial taxa (66.7%). The University of Abuja environment and Giri yielded all three identified fungal taxa (100%), followed by Old Kutunku Abattoir with two taxa (66.7%) and Gwako with one taxon (33.3%). *Salmonella* spp. was recovered from Gwako and Giri, corresponding to isolates C and D, respectively.

Characterization and Identification of Bacterial Isolates

Identification of the bacterial isolates was based on colonial morphology, Gram reaction, cell morphology and biochemical characteristics. The biochemical profile of each isolate is presented in Figure 2**.** Overall, six bacterial taxa were presumptively identified. Gram-positive isolates included *Staphylococcus aureus*, *Streptococcus* sp., and *Bacillus* sp., while Gram-negative isolates included *Escherichia coli*, *Proteus mirabilis*, and *Salmonella* sp.

Characterization and Identification of Bacterial Isolates

Seven bacterial isolate records representing six distinct bacterial taxa were characterized based on Gram reaction and biochemical tests (Table 3).

Characterization of Fungal Isolates

Three fungal taxa were isolated from the cow dung samples. Identification was based on colony morphology and microscopic examination following lactophenol cotton blue staining. *Aspergillus* sp produced colonies that became dark with maturation and exhibited septate hyphae with characteristic conidial heads. *Rhizopus* sp. formed rapidly growing cottony colonies with non-septate hyphae, rhizoids and sporangia, whereas *Mucor* sp. produced fluffy colonies with non-septate hyphae and globose sporangia but lacked rhizoids (Table 4).

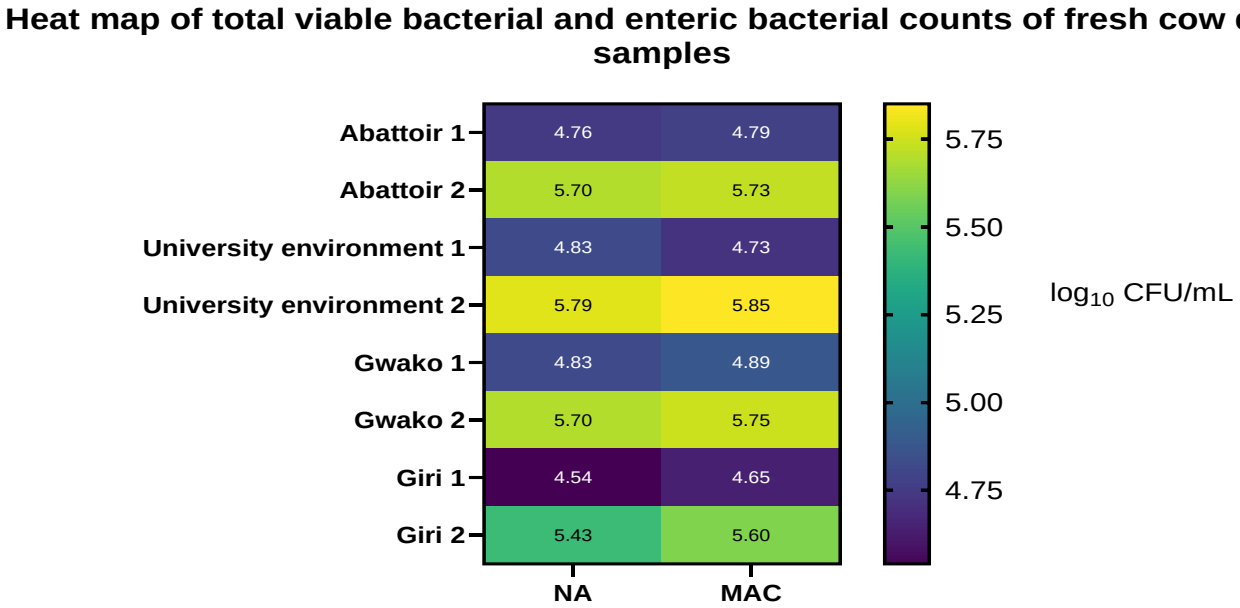


Figure 1: Heat map of total viable bacterial and enteric bacterial counts of fresh cow dung samples. Values are presented as log_{10} CFU/mL

