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Research Article

Presence of Antibiotic-Resistant *Aeromonas caviae* in Bush Meat from the Mulundu Department in Ogooué-Lolo, Gabon

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Abstract

Aeromonas caviae is a bacterium of the genus *Aeromonas* and the family Aeromonadaceae. It is present at the house of fish and animals. Its clinical diagnosis is often uncommon in our medical analysis laboratories. It is a resistant and multi-resistant bacterium to antibiotics of clinical importance. Our study aimed to determine the prevalence of antibiotic resistance of *A. caviae* in wild animals in the Mulundu department of Gabon. Our sampling included 147 terrestrial wild animals of 20 different species. 53 animals of 10 different species tested positive for *A. caviae* after identification tests on API 20 NE, 16 antibiotics were tested and the overall rates of resistance R (49.06%) and sensitivity S (50.94%) indicated a balanced situation between resistant and sensitive strains on a global scale. The highest prevalence of antibiotic resistance was penicillin, oxacillin, vancomycin with 100% resistance for each of them, followed by the combination of ticarcillin + clavulanic acid (98.11%), ceftazidime (94.34%) and rifampicin (94.34%). On the other hand, the most sensitive antibiotics were tetracycline (100%), chloramphenicol (98.11%), gentamicin (96.23%), imipenem (94.34%), ciprofloxacin (84.91%) and tobramycin (71.70%). Several cases of multidrug-resistant bacteria were recorded. Our study highlights the presence of *A. caviae* in the wildlife of the said department, its potential for transmission to populations that consume it and highlights the crucial importance of monitoring the emergence of antibiotic-resistant bacteria in wildlife in Gabon.

Keywords: *Aeromonas caviae*; Resistance; Sensitivity; Antibiotic; Bushmeat; Mulundu; Gabon

Introduction

Antibiotic resistance is a global phenomenon. The presence of bacteria and their antibiotic resistance genes has been reported in humans, the environment, domestic and farm animals and wildlife (terrestrial, aquatic and avifauna) [1]. Most of the emerging diseases of recent decades are zoonoses of animal origin [2]. But the use of antibiotics to combat these zoonoses creates the emergence of antibiotic resistance [3]. In the phenomenon of zoonoses related to antibiotic resistance at the human-wildlife interface, enterobacteria and/or Gram-negative bacteria play a leading role in the spread of bacteria and their antibiotic resistance genes in the environment, but also a sentinel role in the proliferation of antibacterial resistance in terrestrial, aquatic and avifauna [4]. In clinical diagnosis and in the search for bacterial resistance in wildlife, the commonly found enterobacteria *are E. coli, Salmonella spp., Klebsiella spp., Serratia spp., Pseudomonas spp., Enterococcus* [5]. Other emerging pathogens less isolated in clinical routine in the laboratory remain and are possibly responsible for more or less serious infections, this is the case of *Aeromonas caviae* (*A. caviae*) [6]. Indeed, *Aeromonas caviae* is a bacterium responsible for gastroenteritis and other illnesses in humans [6]. *Aeromonas caviae* is a Gram-negative *bacillus* that belongs to the group of dominant *Aeromonas* species. It has been associated with human enteropathologies [7,8]. Bacteria of the genus *Aeromonas* cause infections in fish and other animals, but they also infect and colonize humans [9]. The antibiotic susceptibility of this bacterium varies from individual to individual and from species to species. It has natural resistance to certain beta-lactam antibiotics, including penicillin, oxacillin and ampicillin, but also to rifampicin and more or less to some aminoglycosides [10-14]. *A. caviae* is an etiological agent of several conditions in both immunocompromised or immunocompetent patients [9]. Furthermore, it has been established that animal proteins (meat, chicken, fish), vegetables and even wastewater can act as reservoirs for this bacteria and potential routes of contamination for bacteria from the genus *Aeromonas* for humans [9,15]. Frequent consumption of bushmeat and human intrusion into forest habitats of wildlife through subsistence agriculture, deforestation and hunting maintain frequent contact between humans and wildlife which could constitute health risk to the extent that its presence has been reported in wild fauna consumed by local populations [16-18]. This risk is exacerbated in the event of an epidemic, given the frequent and regular transportation of bush meat (which serves as a natural reservoir of antibiotic-resistant bacteria, such as *Aeromonas caviae*, from one geographical location to another and from one city to another, by land. This phenomenon is a common occurrence in Gabon [19,20]. Anthropogenic activities in the forest habitats of wild animals result in permanent contact between humans and these wild mammals, thereby promoting the exchange of pathogens. This, in turn, leads to therapeutic impasses in human clinical practice. This study is also aligned with an approach based on the "One Health" concept. Its objective is to monitor an emerging bacterium with zoonotic potential, which is rarely diagnosed in our laboratories in Gabon.

Material and Methods

Research Authorization and Study Framework

This study received formal approval from the Scientific Commission for Research Authorizations of the National Center for Scientific and Technological Research (CENAREST) under permit n° AR0033/17/MESRSFC/CENAREST/CG/CST/CSAR, dated July 4, 2017. It was conducted within the framework of the Sustainable Wildlife Management (SWM)-CIRAD-IRET project, aimed at promoting sustainable management of wild fauna and flora in the Mulundu Department of Lastoursville.

