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Presence of *Salmonella enterica* subsp. *arizonae* in bushmeat from the Mulundu department of the Ogooué–Lolo province, Gabon

BEKALE OBAME Aimé Lionel Loïc[1], MBEHANG NGUEMA Pierre Philippe*[1], LENDAMBA Romeo Wenceslas[2,3], MAKANGA Boris Kevin[1], OBAGUE MBEANG Jean Constant[1], NDONG ATOME Guy Roger[4], ZINGA KOUMBA Christophe Roland[1]

[1]Institut de Recherche en Ecologie Tropicale (IRET) / Centre National de la Recherche Scientifique et Technologique (CENAREST)

[2]Centre de Recherche Médicale de Lambaréné (CERMEL), Department of clinical Operations, BP : 242, Lambaréné, Gabon

[3]Ecole Doctorale Régionale (EDR) d'Afrique Centrale en Infectiologie Tropicale de Franceville, PB : 876, Franceville, Gabon

[4]Département de Chimie, Faculté des Sciences, Université des Sciences et Techniques de Masuku (USTM)

ABSTRACT: In Africa, most investigations on *Salmonella* spp. have focused on isolates from humans, poultry, and domestic animals, whereas studies on wild terrestrial mammals remain limited. Consequently, the occurrence of *Salmonella* spp., particularly *Salmonella enterica* subsp. *arizonae*, in African wildlife is underreported. In Gabon, there is little to no information on the presence of antimicrobial-resistant *S. enterica* subsp. *arizonae* in bushmeat. This study aimed to isolate and characterise antibiotic resistance in *S. enterica* subsp. *arizonae* recovered from wildlife in Mulundu department, Lastoursville, Gabon. A total of 147 bushmeat samples representing 20 animal species were collected. After bacterial culture and identification, 23 samples (15.65%) from eight species were positive for *S. enterica* subsp. *arizonae*. The distribution of isolates was as follows: Peters' duiker (34.78%), blue duiker (26.09%), African wood owl (13.04%), moustached monkey (8.69%), pangolin (4.35%), genet (4.35%), crocodile (4.35%), and African brush-tailed porcupine (4.35%). Resistance profiles revealed the presence of multidrug-resistant strains. One isolate from a moustached monkey showed resistance to three antibiotic families, namely sulfonamides (sulfonamide), fluoroquinolones (ofloxacin), and β-lactams (cefoxitin, ampicillin). Another isolate from a Peters' duiker exhibited resistance to six antibiotics: cefotaxime, cefepime, sulfonamide, ertapenem, cefoxitin, and ampicillin. Additionally, isolates from Peters' duiker (n=3), blue duiker (n=2), wood owl (n=1), genet (n=1), and pangolin (n=1) were resistant to ertapenem, cefoxitin, and ampicillin. These findings demonstrate the circulation of *S. enterica* subsp. *arizonae* in wildlife consumed as bushmeat in Gabon. This represents a potential source of antimicrobial-resistant pathogens for human populations relying on game meat.

KEYWORDS: *Salmonella enterica* subsp. *Arizonae*, antimicrobial resistance, wildlife, Mulundu department, Gabon

INTRODUCTION

Bacterial resistance to antibiotics constitutes a global public health concern and falls within the framework of the "One Health" concept – one health for all [1, 2]. The phenomenon of bacteria and genes resistant to antibiotics affects all continents and diverse environments, whether urban, rural, community-based, or hospital settings [3, 4]. This phenomenon is observed not only in humans but also in avifauna, domestic animals, livestock, and terrestrial and aquatic wildlife. Wild animals act both as potential reservoirs of antimicrobial resistance and as sentinels reflecting the presence of bacteria with zoonotic potential in the environment [1, 2]. Enterobacteria play a predominant role in the transmission of resistant bacteria and resistance genes between these different compartments and may be responsible for zoonotic infections. These enterobacteria inhabit the gastrointestinal tract of both humans and animals. Among them, the genus *Salmonella* is of particular interest in this study, as it is potentially responsible for zoonoses and is a causal agent of both invasive and non-invasive disease in humans [5].

