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Selected Aerobic bacterial-based Microbiome of Giant Rat and Squirrel obtained from Abudu and Iguedolor Edo State

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ABSTRACT

Rodents are mammals known for their adaptability, often coexisting with humans and domestic animals, which makes them potential carriers of zoonotic microorganisms. The study is aimed at evaluating the microbial flora of giant rats (Cricetomysgambianus) and squirrels (Xerusrutilus) obtained from Abudu and Iguedolor towns of Edo State, Nigeria. Twenty (20) samples of giant rats and squirrels were collected from the forest of Abudu and Iguedolor. Five (5) samples each of both giant rat and squirrel where obtained from Abudu, while five (5) samples each of giant rat and squirrel from Iguedolor, making 20 samples. These samples were kept in separate cages respectively and were transported from Edo State to the laboratory for microbial analysis. One gram (1g) each of the large intestine, small intestine, stomach and flesh of the samples were homogenized separately, while the anus and skin were swabbed. Serial dilution was carried out in the homogenized samples and the 0.1ml of the diluted samples were inoculated into a sterile petri dish into which sterile molten agar was poured and incubated. These were incubated at 37°C for 18-24hrs for bacterial growth, while plate for fungal growth were plated at 30°C for 3 to 5 days. Several microbiological identification tests were carried out on both bacterial and fungal isolates. Among the recovered bacterial isolates include; Bacillus subtilis, Escherichia coli, Pseudomonas aeruginosa., Enterobacter aerogenes, Staphylococcus aureus, Streptococcus faecalis, Micrococcus sp, Corynebacterium sp. and Lactobacillus sp., while the fungal isolates were Candida albicans, Neurospora sp., Rhizopus sp. and Aspergillus niger. The prevalent bacteria isolated from Giant Rat (Cricetomysgambianus) and Squirrel (Xerusrutilus) were Staphylococcus aureus (40%), followed by Corynebacterium sp. (25%), Bacillus subtilis and Lactobacillus sp. (20%), Streptococcus faecalis had the least percentage occurrence of 5%. Rhizopus sp had the highest occurrence (38.46%), while Neurosporasp and Aspergillus sp had the least occurrence (12.5%) among fungal isolates. Result of

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the antibiotic sensitivity study showed that apart from a strain of Staphylococcus aureus that was resistant to only one antibiotic, other gram-positive bacterial isolates were resistant to 4-10 different antibiotics. Streptococcus faecalis and Bacillus subtilis where resistant to eight of the antibiotics used, however they were only sensitive to pefloxacin and ciprofloxacin. These results indicate considerable combined risks associated with the consumption and interactions between such rodents and humans. The possible transmission of such potential zoonotic pathogens and the potential spread of such antimicrobial resistance dynamics is a principal concern. This study underscored the need for ongoing microbiome monitoring within the One Health framework and suggests the future use of molecular and metagenomic techniques to enhance understanding of microbial diversity and transmission patterns

1. INTRODUCTION

The order Rodentia, comprising around 2,020 living species distributed across 28 families (which is about half of all mammalian species), is the largest group of mammals. These animals inhabit nearly all regions of the world, with the exceptions of Antarctica and certain oceanic islands (Frohlich, 2021). Rodents serve numerous functions: they are utilized as animal models in toxicology studies (Clements *et al.*, 2022), hold essential roles in ecology, medicine, and agriculture (Shah, 2023), and their meat (such as that of the capybara) provides a valuable source of animal protein with considerable nutritional benefits (Ali and Jones, 2020). Among these species, squirrels and rats have a broad geographical presence, yet the African palm squirrel and African giant rat are mostly limited to West Africa.