Study Area and Sampling Periods

The research took place in Ogooué-Lolo Province, Central Gabon, specifically in Lastoursville city and its surrounding Mulundu Department. Bushmeat samples were collected along three primary road axes radiating from Lastoursville to neighboring villages: Axis 1 toward Lipaka 2 (the site of the highest game presence), Axis 2 toward Malendé and Axis 3 toward Dambi on the route to Okondja (Fig. 1). Sampling occurred over three separate periods.: November 10-20, 2022 (34 samples), April 25-May 10, 2023 (57 samples) and October 10-22, 2023 (56 samples), resulting in a total of 147 bushmeat samples. All dissections were carried out under strict biosafety protocols at the field laboratory located at the Water and Forestry Department station in Mulundu.

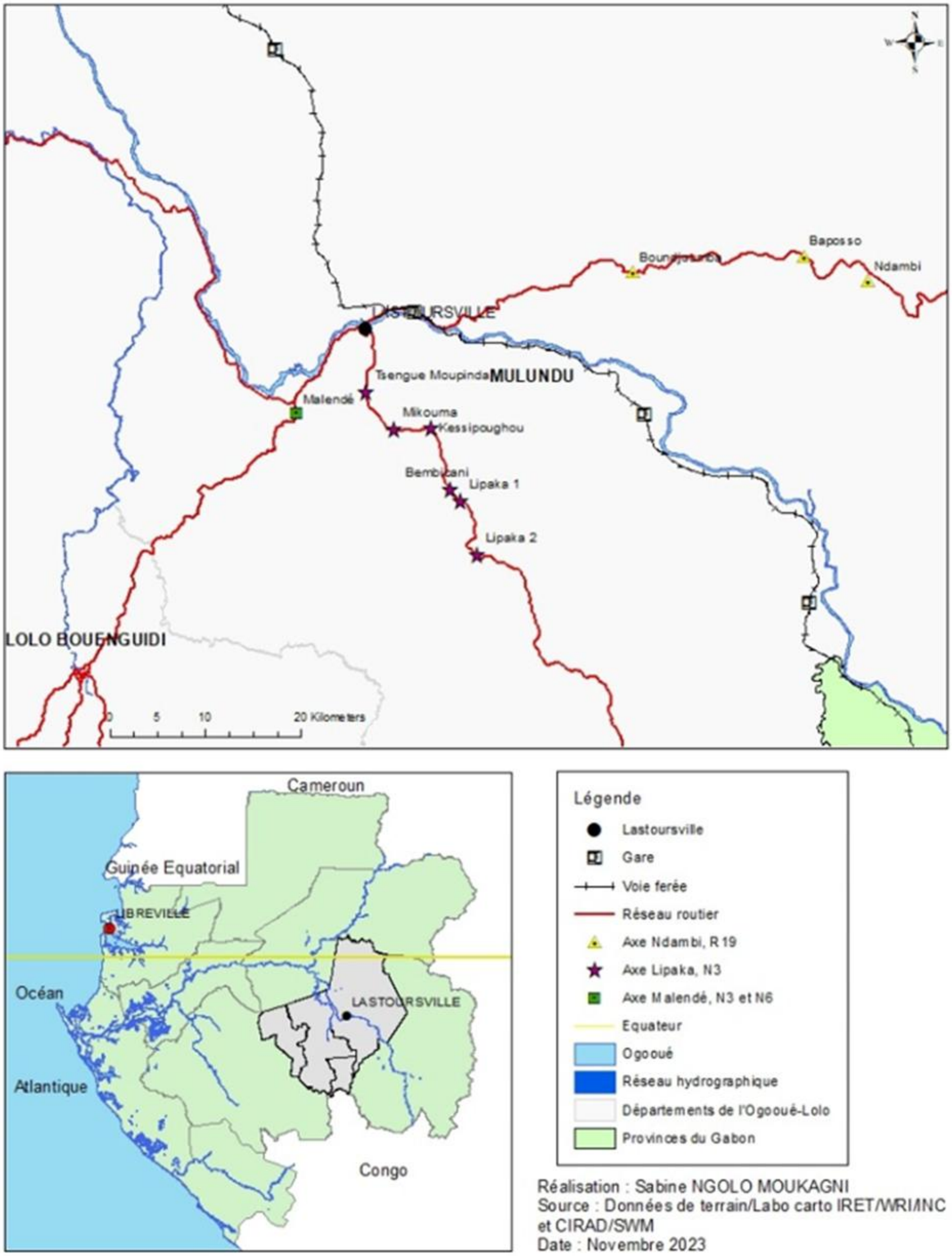


Figure 1: Road axes for collecting bushmeat samples (Source: NGOLO MOUKAGNI Sabine).

Sample Handling and Species Identification

Freshly hunted animals were acquired directly from local hunters at collection sites along the designated road axes and transported promptly to the field laboratory. Upon arrival, species identification was performed using a standardized identification catalog and with assistance from agents of the Water and Forest Service. During processing, data on weight, sex and ectoparasite presence were recorded. Oral and nasal swabs were collected using sterile swabs, followed by fecal samples obtained from dissecting the distal cecum. Each swab was stored in a 2 mL tube containing 700 µL of Phosphate-Buffered Saline (PBS) supplemented with 300 µL of glycerol. Fecal samples (approximately 10 g each) were preserved in 15 mL tubes containing a mixture of 7 mL PBS and 3 mL glycerol.