Salmonellosis is an infectious disease caused by *Salmonella* spp., clinically characterised by acute fever, nausea, abdominal pain, and diarrhoea [5]. It is caused by multiple serotypes of *Salmonella* spp. and ranks as the third leading cause of global mortality among foodborne diseases [5]. Salmonellosis, most emerging infectious diseases, is a zoonosis [6]. For the general public, the role of wildlife as a reservoir of bacterial zoonotic pathogens is often overlooked [7]. This may be attributed to the fact that the severity of bacterial infections is generally more endemic than pandemic in contrast to viral infections such as HIV, Ebola haemorrhagic fever, influenza, or COVID-19. Nevertheless, bacterial infections—particularly those caused by enterobacteria, including salmonellosis—remain highly prevalent, active, and associated with recorded deaths each year. According to a WHO report, an estimated 59,000 deaths worldwide in 2010 were attributable to non-typhoidal *Salmonella* (NTS), with Africa accounting for 32,000 deaths, including 22,000 due to invasive disease, predominantly in children [8, 9]. Non-typhoidal *Salmonella* is reported as one of the leading causes of bacteraemia in neonates, infants, and immunocompromised individuals [9]. The global burden of gastroenteritis due to non-typhoidal *Salmonella* is estimated at 93.8 million cases annually, with 155,000 deaths [10]. In addition, although less frequently reported, human infections with *S. enterica* subsp. *arizonae* have been documented [2, 11, 12]. For example, Waterman et al. reported four cases of severe *S. enterica* subsp. *arizonae* infections in Latino patients [13]; in 2015, Briard et al. described a case of meningitis in an 18-day-old neonate exposed to a corn snake (*Pantherophis guttatus*) [14]; Yi-Chien Lee et al. reported cases of *S. enterica* subsp. *arizonae* infections in adults in southern Taiwan [15]. These cases frequently follow ingestion of, or contact with, reptiles or other animal species. *S. enterica* subsp. *arizonae* is a commensal agent not only found in reptiles but also in a diversity of animal hosts such as wild vultures [16], free-ranging aquatic turtles [17], badgers (*Meles meles*) and foxes (*Vulpes vulpes*) [2], as well as wild crocodiles (*Crocodylus acutus* and *C. moreletii*) [18], among others.

Studies on *Salmonella* spp. in Africa have focused predominantly on isolates from humans, poultry, domestic animals, and livestock used for human consumption, whereas few documented studies address *Salmonella* spp. in wild terrestrial mammals. Consequently, the occurrence of *Salmonella* spp., and specifically *S. enterica* subsp. *arizonae*, within the wildlife environment is under-reported in Africa. Central Africa, and in particular the Congo Basin with its rich biodiversity, represents a significant study population, given that rural communities depend on forest-related activities and consume bushmeat derived from wildlife. Furthermore, Chomel et al. reported that Central Africa and the Amazon Basin consume approximately 1–3.4 million tonnes and 67–164 million kilograms of bushmeat per year, respectively [7]. This practice constitutes a risk factor for the emergence of zoonoses originating from bushmeat.

In Gabon, studies on antibiotic-resistant bacteria in wildlife have been conducted but remain scarce, and they neither cover the entire national territory nor encompass all protected and unprotected areas. Virtually none of the studies investigating antibiotic-resistant bacteria have reported the presence of *Salmonella enterica* subsp. *arizonae* in wildlife. Yet, *S. enterica* subsp. *arizonae* is a zoonotic pathogen of interest for investigating contamination and transmission routes, as well as phenotypic and genotypic antibiotic resistance traits, between humans, wildlife, domestic animals, and livestock.

Given the paucity of information on *Salmonella* in terrestrial wildlife in Gabon, and the absence of a national surveillance programme for such zoonoses, it is relevant to investigate the prevalence of antibiotic-resistant *Salmonella* spp. strains in bushmeat consumed by human populations in the Department of Mulundu, Ogooué-Lolo Province, Gabon.

MATERIALS AND METHODS

Research authorisation and study framework

Research authorisation for this study was granted by the Scientific Commission for Research Permits of the National Centre for Scientific and Technological Research (CENAREST) (Permit No. AR0033/17/MESRSFC/CENAREST/CG/CST/CSAR, issued on 4 July 2017). The study was conducted within the framework of the Sustainable Wildlife Management (SWM) project – CIRAD-IRET (Sustainable management of wild fauna and flora) in the Department of Mulundu, Lastoursville.