The ecological flexibility of these rodents, along with their proximity to human environments, makes them particularly important to public health, as they can harbor numerous zoonotic pathogens. Their close relationships with humans and domestic animals heighten the likelihood of disease transmission (Shah *et al*., 2023). Additionally, the ectoparasites associated with them play a crucial role in the spread of pathogens. For example, a study conducted in Senegal by Demoncheaux*et al*. (2022) documented the isolation, molecular identification, and genetic analysis of *Bartonella* species in wild commensal rodents and their fleas. This study marked the first recorded instance of *Bartonella* strains in African giant rats (*Cricetomysgambianus*) and tropical rat fleas (*Xenopsyllacheopis*), highlighting the necessity for further research into the microbial diversity of rodents in various ecological contexts.

The variety and quantity of ectoparasites found in rodents are shaped by their highly adaptable behaviors, diverse habitats, and their capability to respond to environmental changes (López-Pérez *et al*., 2022). The preferences for different habitats among rodent species impact the types and numbers of ectoparasites they host (Maaz*et al*., 2018). These relationships are further influenced by various factors such as the sex and age of the host, the species of the parasite, and other biological and environmental conditions (López-Pérez *et al*., 2022).

In addition to their role in spreading diseases, rodents host complex and evolving microbial communities. Research has indicated that the composition of gut microbiomes varies among individual rodents, with the phyla Firmicutes and Bacteroidetes largely dominating the gut ecosystems of both captive and wild rodents, making up over 80% of their overall abundance (Bensch*et al*.,

2023). New research by Hanski*et al*. (2025) has established a strong correlation between dietary patterns and gut microbiota composition in rodents. For instance, studies on grassland species *Spermophilusalashanicus, S. dauricus*, and *Merionesunguiculatus* showed that different diets significantly affect gut microbial diversity, with plant-based diets leading to higher richness and diversity compared to diets based on animal products.

Nevertheless, there remains a significant gap in knowledge regarding rodent microflora in West Africa, particularly concerning *Cricetomysgambianus* and *Epixerusebii* in Nigeria. While some local investigations have discussed gut parasites in giant rats, there is still a lack of comprehensive research examining the broader microflora, especially the gut and external microbiomes, of giant rats and squirrels in Edo State.

Abudu, situated in the southern region of Edo State, serves as the administrative center for the Orhionmwon Local Government Area. Abudu and Iguedolor are agricultural communities within Edo State, southern Nigeria. While Abudu operates as the administrative headquarters for Orhionmwon Local Government Area, Iguedolor is a peri-urban community near Benin City in Ovia North-East Local Government Area. Both areas primarily focus on farming and bushmeat hunting, especially of giant rats and squirrels, which serve as significant sources of protein and income. These activities also elevate interactions between humans and wildlife, creating potential avenues for the transmission of zoonotic diseases

2. MATERIALS AND METHODS

Study Area and Sample Collection

Twenty wild rodents, consisting of giant rats (*Cricetomysgambianus*) and squirrels (*Xerusrutilus*), were captured in the forests of Abudu and Iguedolor, Edo State, Nigeria. Trapping took place between March 2025 and April 2025, utilizing wire live traps baited with maize. Five specimens of each species were gathered from each location, resulting in a total of 20 animals. The captured rodents were kept in individual sterile cages, handled minimally, and transported to the microbiology laboratory for further analysis.

Sample Processing and Microorganism Isolation

The rodents were euthanized humanely using cervical dislocation, in accordance with the method describedby Oemcke *et al.* (2021). Aseptic methods were used to obtain samples from the stomach, small intestine, large intestine, flesh, skin, and anus. Gastrointestinal tissues were blended in sterile phosphate-buffered saline (PBS, pH 7.2) and serially diluted (10^{-1}–10^{-9}). The dilutions were processed using the pour-plate method on Nutrient agar (NA) for general bacterial isolation, MacConkey agar (MAC) to selectively isolate Gram-negative enterics, and Potato dextrose agar (PDA) for fungal isolation. The protocols were adapted from Adjei*et al.* (2022). External samples (skin, anus) were obtained with sterile cotton swabs and streaked onto agar plates (Su et al., 2024). Negative controls (PBS blanks) were also processed to check for contamination. Plates were incubated aerobically at 37 °C for 24–48 hours for bacterial cultures, and at 25–28 °C for 3–5 days for fungal cultures. Representative colonies showing distinct morphological characteristics were sub-cultured to secure pure isolates, which were stored on agar slants at 4 °C for future analysis.