Microbiological Analysis of Fecal Samples

At the IRET Microbiology Laboratory, 100 µL of each fecal sample was enriched in 2 mL MacConkey broth and incubated at 30°C for 48 hours. Cultures were then streaked onto MacConkey agar and incubated at 37°C for 24 hours. Colonies exhibiting characteristic white coloration and rounded morphology (2-3 mm diameter) were re-isolated on Tryptone Soy Agar (TSA) and incubated at 30°C for another 24 hours. Bacterial identification was performed using the API 20 NE biochemical gallery. A total of 147 fecal samples from 20 distinct bushmeat species were analyzed (Table 1).

Wild Animal Names	**Number Per Species**
Brush-tailed porcupine (*Atherurus africanus*)	27
Cane rat (*Thryonomys spp.)*	1
Blue duiker (*Philantomba monticola)*	31
Peter's Duiker (*Cephalophus callipygus*)	28
Bay duiker (*Cephalophus dorsalis)*	2
Putty-nosed Monkey (*Cercopithecus nictitans*)	4
Crested mona monkey (*Cercopithecus pongonias*)	1
African Civet (*Civettictis civetta*)	7
Water chevrotain (*Hyemoschus aquaticus)*	6
Crocodile (*Crocodylus spp.)*	1
Genetta (*Genetta spp.)*	1
Mongoose (*Bdeogale nigripes)*	2
Black-legged mongoose (*Herpestes spp.)*	1
Moustached monkey (*Cercopithecus cephus)*	15
African palm civet (*Nandinia binotata)*	1
Long-tailed Pangolin (*Uromanis tetradactyla)*	12
Red river hog (*Potamochoerus porcus)*	2
Potto (*Perodicticus spp.)*	1
Giant pouched rat (*Cricetomys spp.)*	3
Sitatunga (*Tragelaphus spekii)*	1
Total number of species 20	Total number of animals 147

Table 1: Species of animals collected.

Antibiotic susceptibility testing

Antimicrobial susceptibility was evaluated using the disc diffusion method on Mueller-Hinton agar (BioMérieux, France), (Bauer, et al., 1966), following the Clinical and Laboratory Standards Institute (CLSI) 2023 guidelines for interpretive thresholds. The tested antibiotics included: ticarcillin + clavulanic acid (85 µg), piperacillin + tazobactam (100/10 µg), imipenem (10 µg), ceftazidime (30 µg), tobramycin (30 µg), ciprofloxacin (5 µg), chloramphenicol (30 µg), gentamicin (10 µg), tetracycline (30 µg), vancomycin (30 µg), rifampicin (5 µg), amoxicillin + clavulanic acid (20/10 µg), penicillin (10 µg), oxacillin (5 µg), cephalexin (30 µg) and cefepime (30 µg).

Statistical Analysis

Data analyses were conducted using R statistical software. Differences in antibiotic resistance proportions across animal species were assessed using chi-square tests. Data visualization was performed through graphical representations to effectively communicate the results.

Results

Species Composition and Abundance

The 147 bushmeats belonged to 20 species, including Blue duiker (*Philantomba monticola*), Peter's Duiker (*Cephalophus callipygus*), Brush-tailed porcupine (*Atherurus africanus*), Moustached monkey (*Cercopithecus cephus*) and Long-tailed Pangolin (*Uromanis tetradactyla*) were the most abundant in this sampling (Table 1).

Bacterial Identification

Identification of all colonies with the API 20 gallery NE gave the following biochemical characteristics (Table 2).

Oxidase	Mobility	O/F	VP	Indole	Citrate	Urease	Nitrate	H2S	Glucose
+	-/+	-/+	-	+	+	-	+	-	+

Table 2: Biochemical test results for bacterial identification.

The analysis revealed that ten different bushmeat species tested positive for the presence of *Aeromonas caviae* (*A. caviae*), with an overall positivity rate of 36.05% (53 out of 147 animals sampled). The distribution of *A. caviae*-positive cases varied among species, as detailed in Table 3. The blue duiker had the highest number of positive samples, representing 26.42% of the 53 positive cases and 9.52% of the total 147 animals. This was followed by Peters's duiker at 22.64% of positives (8.16% total) and the brush-tailed porcupine at 18.87% of positives (6.80% total). Other species with positive detections included the long-tailed pangolin (7.55% of positives), the water chevrotain and moustached monkey (each 5.66%) and the African civet, putty-nosed monkey, red river hog and sitatunga with lower proportions ranging from approximately 1.89% to 3.77% among positive samples. This variation highlights species-specific differences in the prevalence of *A. caviae* within the bushmeat sample population.