Study area and sampling periods

The study was carried out in the Ogooué-Lolo Province (located in central Gabon), in the city of Lastoursville, Department of Mulundu. Bushmeat was collected along three road axes: Mulundu–Lipaka 2 (the axis yielding the highest number of bushmeat samples), Mulundu–Malendé, and Mulundu–Dambi. Sampling was conducted over three periods. The first collection, in November 2022, yielded 34 bushmeat samples. The second collection, from 25 April to 10 May 2023, comprised 57 animals. The third collection, from 10 to 22 October 2023, yielded 56 animals. In total, 147 bushmeat samples were collected during the study period. All animals were dissected in situ at the provisional laboratory established at the Forestry Department station in Lastoursville

Specimens sampling

Freshly killed animals, obtained from local hunters, were purchased at the designated collection sites along the pre-identified road axes by our research team, which comprised two senior researchers (PhDs) and two doctoral candidates, and subsequently transported to the laboratory.

Upon arrival at the field laboratory, each animal species was identified using an identification catalogue and with the assistance of officers from the Department of Water and Forestry. The weight, sex, and presence of ectoparasites were recorded. Buccal and nasal samples were collected using sterile swabs. Fecal samples were obtained by dissecting the distal portion of the caecum. Each swab was preserved in a 2 mL tube containing a mixture of phosphate-buffered saline (PBS) (700 µL) and glycerol (300 µL). For fecal matter, 10 g of each specimen was preserved in a 15 mL tube containing 7 mL of PBS and 3 mL of glycerol.

Analysis of fecal samples

Bacterial culture, isolation, and identification of colonies

At the Microbiology Laboratory of IRET, 100 µL of each fecal sample was inoculated into Rappaport–Vassiliadis enrichment broth in 2 mL tubes and incubated at 37 °C for 48 hours. Subsequently, 100 µL of each enriched culture was streaked onto Salmonella–Shigella agar and incubated at 37 °C for 24 hours. After incubation, colonies exhibiting a pink or red colouration with a central black spot were considered presumptive *Salmonella* spp. and were further confirmed using the Enterosystem 18R (Liofilchem, Italy) as *Salmonella choleraesuis* subsp. *arizonae*.A total of 147 faecal samples were obtained from 20 species of bushmeat as shown in the table below (Table 1).

Table 1. Species of animals collected

Wild anmals names	Count by species
Atherure	27
Greater Cane Rat (Aulacode)	1
Blue Duiker	31
Peters' Duiker	28
Bay Duiker (Cephalophus dorsalis)	2
Greater Spot-nosed Monkey (Cercopithecus nictitans)	4
Crowned Monkey (Cercopithecus pogonias)	1
Owl	7
Water Chevrotain	6
Crocodile	1
Genet	1
Mongoose	2
Black-footed Mongoose	1
Moustached Monkey (Moustac)	15
African Palm Civet (Nandinia)	1
Pangolin	12
Red River Hog (Potamochoerus porcus)	2
Potto	1
Palm Rat	3
Sitatunga	1
Total number of species: 20	Total number of animals : 147

Antibiotic susceptibility testing

Antibiotic susceptibility was assessed using the disc diffusion method on Mueller–Hinton agar (BioMérieux, France), as described by Bauer et al. (1966), and interpreted according to the clinical breakpoints recommended by the Clinical and Laboratory Standards Institute (CLSI, 2023). The following antibiotics were tested on the faecal isolates: amoxicillin/clavulanic acid (20/10 µg), cefotaxime (30 µg), ceftazidime (30 µg), cefepime (30 µg), aztreonam (30 µg), sulphonamide (23.75 µg), ofloxacin (5 µg), ertapenem (10 µg), cefoxitin, kanamycin (5 µg), and ampicillin. In total, 11 antibiotics were evaluated for the susceptibility of S. arizonae isolates from faecal samples. Extended-spectrum β-lactamase (ESBL) production was investigated using the double-disc synergy test on Mueller–Hinton agar with the following antibiotic discs: amoxicillin/clavulanic acid (20/10 µg), aztreonam (30 µg), cefepime (30 µg), cefotaxime (30 µg), and ceftazidime (30 µg).

RESULTS

Prevalence of *Salmonella choleraesuis subsp. arizonae* in faecal samples

A total of 147 faecal samples, belonging to 20 different species of bushmeat, were analysed. Following bacterial culture and colony identification, 33 samples (22.4%), originating from 8 species, were positive for Salmonella choleraesuis subsp. arizonae. The distribution of positive isolates was as follows: bats (11; 33.3%), Peter's duikers (7; 21.2%), blue duikers (5; 15.6%), African wood owls (3; 9.1%), moustached monkeys (2; 6.1%), brush-tailed porcupines (1; 3.0%), pangolins (1; 3.0%), genets (1; 3.0%), and crocodiles (1; 3.0%) (Table 2).