Bacterial Identification

Bacterial isolates were first characterized by examining colony morphology and performing Gram staining. Further identification was conducted using motility tests and standard biochemical assays,

including catalase, oxidase, citrate utilization, indole production, and triple sugar iron (TSI) reactions, following the procedure described in Clinical Microbiology Procedures Handbookby Garcia (2023)

Fungal Identification

Fungal isolates were purified on Sabouraud Dextrose Agar (SDA) and identified based on features such as macroscopic colony attributes (texture, pigmentation, growth rate) and microscopic characteristics of hyphae, conidia, and reproductive structures stained with lactophenol cotton blue.

Antibiotic Susceptibility Testing

The antibiotic susceptibility of bacterial isolates was evaluated through the Kirby–Bauer disk diffusion method on Mueller–Hinton agar, adapted from the slightly modified method ofAmin*et al*. (2015). Followingincubation at 37 ℃ for 18–24 hours, isolates with zones of inhibition≤10 mm in diameter or no zone of inhibition were considered to be resistant, while isolates with zones of inhibition >10 were considered susceptible. Bacterial suspensions were standardized to a 0.5 McFarland standard before swabbing.The antimicrobial agents tested were Pefloxacin, Gentamicin, Ampicillin, Azithromycin, Amoxicillin, Rifampicin, Ciprofloxacin, Streptomycin, Cotrimoxazole, and Erythromycin.

Data Analysis

Data analysis was performed using SPSS version 23. Microbial prevalence was recorded as percentages

3. RESULTS AND DISCUSSION

A total of 30 bacterial isolates were obtained from various host species and locations (Table 10). The most common were *S. aureus* (26.7%), *Corynebacterium* sp. (16.7%), and B. subtilis (13.3%). The distribution varied according to host and location (Table 4): in Abudu, giant rats were found to carry *B. subtilis, Micrococcus* sp., and *S. aureus*, while squirrels tended to have higher numbers of Lactobacillus sp. and P. aeruginosa. In Iguedolor, the rodent populations were predominantly characterized by *Corynebacterium* sp., *S. faecalis*, *B. subtilis*, and *E. coli*.

A total of 26 fungal isolates were recognized, with *Rhizopus* sp. (38.5%) and *C. albicans* (31.0%) being the most predominant (Table 11). The prevalence of fungi varied by location: in Abudu, both *C. albicans* and *Rhizopus*sp. were the most abundant, whereas samples from Iguedolor exhibited greater diversity, which included *Aspergillus* sp. and *Neurospora* sp. (Table 5).

Microbial loads were observed to be highest in the intestines of both types of hosts (Tables 6–9). Intestinal samples consistently contained *S. aureus*, *B. subtilis*, and *Lactobacillus* sp., while Micrococcus sp. and *C. albicans* were more frequently found at skin and anal sites.

Gram-positive isolates showed varying levels of susceptibility to the tested antibiotics (Table 12). The majority of isolates were susceptible to PEF, CN, CPX, and E, while resistance was mostly observed against APX, Z, AM, and R. Generally, *Lactobacillus* sp. and *S. aureus* were susceptible, whereas *Streptococcus faecalis*, *Micrococcus* sp., *Bacillus subtilis*, and *Corynebacterium* sp. exhibited significant resistance to specific antibiotics.