Species	Quantities	% On 53 Samples	% On 147 Samples
Brush-tailed porcupine	10	18.87	6,802
Blue duiker	14	26.42	9,523
Peters's duiker	12	22.64	8,163
African Civet	2	3.77	1,360
Water chevrotain	3	5.66	2,040
Moustached monkey	3	5.66	2,040
Putty-nosed Monkey	2	3.77	1,360
Long-tailed Pangolin	4	7.55	2,721
Red river hog	2	3.77	1,360
Sitatunga	1	1.89	0.680
Species: 10	Total: 53	Total: 100	Total: 36.05

Table 3: Species tested positive for the presence of *A. caviae.*

Antibiotic Susceptibility Tests

Resistance and Overall Sensitivity

The overall mean antibiotic resistance among the 53 isolates was approximately 49.06%, while the average sensitivity was 50.94%. This near-equal distribution indicates a balanced situation between resistant and susceptible strains at the global level. Table 4 summarizes these findings, showing 416 instances of resistance (49.06%) and 432 instances of sensitivity (50.94%). Fig. 2 visually represents the overall susceptibility pattern to antibiotics across the isolates, reinforcing the evidence of a roughly equal proportion of resistant and sensitive strains.

Overall Sensitivity	N	Proportions
Resistance (R)	416	49.06%
Sensitive (S)	432	50.94%

Table 4: Overall sensitivity.

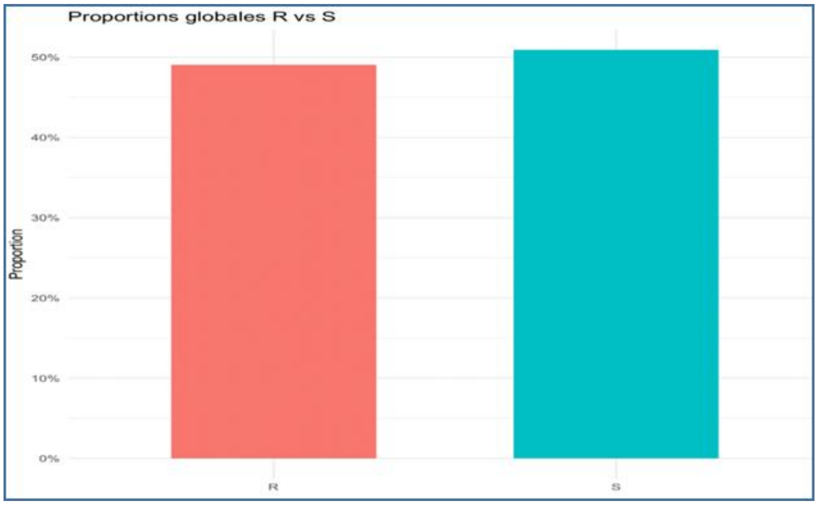


Figure 2: Overall susceptibility to antibiotics.

Resistance and Sensitivity by Species

The proportions of antibiotic resistance and sensitivity vary by species, as shown in Table 5. Species such as the African Civet, Red river hog and Sitatunga exhibit higher resistance levels, with resistance rates of 65.63%, 59.38% and 56.25%, respectively. Conversely, various duiker species, including Peters's Duiker and Blue Duiker, have lower resistance levels, indicating higher susceptibility to antibiotics.

Table 3 details these differences, highlighting that for some species like the Long-tailed Pangolin, Putty-nosed Monkey and several duikers, resistance and sensitivity are nearly balanced, each hovering between 45% and 55%. In these cases, represented by Fig. 3, the lengths of the turquoise bars (sensitivity) and salmon bars (resistance) are nearly equal, reflecting this equilibrium.

Species	R/S	N	Proportions %
Brush-tailed porcupine	R	74	46.25
Brush-tailed porcupine	S	86	56.75
Blue duiker	R	107	47.77
Blue duiker	S	117	52.23
Peters's duiker	R	93	48.44
Peters's duiker	S	99	51.56
African Civet	R	21	65.63
African Civet	S	11	34.38
Water chevrotain	R	23	47.92
Water chevrotain	S	25	52.08
Moustached monkey	R	22	45.83
Moustached monkey	S	26	54.17
Putty-nosed Monkey	R	16	50.00
Putty-nosed Monkey	S	16	50.00
Long-tailed Pangolin	R	32	50.00
Long-tailed Pangolin	S	32	50.00
Red river hog	R	19	59.38
Red river hog	S	13	40.62
Sitatunga	R	9	56.25
Sitatunga	S	7	43.75

Table 5: Contingency by species between resistance R and sensitivity S.

However, Fig. 3 also reveals notable imbalances where resistance exceeds 60% or sensitivity falls below 40%, specifically in the Sitatunga, Red river hog, Moustached monkey, Water Chevrotain and especially the African Civet, which shows the highest resistance rate. This pattern underscores species-specific differences in antibiotic susceptibility within the bushmeat sample population.

Table 6 and Fig. 4 summarize the antibiotic resistance profiles of *A. caviae* isolates. Remarkably, all isolates were resistant to at least five different antibiotics and universally resistant to penicillin, oxacillin and vancomycin, with 100% resistance and no sensitivity detected for these three antibiotics. Resistance to β-lactams showed variability: combinations such as Ticarcillin + Clavulanic Acid (TCC) exhibited very high resistance (98.11%), whereas piperacillin + Tazobactam (TZP) showed lower resistance (32.08%), with only one isolate from a blue duiker sensitive to TCC.