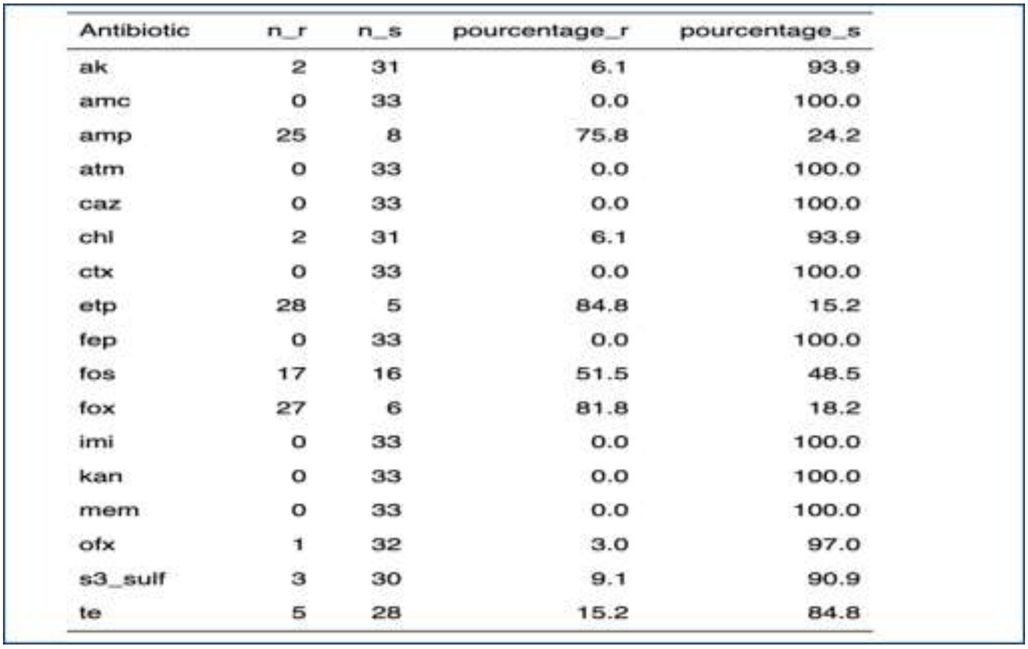
Table 2. Bushmeat species positive for *Salmonella choleraesuis* subsp. Arizonae

Species	Count	%
Atherure (Porcupine)	1	3.0
Peters' Duiker (*Cephalophus dorsalis*)	1	3.0
Crocodile	1	3.0
Genet	1	3.0
Pangolin	1	3.0
Moustached Monkey (*Cercopithecus cephus*, "Moustac")	2	6.1
Owl	3	9.1
Blue Duiker (*Cephalophus monticola*)	5	15.6
Peters' Duiker (*Cephalophus callipygus*)	7	21.2
Bat	11	33.3
Total	33	100

Antibiotic susceptibility testing (Table 3)

This general table presents the frequencies of resistance and susceptibility to the antibiotics tested. From this overview, a clear trend can already be observed, namely, high percentages of susceptibility, reaching up to 100% for certain antimicrobial agents.

Table 3. Overall antibiotic susceptibility



Antibiotic	n_r	n_s	pourcentage_r	pourcentage_s
ak	2	31	6.1	93.9
amc	0	33	0.0	100.0
amp	25	8	75.8	24.2
atm	0	33	0.0	100.0
caz	0	33	0.0	100.0
chl	2	31	6.1	93.9
ctx	0	33	0.0	100.0
etp	28	5	84.8	15.2
fep	0	33	0.0	100.0
fos	17	16	51.5	48.5
fox	27	6	81.8	18.2
imi	0	33	0.0	100.0
kan	0	33	0.0	100.0
mem	0	33	0.0	100.0
ofx	1	32	3.0	97.0
s3_sulf	3	30	9.1	90.9
te	5	28	15.2	84.8

Figure 1 illustrate the trend previously observed in Table 3:

- Five antibiotics demonstrated very high susceptibility rates (84.8%–97%) [TE, AK, CHL, OFX, S3_SUFL].
- Eight antibiotics showed no resistance (100% susceptible).
- Three antibiotics exhibited high resistance rates: ETP with the highest (84.8%), followed by FOX (81.8%) and AMP (75.8%).
- The lowest resistance rate was observed for OFX (3%).
- One antibiotic displayed nearly equivalent proportions of resistance and susceptibility, namely FOS (R = 51.5%, S = 48.5%).