Table 1: Identification of Bacterial Isolates from Giant Rat

S/N	Isolate Code	Gram Stain	Glucose	Lactose	Citrate	Catalase	Motility	Indole	Acid	Gas	H_2S	Organism
1	BS1	+	+	-	-	+	-	-	+	-	-	*Bacillus subtilis*
2	MC2	+	+	-	+	+	+	+	+	+	-	*Micrococcus* species
3	SA3	+	+	-	+	+	+	+	+	-	-	*Staphylococcus aureus*
4	EC4	-	+	+	+	-	+	+	+	+	+	*Escherichia coli*
5	PA5	-	+	+	+	+	+	+	+	+	+	*Pseudomonas aeruginosa*
6	SF6	+	+	+	+	-	+	+	-	-	-	*Streptococcus faecalis*
7	CB7	+	+	+	+	+	+	+	+	+	-	*Corynebacterium* sp.
8	EA8	+	+	+	+	+	+	+	+	+	+	*Enterobacteraerogenes*
9	LB9	+	+	+	+	-	-	+	+	+	-	*Lactobacillus* sp.

Table 2: Identification of Bacterial Isolates from Squirrel

S/N	Isolate Code	Gram Stain	Glucose	Lactose	Citrate	Catalase	Motility	Indole	Acid	Gas	H_2S	Organism
1	BS01	+	+	+	+	+	+	-	+	-	-	*Bacillus subtilis*
2	SA02	+	+	-	+	+	-	-	+	-	-	*Staphylococcus aureus*
3	EA03	-	+	+	+	+	+	-	+	+	+	*Enterobacteraerogenes*
4	CB04	+	-	-	+	-	-	-	-	-	-	*Corynebacterium* sp.
5	LB05	+	+	-	-	-	-	-	+	-	-	*Lactobacillus* sp.

Table 3: Identification of Fungi Isolates

S/N	Color / Growth	Morphology	Appearance	Spore	Organism
1	Cream, raised growth	Yeast hyphae	Hyphae small, glossy, raised, smooth	Spore	*Candida albicans*
2	White, woolly growth	Yeast hyphae	Hyphae and spore growth	Spore	*Rhizopus*sp.
3	Brown, woolly growth	Yeast hyphae	Hyphae glossy and smooth	Spore	*Aspergillus* sp.
4	Black, woolly growth	Elongation of hyphae	Nerve spore	Spore	*Neurospora*sp.

Table 4: Predominant bacteria isolated from Giant Rat and Squirrel from Abudu and Iguedolor

Abudu (Giant Rat)	Abudu (Squirrel)	Iguedolor (Giant Rat)	Iguedolor (Squirrel)
Staphylococcus aureus	*Corynebacteriumfaecalis*	*Streptococcus faecalis*	*Corynebacterium*specie
Streptococcus faecalis	*Bacillus subtilis*	*Escherichia coli*	*Lactobacillus* sp.
Lactobacillus sp.	*Lactobacillus* sp.	*Pseudomonas aeruginosa*	*Bacillus subtilis*
Corynebacteriumsp	*Micrococcus specie*	*Micrococcus* sp	*Staphylococcus aureus*
Micrococcus sp.	*Staphylococcus aureus*	*Staphylococcus aureus*	*Enterobacteraerogenes*
Bacillus subtilis		*Lactobacillus* sp.	

Table 5: Predominant fungi isolated from Giant Rat and Squirrel from Abudu and Iguedolor

Abudu (Giant Rat)	**Abudu (Squirrel)**	**Iguedolor (Giant Rat)**	**Iguedolor (Squirrel)**
Candida albicans	*Rhizopus* sp.	*Aspergillus niger*	*Neurospora* specie
Aspergillus niger	*Neurospora* sp.	*Candida albicans*	*Rhizopus* sp.
Rhizopus sp.	*Candida albicans*	*Neurospora* sp.	*Aspergillus niger*
Neurospora sp.	*Aspergillus niger*	*Rhizopus* sp.	*Candida albicans*

Table 6: Prevalence of microorganisms in the various parts of the giant rat examined (large intestine, small intestine, flesh, stomach, and anus) from Abudu

