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Research Article

ANALYTICAL REVIEW ON ANTIMICROBIAL RESISTANCE IN BUSHMEAT: RESISTANCE PROFILES AND GENETIC DETERMINANTS IN BACTERIA ASSOCIATED WITH ANIMAL SPECIES ACROSS CONTINENTAL GEOGRAPHIC ZONES

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Abstract

This literature review focuses on Antimicrobial resistance (AMR) in bushmeat consumed in Africa, Asia, the Americas, and Europe. We analysed 119 articles, including 18 on Gram-negative bacteria in protected areas, 66 on Gram-negative bacteria in non-protected areas, and 35 on Gram-positive bacteria in wildlife. Our findings revealed the presence of AMR and resistance genes in all regions, in both protected and non-protected areas. Africa had the highest number of publications on protected areas, followed by Europe, the Americas, and Asia. In non-protected areas, Europe ranked first, followed by Asia, the Americas, and Africa. Gram-negative bacteria such as *Pseudomonas spp*., *Escherichia coli*, *Klebsiella pneumoniae*, and *Salmonella* spp. exhibited resistance and multidrug resistance. Resistance genes were also identified, including those targeting tetracyclines, carbapenems, vancomycin, fluoroquinolones, and chloramphenicol. Wildlife plays a critical role in the dissemination of resistant bacteria and genes, highlighting the need for continuous monitoring and preventive measures to combat zoonotic antibiotic resistance.

Keywords: Wildlife, Antibiotic resistance, Bushmeat.

INTRODUCTION

The term "bushmeat" refers to any terrestrial mammal, bird, reptile, or amphibian harvested from the wild for consumption and encompasses all stages of the supply chain, including acquisition, trade, and consumption of wild meat (1). Bushmeat is both a source of protein and income for many communities. However, this highly valued bushmeat can act as a significant reservoir of zoonotic pathogens, such as antibiotic-resistant bacteria (2, 3). Antibiotic resistance represents a major global public health issue (4, 5). The rising incidence of AMR bacteria poses one of the greatest medical challenges of our time. Bacteria once sensitive to clinically relevant antimicrobials now exhibit resistance, impacting public health, domestic animals, and bushmeat (4). Carbapenems, often considered antibiotics of last resort for life-threatening infections in humans, are increasingly compromised by carbapenemases and extended-spectrum β-lactamases (ESBLs) (6). Over the last decade, clinically significant AMR bacteria have been isolated from various wildlife species across all continents, including Antarctica (7-11). The presence of multidrug-resistant bacteria (MDR) and antibiotic-resistance genes in wildlife is influenced by host biology and ecology, as well as anthropogenic impact in areas inhabited by these animals (6, 12). While healthcare facilities, livestock farming, and agriculture are the primary drivers of antibiotic resistance, other contributors include wastewater, farm animals, domestic pets, and wildlife, such as bushmeat (4).

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In rural areas of Central Africa, bushmeat is a crucial source of animal protein (6). However, Gram-negative bacteria carrying antibiotic resistance have been identified in wildlife, raising concerns about zoonotic transmission between humans and wildlife. Several studies have revealed similarities between bacterial gene sequences found in wildlife and those in humans, both in terms of sequence types and clinically significant antibiotic resistance determinants (6, 13). This highlights the importance of examining the impacts, consequences, and quantitative data on AMR to better justify the issue at hand. The presence of MDR bacteria, antimicrobial resistance genes, and their resistance mechanisms in wildlife necessitates close monitoring to prevent zoonotic risks at the human-wildlife interface. The purpose of this review is to provide an overview of bacterial resistance profiles and their genetic determinants in protected and non-protected areas.

MATERIALS AND METHODS

For this study, we searched for relevant articles on bacterial antibiotic resistance in wildlife consumed by humans and in game meat. Searches were conducted in databases such as Google Scholar, PubMed, and CrossRef. We included publications from 10 years (2013–2023), combining keywords with the names of specific countries.