Overall, the majority of antibiotics tested remained highly effective, with susceptibility rates exceeding 90%. Nevertheless, certain antibiotics presented concerning resistance patterns, particularly AMP, ETP, and FOX, which exhibited markedly elevated resistance rates.

In conclusion, this figure highlights the need to adapt antibiotic prescriptions for local populations consuming bushmeat in accordance with the regional resistance profiles. It further underlines the importance of continuous surveillance of bacterial resistance to safeguard the effectiveness of available treatments.

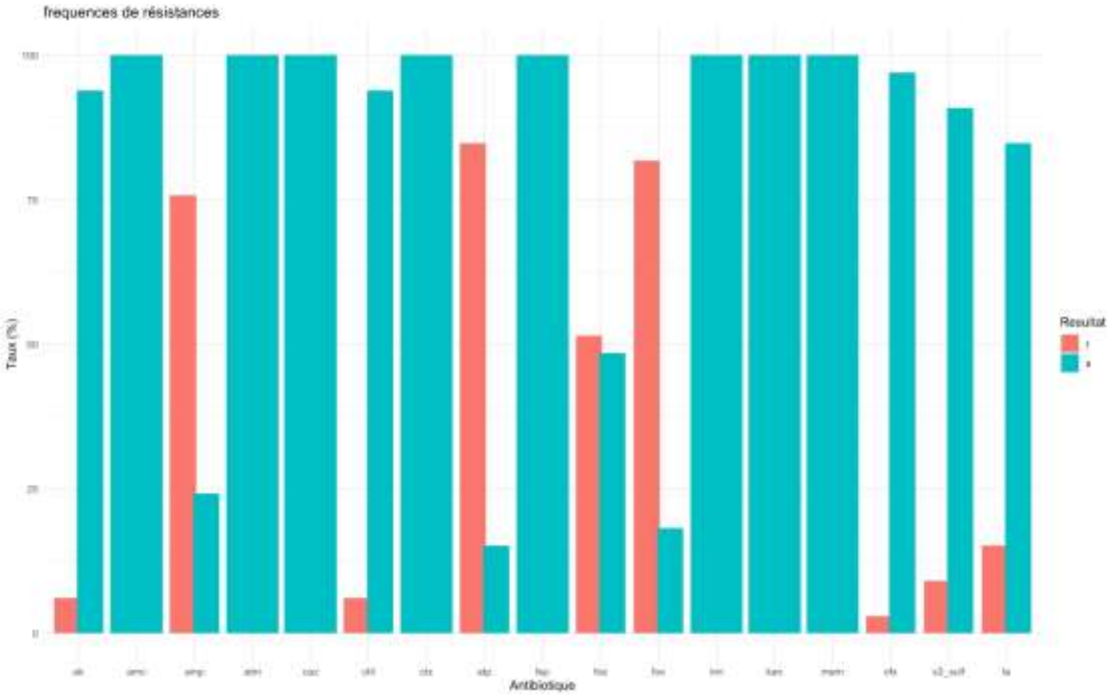


Figure 1: The trend of *Salmonella* susceptibility to antibiotics

Table 4. *Salmonella* susceptibility to antibiotics in different bushmeat species.

Molécules	Resistance (R)	Sensitivity (S)
Ak	**Very weak**	**Very high**
Amc	**-**	**Total (100%)**
Amp	**High**	**Weak**
Atm	**-**	**Total (100%)**
Caz	**-**	**Total (100%)**
Chl	**Very weak**	**Very high**
Ctx	**-**	**Total (100%)**
Etp	**High**	**Weak**

Fep	**-**	**Total (100%)**
Fos	**Moderate**	**Moderate**
Fox	**High**	**Weak**
Imi	**-**	**Total (100%)**
Kan	**-**	**Total (100%)**
Mem	**-**	**Total (100%)**
Ofx	**Very weak**	**Very high**
S3_sulf	**Very weak**	**Very high**
Te	**Weak**	**Very**

Resistance (R) analysis

By filtering the dataset to retain only the resistant isolates (R), a total of 110 occurrences were recorded across 10 species. The Cape fruit bat (39), Peter's duiker (25), and the blue duiker (15) together accounted for 70% of the sample (Figure 2/Table 4).