Keys: NA = Nutrient Agar, MAC = MacConkey Agar. Values are presented as log_{10} CFU/mL

Table 1: Colonial characteristics and presumptive identification of bacterial isolates from fresh cow dung samples

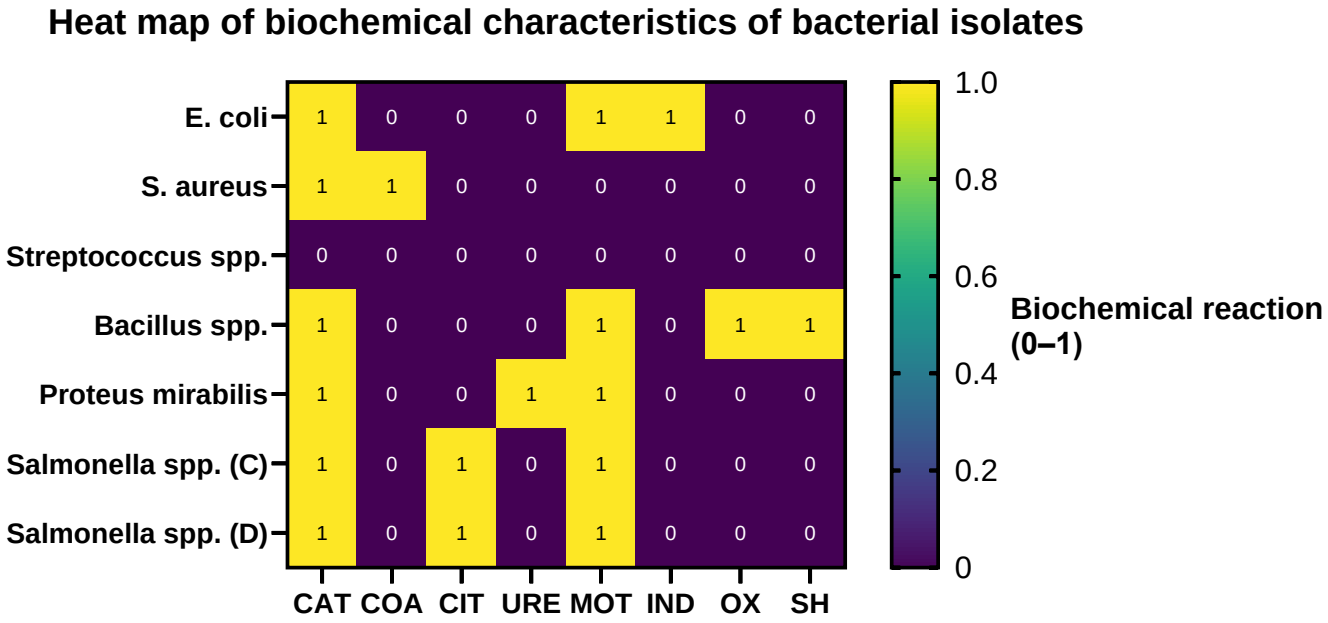
Isolates	Shape	Pigmentation	Margin	Surface texture	Elevation	Transparency	Presumptive identification
1	Circular	Orange	Entire	Smooth/Shiny	Raised	Opaque	*Escherichia coli*
2	Circular	Cream	Entire	Smooth/Shiny	Raised	Opaque	*Staphylococcus aureus*
3	Round	Cream	Lobate	Rough	Raised	Opaque	*Streptococcus* sp.
4	Round	Cream	Entire	Rough	Flat	Opaque	*Bacillus* sp.
5	Irregular	Milky	Undulate	Smooth	Raised	Transparent	*Proteus mirabilis*
6	Round	Black	Entire	Smooth	Raised	Opaque	*Salmonella* spp.