Large Intestine	**Small Intestine**	**Flesh**	**Skin (external body surface)**	**Stomach**	**Anus**
Staphylococcus aureus	*Bacillus subtilis*	*Corynebacterium*sp.	*Staphylococcus aureus*	*E. coli*	*Micrococcus* sp.
Streptococcus faecalis	*Pseudomonas aeruginosa*	*Staphylococcus aureus*	*Micrococcus* specie	*Streptococcus faecalis*	*Staphylococcus aureus*
Lactobacillus sp.	*Enterobacterae rogenes*	*Lactobacillus* sp.	*Bacillus subtilis*	*Lactobacillus* sp.	*Micrococcus* specie
E. coli	*Micrococcus* sp.	*Streptococcus faecalis*	*Corynebacterium*sp.	*Staphylococcus aureus*	*Corynebacterium*sp.
*Corynebacterium*sp.	*Staphylococcus aureus*	*Enterobacterae rogenes*	*Candida albicans*	*Aspergillus niger*	*Corynebacterium*sp.
Pseudomonas aeruginosa	*E. coli*	*Nurospora*sp.			*Candida albicans*

Micrococcus sp.	*Streptococcus faecalis*
*Rhizopus*sp.	*Candida albicans*

Table 7: Prevalence of microorganisms in the various parts of giant rat examined (large intestine, small intestine, flesh, stomach, and anus) from Iguedolor

Large Intestine	**Small Intestine**	**Flesh**	**Skin (external body surface)**	**Stomach**	**Anus**
*Corynebacterium*sp	*Bacillus subtilis*	*Lactobacillus* sp.	*Corynebacterium*specie	*Lactobacillus* sp.	*Streptococcus faecalis*
Streptococcus faecalis	*Escherichia coli*	*Enterobacterae rogenes*	*Micrococcus* sp	*Streptococcus faecalis*	*Micrococcus* sp
Pseudomonas sp.	*Enterobacterae rogenes*	*Staphylococcus aureus*	*Bacillus subtilis*	*Staphylococcus aureus*	*Corynebacterium*sp
Micrococcus sp	*Micrococcus* sp	*Streptococcus* sp.	*Staphylococcus aureus*	*Escherichia coli*	*Micrococcus* sp
Lactobacillus sp.	*Staphylococcus aureus*	*Corynebacterium*sp	*Rhizopus*sp.	*Neurospora*sp.	*Staphylococcus aureus*
Staphylococcus aureus	*Staphylococcus aureus*	*Staphylococcus aureus*	*Staphylococcus aureus*	*Aspergillus niger*	*Candida albicans*
Staphylococcus aureus	*Streptococcus faecalis*	*Pseudomonas* sp.			*Rhizopus*sp.
Aspergillus sp.	*Neurospora*sp.	*Rhizopus*sp.			

Table 8: Prevalence of microorganisms in the various parts of Squirrel examined (large intestine, small intestine, flesh, stomach and anus) in Abudu

Large Intestine	**Small Intestine**	**Flesh**	**Skin (external body surface)**	**Stomach**	**Anus**
Bacillus subtilis	*Lactobacillus* sp.	*Enterobacteraerogenes*	*Lactobacillus* sp.	*Lactobacillus* sp.	*Corynebacterium*sp.
Staphylococcus aureus	*Enterobacteraerogenes*	*Corynebacterium*sp.	*Staphylococcus aureus*	*Streptococcus faecalis*	*Micrococcus* sp.
Lactobacillus sp.	*Staphylococcus aureus*	*Lactobacillus* sp.	*Bacillus subtilis*	*E. coli*	*Staphylococcus aureus*
Micrococcus sp.	*Micrococcus* sp.	*Candida albicans*	*Micrococcus* sp.	*Staphylococcus aureus*	*Lactobacillus* sp.
Candida albicans	*Neurospora*sp.		*Rhizopus*sp	*Candida albicans*	*Aspergillus* sp

Table 9: Prevalence of microorganisms in the various parts of squirrel examined (large intestine, small intestine, flesh, stomach and anus) in Iguedolor