Figure 2: Antibiotics susceptibility by animal species

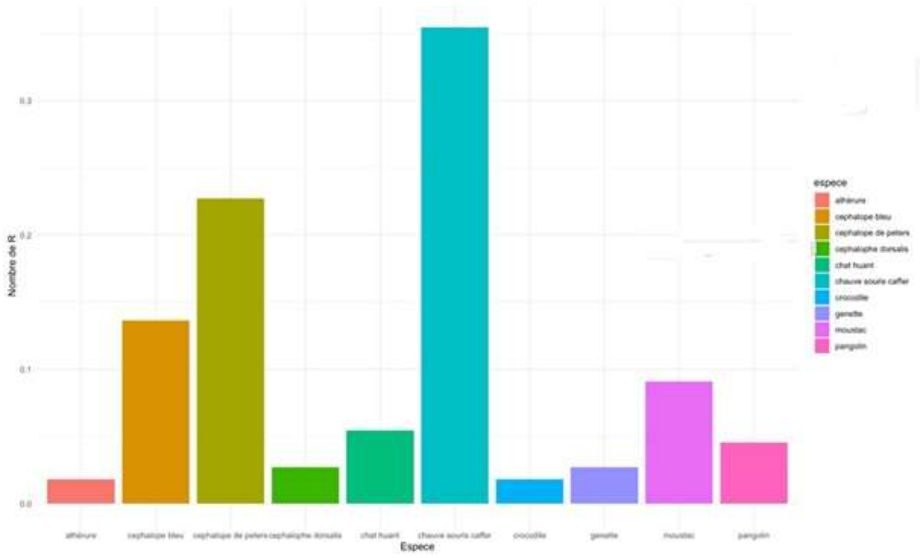


Figure 2. *Salmonella* resistance to antibiotics in different bushmeat species.

This graph shows an uneven distribution, as resistance is not uniformly spread across species; some species are more strongly represented than others.

Most affected species: The Cape fruit bat (Eidolon helvum caffer) clearly stands out, with the highest number of resistant isolates among all species represented.

Species with moderate resistance: Peter's duiker also exhibited a relatively high level of resistance, although lower than that of the Cape fruit bat. The blue duiker also demonstrated a notable level of resistance, followed by the moustached monkey.

Species with low resistance: The brush-tailed porcupine, bay duiker, African wood owl, crocodile, genet, and pangolin displayed low to moderate levels of resistance. Among them, the crocodile and the genet were the least affected.

Susceptibility (S) distribution

Here, only susceptible (S) isolates were considered, following the same filtering approach applied to resistance. The most represented species were once again the Cape fruit bat, Peter's duiker, and the blue duiker, together accounting for approximately 70% of the total sample. These were followed by the African wood owl, the moustached monkey, and others (Figure 3).

Figure 3: Distribution of antibiotics susceptibility in bushmeat species

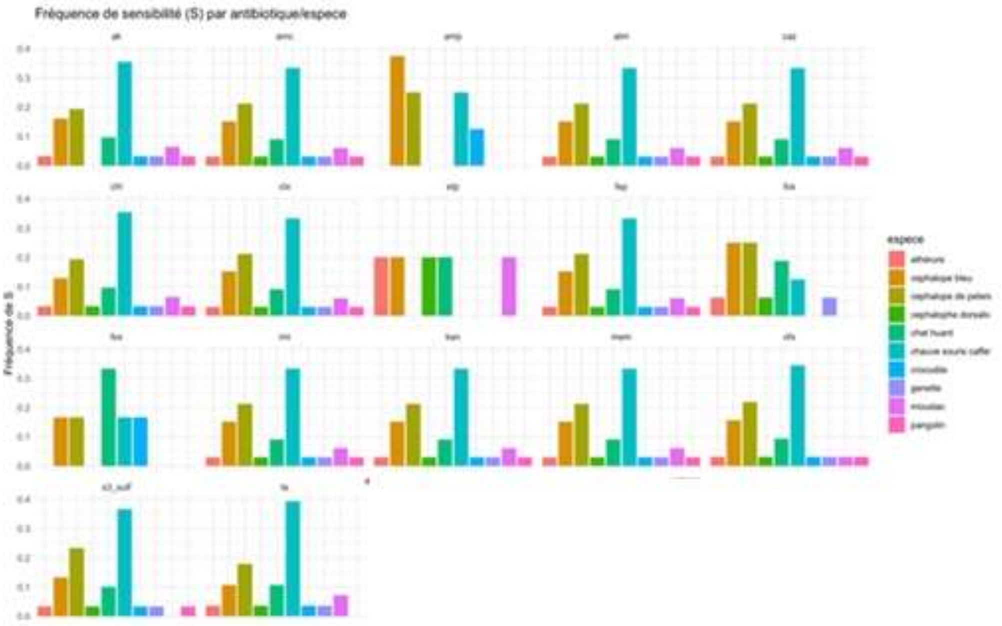


Figure 3 illustrates the frequency of antibiotic susceptibility (S) across different animal species. Each subplot (facet) represents a specific antibiotic, and each bar depicts the susceptibility frequency of a given species to that antibiotic.