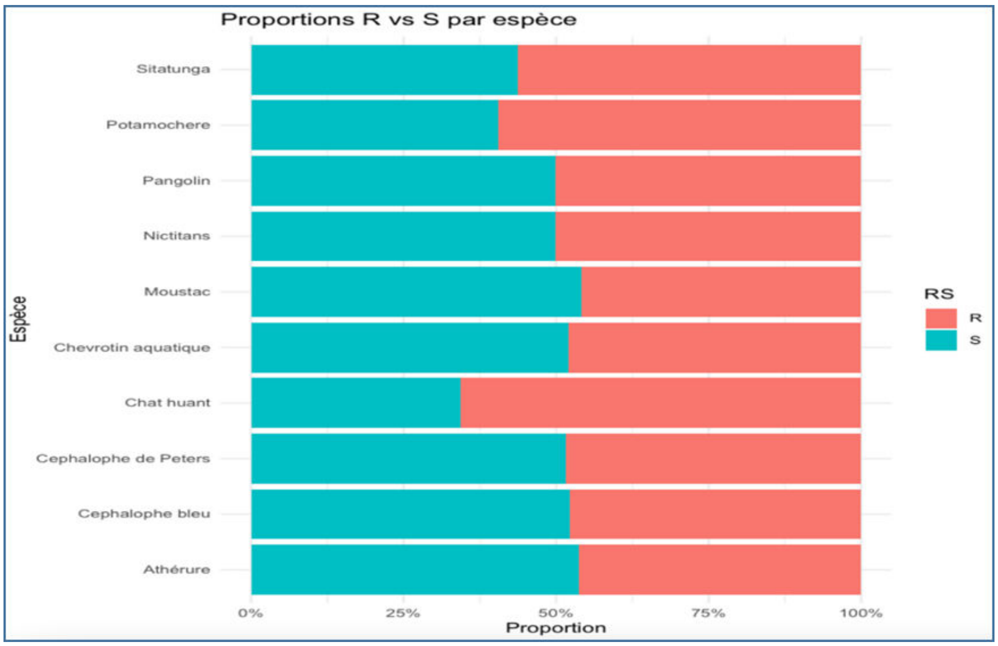


Figure 3: Antibiotic susceptibility by species.