RESULTS AND DISCUSSION

Antibiotic resistance in protected areas

National parks play a critical role in biodiversity conservation, safeguarding natural heritage and resources essential to

national economies. Established over vast, sparsely populated regions, these reserves are crucial for economic development. Africa, Asia, the Americas, and Europe have the highest number of protected areas, with studies examining diverse wildlife species and antibiotic-resistant bacteria. Antibiotic-resistant bacteria isolated from this biodiversity, classified by continent, are summarised in Figure 1.

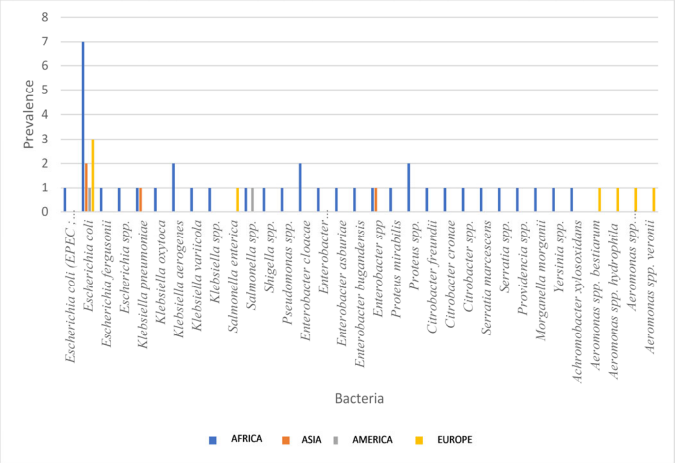


Figure 1. Profile of Antimicrobial-Resistant Bacteria Isolated from the Four Continents

Figure 1 present a diverse array of wild animals associated with a wide variety of bacteria. Non-human primates share a genetic heritage that is closely related to that of humans. The fact that these primates harbour bacteria which exhibit resistance and multidrug resistance to antimicrobials is concerning. These pathogens are responsible for human diseases, raising the possibility of bacterial transmission between humans and wildlife (11, 14). Indeed, several studies have highlighted the potential role of wildlife in the transmission of pathogens to humans (15, 16). Furthermore, multidrug-resistant (MDR) pathogens, particularly enterobacteria, are associated with increased mortality rates in both humans and animals, including non-human primates (NHPs) (17). Increased contact between animal species inhabiting the same geographical environment further facilitates the potential exchange of pathogens with wildlife such as NHPs (4, 14) probably due to hunting. However, NHPs are now prohibited from being hunted as they are monitored and protected by local authorities. A study conducted by Leresche Even Doneilly Oyaba Yinda et al in Gabon's Moukalaba-Doudou National Park on western lowland gorillas (*Gorilla gorilla gorilla*) revealed pathogenic *E. coli* strains resistant to more than three classes of antibiotics, indicating multidrug-resistant *E. coli* (14). Another study by Mbehang Nguema et al in Gabon, also involving western lowland gorillas, identified multidrug-resistant strains of *Achromobacter xylosoxidans* and *Providencia sp.*, with resistance to several antibiotic classes, including ampicillin, cefazolin, cefotaxime, streptomycin, gentamicin, kanamycin, tetracycline, nalidixic acid, ciprofloxacin, colistin, chloramphenicol, and trimethoprim (18). In South Africa, the study by Glover et al found that both *Escherichia fergusonii* and *E. coli* exhibited multidrug resistance, including resistance to carbapenems (19). Additionally, research conducted by Julio Andre Benavides et al in Gabon's Lopé National Park revealed that *E. coli* displayed multidrug resistance to several antibiotic classes, including tetracycline, ampicillin, streptomycin, sulfamethoxazole, and rifampicin (20). Lastly, Mbehang Nguema et al conducted a study in Gabon involving various terrestrial mammals, including non-human primates (11). They identified antibiotic-resistant *E. coli* strains in *Colobus satanas* (resistance to levofloxacin), *Gorilla gorilla gorilla* (resistance to amoxicillin, ticarcillin, nalidixic acid, and chloramphenicol), and *Mandrillus sphinx* (resistance to amoxicillin, ticarcillin, chloramphenicol, and sulfamethoxazole-trimethoprim). Additionally, *Mandrillus sphinx* demonstrated resistance to amoxicillin, amoxicillin-clavulanic acid, aztreonam, ticarcillin, ticarcillin-clavulanic acid, piperacillin-tazobactam, and cephalexin (11). The emergence of resistance to last-resort antimicrobials, such as carbapenems, colistin, and third-generation cephalosporins, within wildlife suggests potential anthropogenic contamination via various transmission pathways between humans and animals (21, 22). Furthermore, given the close genetic proximity between humans and non-human primates, the presence of antimicrobial-resistant bacteria in the latter could indicate that non-human primates act as reservoirs of pathogenic infectious agents. It is noteworthy that these primates harbour such bacteria without displaying apparent clinical signs of infectious diseases (14, 23). Figure 1 demonstrates that the most frequently isolated bacteria include *Escherichia coli*, *Salmonella spp.*, and *Klebsiella pneumoniae*, with Africa being the most affected continent. These enterobacteria exhibit resistance to carbapenems and produce extended-spectrum beta-lactamases (ESBL), are listed as priority pathogens by the WHO (24). Antibiotic resistance profiles vary across continents, with Africa exhibiting the highest number of tested antibiotic classes and consequently the greatest diversity of antibiotic resistance in wildlife. Figures 2 and 3 below further illustrate this trend.