Table 2: Distribution and number of bacterial and fungal taxa recovered from fresh cow dung samples across the sampling locations

Sampling location	Bacterial isolates recovered	Bacterial taxa, n (%)	Fungal isolates recovered	Fungal taxa, n (%)
Old Kutunku Abattoir	*Staphylococcus aureus*, *Escherichia coli*, *Proteus mirabilis*, *Bacillus* sp.	4 (66.7%)	*Aspergillus* sp, *Mucor* sp.	2 (66.7%)
University of Abuja environment	*Escherichia coli*, *Staphylococcus aureus*, *Streptococcus* sp., *Bacillus* sp., *Proteus mirabilis*	5 (83.3%)	*Rhizopus* sp., *Mucor* sp., *Aspergillus* sp	3 (100%)
Gwako	*Staphylococcus aureus*, *Proteus mirabilis*, *Salmonella* spp., *Escherichia coli*	4 (66.7%)	*Rhizopus* sp.	1 (33.3%)
Giri	*Salmonella* spp., *Escherichia coli*, *Bacillus* sp., *Staphylococcus aureus*	4 (66.7%)	*Rhizopus* sp., *Mucor* sp., *Aspergillus* sp	3 (100%)

Note: ***n*** represents the number of distinct taxa recovered at each sampling location. Percentages represent the proportion of the total distinct taxa identified in the study (six bacterial taxa and three fungal taxa) and do not represent sample-level prevalence

Figure 2: Heat map of biochemical characteristics of bacterial isolates



Note: Values are coded as 1 = positive reaction and 0 = negative reaction. *Salmonella* spp. was recovered from both samples C and D. CAT = catalase; COA = coagulase; CIT = citrate; URE = urease; MOT = motility; IND = indole; OX = oxidase; SH = starch hydrolysis

Table 3: Biochemical characterization and presumptive identification of bacterial isolates

Sample	Gram reaction	Cell shape	CAT	COA	CIT	URE	MOT	IND	OX	SH	Presumptive Identification
A	-	Rod	+	-	-	-	+	+	-	-	*Escherichia coli*
A	+	cocci	+	+	-	-	-	-	-	-	*Staphylococcus aureus*
B	+	Cocci (chain)	-	-	-	-	-	-	-	-	*Streptococcus* sp.
B	+	Rod	+	-	-	-	+	-	+	+	*Bacillus* sp.
C	-	Rod	+	-	-	+	+	-	-	-	*Proteus mirabilis*
C	-	Rod	+	-	+	-	+	-	-	-	*Salmonella* sp.
D	-	Rod	+	-	+	-	+	-	-	-	*Salmonella* sp.

Key: CAT = Catalase; COA = Coagulase; CIT = Citrate utilization; URE = Urease; MOT = Motility; IND = Indole; OX = Oxidase; SH= Starch hydrolysis. **Note:** Sample letters A–D represent the sampling locations: A = Old Kutunku Abattoir, B = University of Abuja environment, C = Gwako, and D = Giri. *Salmonella* spp. was recovered from both samples C and D, resulting in seven isolate records representing six distinct bacterial taxa.

Table 4: Cultural and microscopic characteristics of fungal isolates

Fungal isolate	Cultural characteristics	Microscopic characteristics
Aspergillus sp	White colonies becoming dark with age	Septate hyphae with conidial heads
Rhizopus sp	Rapidly growing cottony colonies	Non-septate hyphae with rhizoids and sporangia
Mucor sp	White fluffy colonies	Non-septate hyphae with globose sporangia and no rhizoids

Discussion

This study investigated the occurrence and characterization of bacteria and fungi associated with fresh cow dung collected from selected locations within Gwagwalada Area Council, Abuja, Nigeria. The results demonstrated that fresh cow dung harbours diverse bacterial and fungal populations, including microorganisms of environmental, agricultural and public health significance (Gurmessa et al., 2021; Zalewska et al., 2024; Neupane et al., 2021).