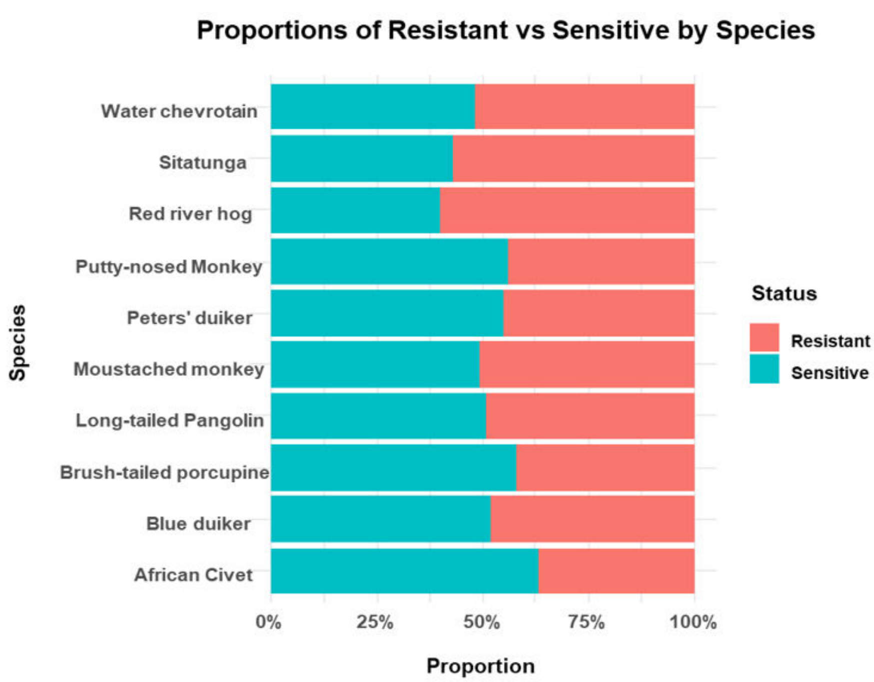


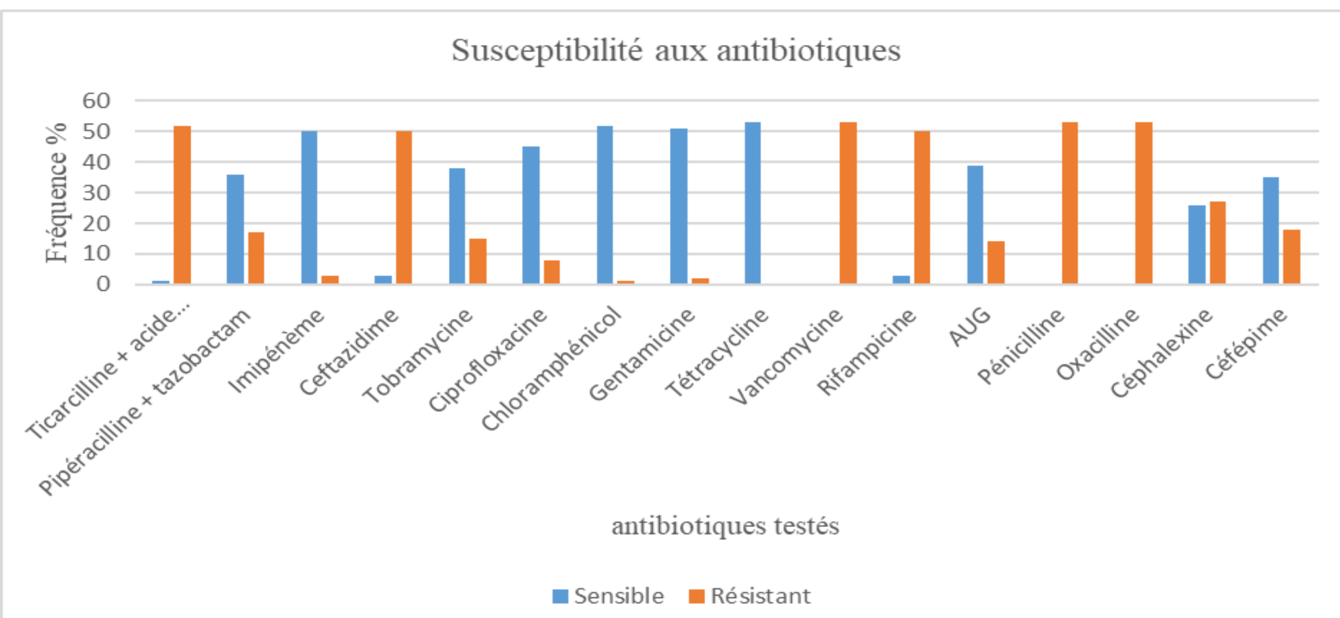
Figure 4: Proportions of resistant sensitive by species.

Cephalosporins also had high resistance rates: ceftazidime (94.34%), cephalexin (50.94%) and cefepime (66.04%). Imipenem (IMI) stood out as the only β-lactam with predominantly high sensitivity, showing just 5.66% resistance. Several other antibiotics showed high sensitivity levels, including ciprofloxacin (84.91%), gentamicin (96.23%), tobramycin (71.70%), chloramphenicol (98.11%) and amoxicillin + clavulanic acid (73.59%). Notably, tetracycline was fully effective against all isolates, with 100% sensitivity.

Statistical analysis based on the resistance/sensitivity contingency table yielded a chi-square value of 6.15 and a p-value of 0.72, indicating no significant difference in antibiotic resistance distribution between species. This suggests that resistance proportions are generally consistent across the different bushmeat species sampled (Fig. 5).

Antibiotics	Sensitive (S)	Resistant (R)
TCC	1 (1.89%)	52 (98.11%)
TZP	36 (67.92%)	17 (32.08%)
IMI	50 (94.34%)	3 (5.66%)
CAZ	3 (5.66%)	50 (94.34%)
TOB	38 (71.70%)	15 (28.30%)
CIP	45 (84.91%)	8 (15.09%)
CHL	52 (98.11%)	1 (1.89%)
GEN	51 (96.23%)	2 (3.77%)
TET	53 (100%)	0%
VAN	0%	53 (100%)
RIF	3 (5.66%)	50 (94.34%)
AUG	39 (73.59%)	14 (26.41%)
PEN	0%	53 (100%)
OXA	0%	53 (100%)
CN	26 (49.06%)	27 (50.94%)
CEF	35 (66.04%)	18 (33.96%)

Table 6: Frequency of resistance to antibiotics tested on *A. caviae*.