Inter-species variability:

Antibiotic susceptibility varies considerably between species. Certain species exhibit markedly higher susceptibility frequencies to specific antibiotics.

Most susceptible species:

The African straw-coloured fruit bat (*Chauve-souris caffer*) consistently shows the highest susceptibility frequencies for the majority of tested antibiotics. The Peters' duiker (*Cephalophus callipygus*) and the blue duiker (*Philantomba monticola*) also display notable susceptibility frequencies for several antibiotics.

Antibiotics with high overall susceptibility:

Antibiotics such as amikacin (AK), amoxicillin–clavulanic acid (AMC), aztreonam (ATM), ceftazidime (CAZ), cefepime (FEP), and meropenem (MEM) show pronounced susceptibility peaks in certain species, particularly the African straw-coloured fruit bat. For ampicillin (AMP), susceptibility is primarily observed in Peters' duiker and blue duiker.

Antibiotics with low overall susceptibility:

Some antibiotics, including ertapenem (ETP), fosfomycin (FOS), ofloxacin (OFX), and tetracycline (TE), exhibit low or negligible susceptibility frequencies across most species, with isolated peaks (e.g., pangolin for ETP).

Least susceptible species:

Species such as the African brush-tailed porcupine (*Atherurus africanus*), genet (*Genetta spp.*), moustac monkey (*Cercopithecus cephus*), and pangolin generally display low susceptibility frequencies for most antibiotics.

Overall, the African straw-coloured fruit bat emerges as the most susceptible species to the majority of tested antibiotics. The distribution of susceptibility frequencies is heterogeneous among species: some antibiotics are effective primarily in one or two species.

DISCUSSION

This study is framed within a One Health approach, recognising that the phenomenon of antibiotic-resistant bacteria affects both humans and terrestrial wildlife. The aim was to improve understanding of the potential sources and reservoirs contributing to the emergence of zoonoses at the human–wildlife interface. Investigations into the presence of *Salmonella* spp., particularly *Salmonella choleraesuis* subsp. *arizonae*, in wildlife remain scarce in Central Africa, including in Gabon. Our study, conducted in Gabon, revealed the presence of *S. choleraesuis* subsp. *arizonae* in bushmeat consumed by local populations in the Mulundu Department, Ogooué–Lolo Province. Out of 147 bushmeat faecal samples analysed, only 33 (22.5%) tested positive for *Salmonella* spp., all of which were identified as *S. choleraesuis* subsp. *arizonae*.

These findings are comparable to those of a previous Gabonese study on indigenous foods, which reported a prevalence of 18.69% [19]. This could be explained either by the fact that the analyzed specimens were obtained from uncooked bushmeats at the time of collection, thus allowing persistence of *Salmonella* spp [20], or by the inefficacy of potential heat treatments due to a high initial bacterial load or the presence of high fat content in wild animal meat. Other studies report varying prevalence across regions. For instance, Belo et *al*. (2022) identified *Salmonella* spp. 23/210 (10.9%) in wild birds in the Amazon rainforest of Brazil [21]; Casalino et *al*. (2021) isolated *Salmonella* spp. from 42/69 (60.9%) turtles housed in a regional wildlife rescue centre in Apulia [22] (southern Italy); while Mafizur et *al*. (2024) reported detection of *Salmonella* spp. in 3% (21/699) of fecal samples from free-ranging wild animals in South Korea [23]. In contrast to these findings, our results suggest that *Salmonella* spp. prevalence in wildlife may vary substantially between geographical regions.

Salmonella choleraesuis subsp. *arizonae* is a bacterial subspecies associated with joint infections, soft tissue infections, and dermatological disorders [24]. It predominantly affects neonates and immunocompromised individuals. Other clinical manifestations include gastroenteritis, vomiting, headaches, and fever. In reptiles such as crocodiles, this subspecies may cause enteritis and septicaemia under severe stress conditions [25]. Although relatively low in prevalence within our sampling, the detection of *Salmonella choleraesuis* subsp. *arizonae* is nonetheless concerning, particularly given its resistance to clinically important antibiotics, including ampicillin, cefoxitin, and ertapenem, all belonging to the β-lactam family [26]. Moreover, all 33 isolates of *S. choleraesuis* subsp. *arizonae* exhibited resistance to at least one antibiotic.