The total viable bacterial counts obtained in this study ranged from 3.50×10^4 to 6.10×10^5 CFU/mL on Nutrient Agar, while total enteric bacterial counts on MacConkey Agar ranged from 4.50×10^4 to 7.00×10^5 CFU/mL. The highest counts were recorded at the University of Abuja environment, with 6.10×10^5 CFU/mL on Nutrient Agar and 7.00×10^5 CFU/mL on MacConkey Agar, whereas the lowest counts were recorded at Giri, with 3.50×10^4 and 4.50×10^4 CFU/mL, respectively. The higher microbial loads at the University of Abuja environment may reflect differences in animal management practices, feeding habits, environmental exposure and manure handling. Conversely, the lower counts observed at Giri may be associated with differences in environmental conditions, manure accumulation and exposure. Although variations in bacterial counts were observed among the sampling locations, the differences were not statistically significant for Nutrient Agar ($H(3) = 6.667$, $p = 0.083$) or MacConkey Agar ($H(3) = 4.500$, $p = 0.212$). This suggests that the observed differences in microbial loads among the locations were not statistically significant. Similar observations have been reported in studies showing that manure microbiota may vary according to livestock

management systems, environmental conditions, feed composition and manure storage practices (Gurmessa et al., 2021; Zalewska et al., 2024; Neupane et al., 2021).

The microbial counts obtained are consistent with previous reports demonstrating that untreated cattle manure contains abundant microbial populations because of its high organic matter and nutrient content. Fresh cow dung provides a favourable environment for the survival and multiplication of microorganisms involved in the degradation of organic materials. However, untreated manure may also serve as a reservoir of potentially pathogenic microorganisms capable of contaminating agricultural soils, irrigation water, vegetables and other food products if applied without appropriate treatment (Staley et al., 2021; Jauregi et al., 2021; Sharma et al., 2021). These findings further support the need for appropriate manure treatment before agricultural application to reduce microbial contamination risks.

Six bacterial taxa were presumptively identified from the cow dung samples, namely *Staphylococcus aureus*, *Streptococcus* sp., *Bacillus* sp., *Escherichia coli*, *Proteus mirabilis* and *Salmonella* spp. The occurrence of *Escherichia coli* and *Salmonella* spp. indicates the presence of faecal-associated bacteria in the cow dung. Their presence in untreated cow dung is of public health concern because some members of these groups are capable of causing foodborne and other infections and may contribute to environmental contamination (WHO, 2022). Similar bacterial genera have been reported in cattle manure and livestock-associated environments, highlighting the importance of animal wastes as reservoirs of enteric microorganisms (Gurmessa et al., 2021; Sukhum et al., 2021; Nwanta et al., 2010). The isolation of *Proteus mirabilis* further supports the presence of enteric-associated bacteria in the samples.

The recovery of *Staphylococcus aureus* from the samples also has public health implications. Although *Staphylococcus* species may occur naturally on the skin and mucous membranes of animals, *S. aureus* can produce enterotoxins associated with food poisoning when introduced into foods under favourable conditions (WHO, 2022). Likewise, members of the genus *Bacillus* are widely distributed in soil and animal manure because of their ability to produce resistant endospores that enable survival under adverse environmental conditions. While many *Bacillus* species contribute to nutrient cycling, some members of the genus are recognized as opportunistic or foodborne pathogens (Madigan et al., 2021; Tortora et al., 2021).

Three fungal taxa, namely *Aspergillus* sp, *Rhizopus* sp. and *Mucor* sp., were also recovered from the cow dung samples. These fungi are common environmental saprophytes that play important roles in the decomposition of organic matter, making their occurrence in cow dung unsurprising. Nevertheless, some species within these genera may present health concerns under favourable conditions. For example, some *Aspergillus* species are capable of producing mycotoxins, while *Rhizopus* and *Mucor* species have been associated with opportunistic infections, particularly in susceptible individuals (Madigan et al., 2021). Similar fungal genera have also been reported from livestock manure and other organic wastes, reflecting their ecological role in organic matter degradation (Khoshnevisan et al., 2021).