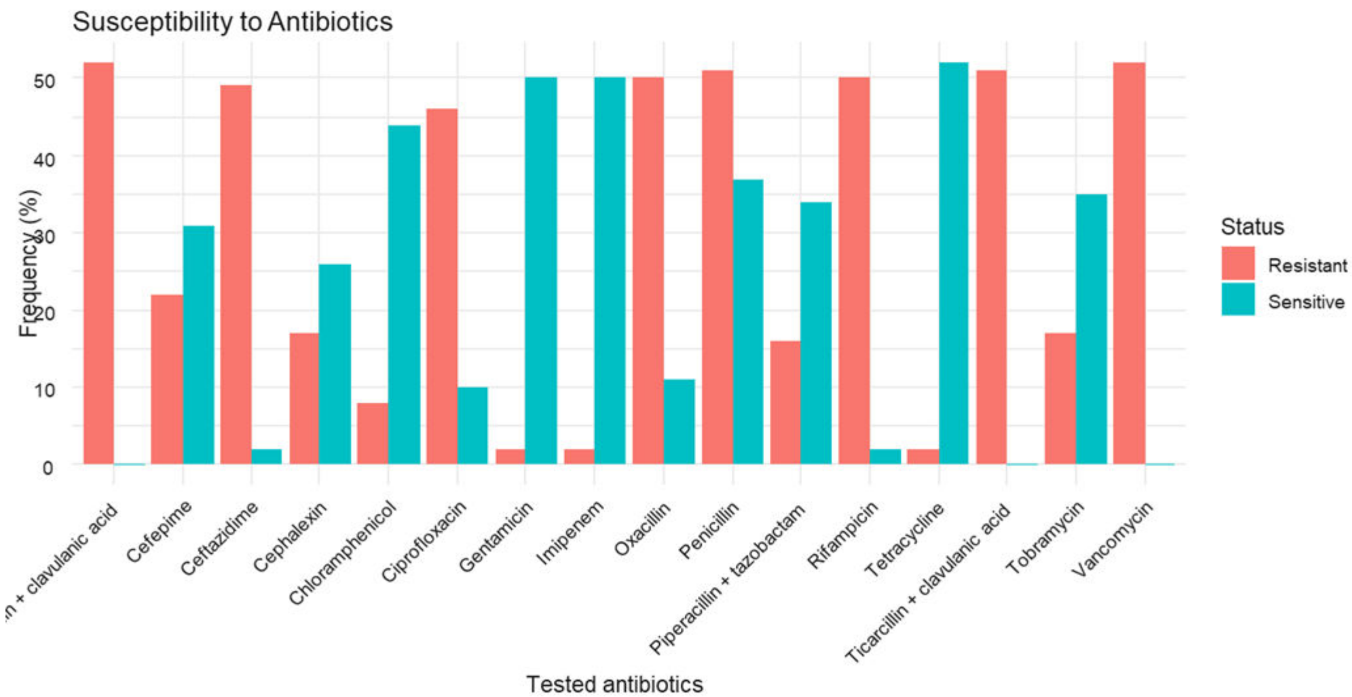


Figure 5: Antibiotic susceptibility *of A. caviae*.

Discussion

This study is one of several investigations to identify pathogens in bush meat consumed by people in the Mulundu district, in order to protect their health. Analyses of feces from purchased bushmeats animals showed the detection of *Aeromonas caviae* (*A. caviae*). The genus *Aeromonas* is a bacterium commonly found in fish and marine animals, but also isolates infections in humans [9]. The diagnosis of this bacterium is somewhat rare in clinical routine, which makes it a bacterium less identified in human pathologies. Nevertheless, in humans it is responsible for various infections ranging from acute gastroenteritis to soft tissue infections and even severe septicemia [9,12]. The interest of studying *A. caviae* in the wildlife of the department of Mulundu lies essentially in its capacity for zoonotic transmission between bushmeat and the populations that consume it. In this study, the number of wild mammal species (10/20 species, 1/2 of the animals) being positive for the presence of this bacterium and the overall antibiotic resistance rate estimated at 49.06% seem to be important and alarming on the potential for transmission of antibacterial resistance found in this bacterium. The identical frequencies of overall resistance (49.06%) and overall sensitivity (50.94%) in the tested animals indicate a balanced situation between resistant and sensitive strains on a global scale. The prevalence rate of *A. caviae* in the stools of this study was estimated at 36.05%. In Spain, a study carried out from January 2015 to December 2017 at the Galdakao-Usansolo Hospital revealed the presence of *A. caviae* from the stools of 85 out of 98 patients, i.e. 86.73% [21]. This result is significantly higher than the prevalence in our study. In Kenya, out of 188 human fecal samples that were analyzed to determine the etiological agents of diarrhea, only three cases were positive for *A. caviae* [9]. *A. caviae* and other *Aeromonas* (*A. hydrophila* and *A. veronii*) were identified in another study of 109 clinical isolates isolated from individuals with gastroenteritis in Spain and Mexico [22].

Overall antibiotic susceptibility shows a heterogeneous distribution by species. Some species have higher prevalences of antibiotic resistance than others (the African Civet, the red river hog and the sitatunga); while others have the highest rates of antibiotic susceptibility (the blue duiker, the Peters' duiker, the Brush-tailed porcupine, the Moustached monkey and the water chevrotain). This distribution could be explained by the fact that *A. caviae* is a heterogeneous bacterium found on a variety of hosts and whose antibacterial resistance varies greatly [23]. These results also seem to show that wild mammals with the highest resistance rates most frequently frequent forest areas most frequented by humans [24, 25]. It should also be emphasized that the overall resistance is influenced by the natural resistance of' *Aeromonas* with respect to rifampicin, there penicillin and oxacillin [10-12]. However, the estimated p-value of 0.7247259 confirms that the overall proportions of susceptibility (S) and resistance R, although S slightly exceeds R in this dataset, the resistance proportions are broadly similar between species; and the chi-square test shows no significant difference in the R/S distribution between species ($p > 0.05$).