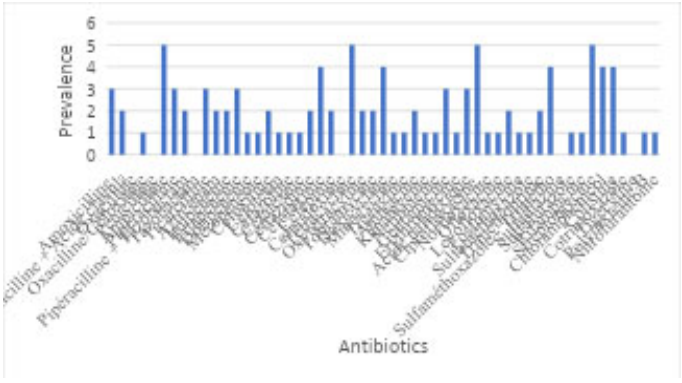


Figure 2. Profile of antibiotics exhibiting resistance in bacteria from protected areas in Africa

The prevalence on the y-axis corresponds to the total number of instances a resistant bacterium was reported across all the articles collected from Africa.

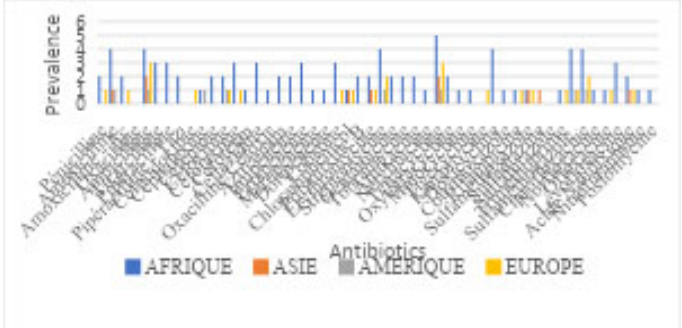


Figure 3. Profile of antibiotics exhibiting resistance in bacteria from protected areas across four continents

The prevalence on the y-axis corresponds to the total number of instances a resistant bacterium was reported across all the articles collected. These findings highlight the most frequently observed resistances in wildlife from protected areas across the four continents, particularly concerning clinically significant last-resort antibiotics, such as carbapenems (imipenem, ertapenem, doripenem, meropenem) and third-generation cephalosporins, including colistin (25, 26).