The distribution of microbial taxa varied among the sampling locations. The University of Abuja environment and Giri showed relatively greater taxonomic diversity than the other locations, despite the University environment recording the highest bacterial counts and Giri recording the lowest. This demonstrates that microbial abundance and taxonomic diversity are not necessarily directly related. Differences in the number and composition of recovered taxa may be influenced by environmental exposure, animal density, sanitation practices, manure characteristics and local ecological conditions. Previous studies have similarly reported that geographical location, animal diet, environmental hygiene and manure storage conditions can influence the microbial composition of livestock wastes (Gurmessa et al., 2021; Zalewska et al., 2024; Neupane et al., 2021).

A limitation of this study is that bacterial and fungal identification was based primarily on cultural characteristics, microscopy and

conventional biochemical tests. Although these methods are useful for preliminary identification, they may not provide definitive species-level identification; therefore, the identities of the isolates should be regarded as presumptive. Molecular methods, such as 16S rRNA gene sequencing for bacteria and appropriate fungal barcoding approaches, would provide greater taxonomic resolution and help confirm the identities of the isolates. In addition, culture-based methods may not recover all microorganisms present in the samples, particularly those requiring specific growth conditions. The relatively small sample size, with two samples collected from each location, may also limit the generalizability of the findings to other cattle-manure environments. Nevertheless, the recovery of enteric and environmental bacteria is consistent with reports from Nigerian livestock and abattoir-associated environments (Nwanta et al., 2010; Gurmessa et al., 2021), providing further evidence that untreated livestock manure can harbour microorganisms of environmental and public health importance.

Overall, the findings of this study highlight the importance of safe handling and proper treatment of fresh cow dung before agricultural application. Although cow dung is a valuable organic fertilizer that can improve soil fertility and crop productivity, the use of untreated manure may facilitate the dissemination of microorganisms into agricultural environments, surface waters and food production systems (FAO, 2001; WHO, 2022; Sharma et al., 2021). Composting or other appropriate manure-treatment methods may reduce microbial risks while preserving its agronomic benefits (Staley et al., 2021; Zalewska et al., 2024; United States Environmental Protection Agency [USEPA], 2023).

Conclusion and Recommendations

This study demonstrated that fresh cow dung collected from four locations within Gwagwalada Area Council, Abuja, contains diverse bacterial and fungal taxa of agricultural, environmental and potential public health importance. Bacterial counts ranged from 3.50×10^4 to 6.10×10^5 CFU/mL on Nutrient Agar and 4.50×10^4 to 7.00×10^5 CFU/mL on MacConkey Agar, with the highest counts recorded at the University of Abuja environment and the lowest at Giri. Six bacterial taxa, namely *Staphylococcus aureus, Streptococcus* spp., *Bacillus* sp., *Escherichia coli, Proteus mirabilis* and *Salmonella* spp., and three fungal taxa, *Aspergillus* sp, *Rhizopus* sp. and *Mucor* sp., were presumptively identified. Although bacterial counts varied among the sampling locations, the differences were not statistically significant.

The recovery of enteric and other potentially significant microorganisms indicates that raw cow dung should be handled as a potential source of environmental contamination**.** Direct handling or indiscriminate application of untreated dung may facilitate the transfer of microorganisms to agricultural soils, water sources, vegetables and other food production environments. Therefore, the use of fresh cow dung without adequate treatment may present avoidable environmental and public health risks.

Farmers and other users of cow dung in Gwagwalada and similar communities should be encouraged to compost or otherwise adequately treat manure before applying it to agricultural fields. Appropriate personal hygiene, including the use of gloves and handwashing after handling manure, should also be encouraged. Local agricultural and environmental health authorities should promote farmer education on safe manure handling, storage and application practices and support appropriate manure-treatment practices. Further studies using molecular identification methods and antimicrobial susceptibility testing are recommended to provide more comprehensive information on the microbial diversity and potential public health significance of microorganisms associated with cow dung.

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Conflict of Interest

The authors declare that there are no conflicts of interest regarding the publication of this manuscript.

Author Contributions

EE: Conceptualization, study design, sample collection, laboratory analyses, data analysis, interpretation of results and preparation of the original manuscript draft. OOA: Supervision of the study, methodological guidance, critical review and editing of the manuscript, and approval of the final version for publication. All authors read and approved the final manuscript.

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