Regarding the antibiotics tested, only one antibiotic, tetracycline, was sensitive to all isolates. However, all aminoglycosides tested, tetracycline (100%), gentamicin (96.23%) and tobramycin (71.70%), showed high sensitivities. Other studies on *A. caviae* have also shown it to be sensitive to tetracycline and aminoglycosides, including the studies by Monika Nowrotek, et al., and Yiling Dai, et al., and the study by Arun Sharma, et al., also noted the sensitivity of *A. caviae* to gentamicin and tetracycline [26,27]. On the other hand, the study by Xue, et al., presented *A. caviae* resistant to tetracyclines and doxycycline [28]. In our study, penicillin and oxacillin were 100% resistant, ceftazidime 94.34%, cephalexin 50.94% and cefepime 33.96%. In general, *Aeromonas* carry intrinsic resistance to beta-lactams [12,29]. On the other hand, other studies have also revealed *A. caviae* to be 100% resistant to penicillin. Herawati, et al., high resistance to penicillin and other beta-lactams, including oxacillin, ampicillin and first-generation cephalosporins [9,26,27]. In addition, ceftazidime and cefepime, third and fourth generation cephalosporins respectively, have a very high prevalence of resistance for ceftazidime (94.34%) and a fairly high prevalence for cefepime (33.96%). These resistance rates are quite worrying, as these antibiotics are used clinically to combat severe bacterial resistance as a last resort. Other antibiotics have also shown high prevalence of resistance, namely the combination of ticarcillin + clavulanic acid (98.11%), piperacillin + tazobactam (32.08%) and amoxicillin + clavulanic acid (26.41%). Cases of *A. caviae* resistant to beta-lactam/beta-lactam inhibitor combinations have already been reported [30]. Resistance to rifampicin (94.34%) and vancomycin (100%) is also significant, even though these antibiotics are used in cases of Mycobacterium infections and infections with Gram-positive bacteria such as *Enterococci*, respectively. However, the use of these two antibiotics confirms the natural resistance of the *Aeromonas* genus to them [9]. One study did show *Aeromonas* hydrophila isolates with resistance rates above 70% [31]. Which suggests that this bacteria appears to have a natural resistance to glycopeptides.

Several isolates were multiresistant to at least five antibiotics of different classes [32] and on several different host species. Most of the Brush-tailed porcupine (*Atherurus africanus*) were resistant to penicillin, oxacillin, ticarcillin + clavulanic acid, ceftazidime, vancomycin and rifampicin (MDR isolate). Except for these antibiotics, one *Atherurus africanus* was resistant to these antibiotics but also to tobramycin, chloramphenicol, vancomycin and all beta-lactams (MDR isolate). One blue duiker was resistant to all beta-lactams except imipenem, but also to ciprofloxacin, vancomycin and rifampicin. All Peters' duikers were resistant to the combination of ticarcillin + clavulanic acid, ceftazidime, vancomycin, rifampicin, penicillin and oxacillin (MDR isolate). One Peters' duiker was resistant not only to the above antibiotics, but also to imipenem, tobramycin and ciprofloxacin (MDR isolate). One tawny cat showed resistance to twelve out of fourteen antibiotics, only four antibiotics were sensitive (chloramphenicol, gentamicin, tetracycline and cephalexin). *Aeromonas* are generally resistant to beta-lactams. However, the cases of multidrug resistance recorded in bushmeat, isolated from several different species is not a negligible fact and requires monitoring. In addition, several bushmeat species showed a quite high sensitivity to imipenem (94.34%), tobramycin (71.70%), ciprofloxacin (84.91%), chloramphenicol (98.11%), gentamicin (96.23%) and tetracycline (100%). Resistance to chloramphenicol is not common, it is an antibiotic of restricted use [33]. Other studies have also mentioned the sensitivity of *A. caviae* to these antibiotics, at fluoroquinolones (ciprofloxacin), tetracycline and aminoglycosides and carbapenems [9,28].

Strength and Limitations of Study

Strength

This study was conducted as part of a collaboration between the Institute for Research in Tropical Ecology (IRET) and the Center for International Cooperation in Agricultural Research for Development (CIRAD). CIRAD covered the cost of samples bushmeat and laboratory reagents for all field missions. In Mulundu, bushmeat was easily purchased from hunters grouped into three Sustainable Management Units (SMUs) by CIRAD researchers who had informed them about our study.

Limitations

The amount of money we had to buy the game wasn't enough to get a really big sample. Some species of wild mammals are fully protected in Gabon. This explains the low diversity of species in our sampling. In Gabon, it rains almost all the time. Hunting could only take place when it wasn't raining. This made it impossible for us to access certain areas to purchase bushmeat, thereby reducing the diversity of species.

Conclusion

This study highlighted the presence of resistant and multi-resistant *A. caviae* in bushmeat consumed by local populations in the Mulundu department of Gabon, a resistance to clinically important antibiotics such as several beta-lactams, rifampicin, vancomycin. Overall, the resistance rate and the sensitivity rate were approximately equal. This indicates a balanced situation between resistant and sensitive strains on a global scale. This study also explores the risks associated with bushmeat consumption and the emergence of a pathogen often ignored in our clinical diagnoses, but with the potential to be a causative agent of acute gastroenteritis, soft tissue infections, septicemia and uremic syndrome. Finally, our research highlights the importance of monitoring the emergence of antibiotic-resistant bacteria in bushmeat consumed by local populations.

Conflict of Interest

The authors declared no potential conflicts of interest with respect to the research, authorship and/or publication of this article.

Financial Disclosure

This research did not receive any grant from funding agencies in the public, commercial or not-for-profit sectors.

Consent To Participate

The authors certify that they have obtained all appropriate patient consent.

Data Availability and Consent of Patient

Data is available for the journal. Informed consents were not necessary for this paper.

Author's Contribution

All authors contributed equally for this paper.

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