Large Intestine	**Small Intestine**	**Flesh**	**Skin (external body surface)**	**Stomach**	**Anus**
Lactobacillus sp.	*Micrococcus* sp.	*Lactobacillus* sp.	*Lactobacillus* sp.	*E. coli*	*Staphylococcus aureus*
Micrococcus sp	*Lactobacillus specie*	*Micrococcus sp*	*Enterobacteraerogenes*	*Lactobacillus specie*	*Corynebacterium*sp.
Staphylococcus aureus	*Lactobacillus* sp.	*Enterobacteraerogenes*	*Micrococcus* sp.	*Streptococcus faecalis*	*Lactobacillus* sp.
Bacillus subtilis	*Staphylococcus aureus*		*Staphylococcus aureus*	*Staphylococcus aureus*	*Micrococcus* sp.
Aspergillus sp	*Candida albicans*	*Rhizopus*sp.	*Neurospora*sp.	*Candida albicans*	*Aspergillus* sp

Table 10: Prevalence (%) of bacterial isolates according to genera

Isolates	**Number of Isolates**	**Percentage rate (%)**
Staphylococcus aureus	8	26.7
Bacillus subtilis	4	13.3
Corynebacterium sp.	5	16.7
Lactobacillus sp	4	13.3
Streptococcus faecalis	1	3.3
Pseudomonas aeruginosa	2	6.7
Micrococcus sp.	2	6.7
Escherichia coli	2	6.7
Enterobacteraerogenes	2	6.7
Total	30	100

Table 11: Prevalence (%) of fungal isolates according to genera

Isolates	**Number of Isolates**	**Percentage rate (%)**
Candida albicans	8	31.0
*Neurospora*sp	4	12.5
*Rhizopus*sp	10	38.46
*Aspergillus*sp	4	12.5
Total	26	100

Table 12: Antibiotic susceptibility profiles of representative Gram-positive isolates

Isolate	**PEF**	**CN**	**APX**	**Z**	**AM**	**R**	**CPX**	**S**	**SXT**	**E**
Lactobacillus spp	S	S	R	R	S	S	S	S	S	S
S. aureus	S	S	S	S	S	S	S	S	S	R
Enterobacteraerogenes	S	S	S	S	R	S	S	R	S	S
Streptococcus faecalis	S	R	R	R	R	R	S	R	R	R
Micrococcus sp	S	S	R	R	R	S	S	R	R	R
Bacillus subtilis	S	R	R	R	R	R	S	R	R	S
Corynebacteriumsp	S	R	R	R	R	R	S	R	R	R

Keys:

PEF: Pefloxacin, CN: Gentamycin, AMPX: Ampiclox, AM: Amoxicillin, R: Rifampicin, CPX: Ciprofloxacin, S: Streptomycin, SXT: Cotrimoxazole, E: Erythromycin, Z: Azithromycin.
R = resistant, S = sensitive.

3.1 Discussion

This research offers an in-depth analysis of the bacterial and fungal communities found in giant rats (*Cricetomysgambianus*) and squirrels (*Xerusrutilus*) from Abudu and Iguedolor, Edo State, Nigeria. A total of 30 bacterial isolates and 26 fungal isolates were obtained, with *Staphylococcus aureus* (26.7%) and *Rhizopus* spp. (38.46%) being the most commonly identified species. The presence of clinically significant bacteria and opportunistic fungi in wildlife hosts highlights the role of rodents as reservoirs for zoonotic pathogens that can spread via direct contact, environmental contamination, or consumption as bushmeat (Ziarati*et al.*, 2022). Notably, the discovery of multidrug-resistant (MDR) *Corynebacterium* spp. and *Streptococcus faecalis* raises concerns about potential treatment difficulties if these pathogens are transmitted to humans.