In this study, ertapenem demonstrated the highest resistance rate, with 28 out of 33 isolates (84.8%) resistant, followed by cefoxitin (27/33, 81.8%) and ampicillin (25/33, 75.8%). Ertapenem, a carbapenem antibiotic, is of major clinical importance and considered a last-resort treatment. Resistance of *S. choleraesuis* subsp. *arizonae* to ertapenem may reflect contamination of wildlife environments by human activity, either via waterways, hunting practices, or deforestation for subsistence agriculture. In the study area, bushmeat hunting sometimes occurs in close proximity to human dwellings, occasionally within 100 meters of villages, which may increase the risk of cross-contamination [27]. Ampicillin also showed a high resistance rate (75.8%) in our study. Similarly, Gargano et al. (2021), investigating antibiotic susceptibility profiles in wildlife, reported resistance to ampicillin (21.6%), kanamycin (10%), and cefotaxime (5%) [28]. In addition, O'Hagan et al. (2021) identified 14 *Salmonella* spp. isolates, including a single *S. choleraesuis* subsp. *arizonae* isolate from 146 badger fecal samples, which exhibited multidrug resistance to several β-lactam antibiotics, including ampicillin, ceftazidime, cefoxitin, cefotaxime, and ertapenem [2]. The resistance patterns observed in our isolates may also be explained by genetic mechanisms such as spontaneous mutations [29] or the presence of integrons and plasmids [30]. Indeed, antimicrobial resistance (AMR) is a natural evolutionary phenomenon, although its frequency is substantially amplified by the inappropriate and excessive use of antibiotics in humans and livestock [31, 32]. Resistance to sulphonamides was relatively low in our study, with 3/33 isolates (9.1%) resistant. Sulphonamides are bacteriostatic agents that inhibit folic acid synthesis [33]. Similar findings have been reported in other studies, where resistance was detected against combinations such as sulphamethoxazole–trimethoprim and sulphadiazine–sulphamerazine–sulphamethazine [28, 33]. Screening for extended-spectrum β-lactamase (ESBL) production by agar disc diffusion did not reveal any "champagne cork" effect. This result is consistent with the findings of O'Hagan et *al*. (2021)[2], who reported that *S. enterica* subsp. *arizonae* (syn. *S. choleraesuis* subsp. *arizonae*) isolated from badgers was resistant to multiple antimicrobials but did not produce ESBLs. Regarding wildlife species, the blue duiker (*Philantomba monticola*) and Peters' duiker (*Cephalophus callipygus*) are African bovids, while the brush-tailed porcupine (*Atherurus africanus*) and moustached monkey (*Cercopithecus cephus*) are also endemic to Africa. In contrast, species such as the genet (*Genetta*), crocodile, and pangolin are distributed across several continents. The presence of *S. choleraesuis* subsp. *arizonae* across such taxonomically and geographically diverse hosts suggests its potential as a sentinel marker for predicting the emergence of zoonoses linked to this bacterial subspecies.

Limitations of the study: A limitation of this study was the absence of molecular analyses to confirm the presence of *Salmonella* through the detection of virulence-associated genes, particularly the *invA* gene, which is directly associated with pathogenicity in *Salmonella*.

CONCLUSION

This study reports the circulation of *Salmonella cholerasius* spp. *arizonae* in wildlife species consumed as bushmeat in the Mulundu department, Ogooué–Ivindo, Gabon. The bacterium represents a potential threat to human health, either through direct consumption of contaminated meat or indirectly via ecological disturbances linked to human activities. Although overall antimicrobial resistance (AMR) rates were relatively low, the detection of elevated resistance to ertapenem and cefoxitin—antibiotics of high clinical relevance—raises concern and highlights the need for preventive measures against AMR emergence. The study underlines the necessity of establishing a dedicated AMR surveillance programme targeting bushmeat, alongside broader wildlife monitoring strategies. Notably, it also provides the first evidence of *S. cholerasius* spp. *arizonae* in species not previously identified as hosts, including Peters' duiker, blue duiker, moustached monkey, African brush-tailed porcupine, genet, and pangolin.

By advancing knowledge on the ecology and resistance of this pathogen in wild fauna, the findings reinforce the role of wildlife as reservoirs and potential transmission sources, while offering valuable guidance for prophylaxis and therapy in the event of emerging infections linked to bushmeat consumption.

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