Our results emphasize geographical and host-specific differences in rodent microbiomes. In Abudu, giant rats were primarily inhabited by *Bacillus subtilis, Corynebacterium* spp., and *S. aureus*, while squirrels contained more *Lactobacillus* spp. and *Pseudomonas aeruginosa*. Conversely, both rodent species in Iguedolor shared overlapping communities of *Corynebacterium* spp., *S. faecalis*, *B. subtilis*, and *E. coli*. In terms of fungal populations, similarities were found with Wu *et al*. (2024), who indicated that geography and host species significantly influence

rodent microbiomes, but our findings contrast with those of Oduro*et al*. (2025), who reported *E. coli* and *Klebsiella* spp. as the most dominant bacteria in Ghanaian rodent bush-meat. Additionally, our observations differ from those of Katani*et al*. (2019), who identified Firmicutes as the leading phylum in bush-meat samples from the Serengeti, indicating strong ecological and methodological factors affecting observed microbiota.

Differences noted across host species and anatomical sites suggest specialization in ecological niches. The bacterial load was greatest in the large intestine, where S. aureus, B. subtilis, and *S. faecalis* were prevalent, consistent with previous studies indicating increased microbial density towards the distal end of the gastrointestinal tract (Yang *et al*., 2023). The increased presence of *Lactobacillus* spp. in the intestines of squirrels corroborates earlier research showing that lactic acid bacteria thrive in areas rich in carbohydrates (Liu *et al*., 2021). Opportunistic fungi like *C. albicans* and *Neurospora* spp. were found in greater numbers in the stomach and anus, while *Micrococcus* spp. and *Enterobacter* spp. were consistently present on the skin, illustrating microbial adaptability to the surfaces of their hosts (Egbagba*et al*., 2021). Antibiotic resistance profiling indicated sensitivity to pefloxacin and ciprofloxacin yet demonstrated resistance to ampicillin, azithromycin, and streptomycin, especially among *Corynebacterium* spp. Similar resistance trends have been observed in rodent samples from Europe and Asia (Jalal *et al.*, 2019; Smoglica*et al*., 2023), suggesting that environmental exposure to antibiotics—likely stemming from agricultural or veterinary use- may promote resistance development in wildlife.

The identification of MDR Corynebacterium spp. and S. faecalis is particularly alarming given their potential to lead to opportunistic infections, ranging from skin and soft-tissue infections to bacteremia and endocarditis (Arnés-García*et al*., 2024). In Abudu and Iguedolor, where giant rats and squirrels are commonly consumed as bush meat, the risk of exposure to pathogens such as *S. aureus*, *E. coli*, *C. albicans*, and *Rhizopus* spp. may arise from inadequate preparation or the consumption of undercooked meat. The threat extends beyond zoonotic diseases to encompass the potential spread of antimicrobial resistance factors, as highlighted by recent research from Nigeria and various other African regions (Odetokun*et al*., 2023; Amuasi*et al*., 2023). This dual risk underscores the potential for bushmeat to act as a conduit for zoonotic disease transmission and contribute to the development of antimicrobial resistance (Olaru*et al*., 2023; Oduro*et al*., 2025).

4. CONCLUSION

This research shows that giant rats (Cricetomys spp.) and squirrels (Funisciurus spp.) found in Abudu and Iguedolor carry a variety of microbial communities, including zoonotic pathogens like *Staphylococcus aureus* and *Candida albicans*. The detection of antimicrobial resistance, particularly in *Corynebacterium* spp., suggests that these rodents could serve as reservoirs for resistance genes within the One Health framework.

However, the dependence on culture-based methods may have led to an underestimation of microbial diversity and hindered the identification of unculturable or low-abundance organisms. The size of the sample was also relatively small, and the molecular level resistance mechanisms were not investigated. Future investigations that utilize molecular typing, resistance gene profiling, and metagenomic sequencing will be essential for elucidating transmission routes and enhancing strategies to reduce the risks

associated with zoonotic diseases and antimicrobial resistance.

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Conflict of Interest

Authors declared non

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