The majority of these resistant antibiotics are found in Africa, which could be attributed to the effects of various antimicrobial dissemination pathways in the environment. Resistant antibiotics spread through untreated wastewater, pathogen vectors, and poor hospital waste management, primarily found in Africa, affecting wildlife and distributing antibiotic resistance genes, highlighting the need for effective environmental solutions (4, 6). Among this fauna, it is significant to highlight the presence of protected animal species such as the giant panda (*Ailuropoda melanoleuca*), western lowland gorilla (*Gorilla gorilla gorilla*), mandrill (*Mandrillus sphinx*), forest elephant (*Loxodonta cyclotis*), giraffe (*Giraffa camelopardalis*), and chimpanzees (*Pan troglodytes verus*) (27, 28). Although bushmeat species vary from continent to continent, almost identical bacterial strains are found in all four regions, with similar antibiotic resistance profiles. Among the protected species such as forest elephant (*Loxodonta cyclotis*) plays a crucial role in forest regeneration through its dung (faecal matter) (29). These droppings, which carry bacteria and resistance genes, disperse across various environments, thereby facilitating the persistence and dissemination of these microbes within wildlife populations, including game consumed by human populations (29). Despite their herbivorous diet, these animals harbour antibiotic-resistant *E. coli* strains (1) similar to other bacterial species detected in bushmeat. The red river hog (*Potamochoerus porcus*), akin to the European wild boar, is one of eight wild suids in Africa (30). It inhabits the humid forests of West and Central Africa's forest belt (30). These animals live in groups of approximately fifteen to forty individuals (30). Their diet includes seeds and fruits. Their gregarious nature and close contact foster the sharing of microbes, which may lead to the exchange of antibiotic-resistance genes (4, 30). They also consume plant roots and occasionally small animals (30). Roots, which are in contact with soil, may act as vectors of bacterial contamination, as soil harbours ubiquitous bacteria originating from human waste, animal excrement, and polluted water (31, 32). The red river hog's consumption of small animals, which serve as game for them, further contributes to the acquisition of novel bacteria and antimicrobial resistance genes (30). Omnivores such as the Guinea baboon (*Papio papio*), the chimpanzee (P*an troglodytes verus*) found exclusively in certain African savannas and tropical forests and the South American coati (*Nasua nasua*), also carry the same enterobacteria found in other game species mentioned previously (33, 34). Across all continents, antibiotic-resistance to beta-lactams, quinolones/fluoroquinolones, tetracyclines, and sulphonamides is widespread (14, 35). Colistin resistance is confined to Africa and Europe, possibly due to the limited number of articles addressing this topic in protected areas and the fact that colistin resistance is not systematically examined in these studies. Resistance to other cyclins (tigecycline, oxytetracycline), meropenem, and erythromycin also appears limited to Africa and Europe, potentially explained by the proximity between these two continents via game trade and the transfer of resistant bacteria by migratory birds such as gulls (36, 37). Furthermore, other enterobacteria, such as *Shigella* spp. (responsible for shigellosis in humans), *Klebsiella* spp. (*K. pneumoniae, K. oxytoca, K. variicola, K. aerogenes*), which cause digestive and pleuropulmonary infections in humans, *Serratia* spp., *Salmonella enterica*, *Enterobacter* spp., *Proteus*, and *Morganella morganii*, are all found in the digestive tracts of humans and animals. In immunocompromised individuals, these bacteria may lead to infectious diseases with therapeutic dead ends (38, 39).

Antibiotic resistance genes such as beta-lactamases (*blaCMY-2, blaCMY-1, blaCTX-M-15*) are widespread in all over the world. Genes conferring resistance to sulphonamides (*sul1, sul2, sul3*), tetracyclines (*tetA, tetB, tetC*), quinolones (*qnS1*), and aminoglycosides (*acc(3)-IIa and ant(3")-Ia*) are predominantly found in Africa and Asia. Antibiotic resistance in unprotected areas represent the most abundant locations for antibiotic-resistant bacteria and antibiotic-resistance genes compared to protected areas due to a more important human activity in these areas.

Our results indicate the presence of several bacterial species are studied, including those on the list of priority bacteria for research and the development of new antimicrobials effective against therapeutic dead-ends in clinical settings (24). Bacteria such as multidrug-resistant *Acinetobacter*, multidrug-resistant *Pseudomonas aeruginosa*, *E. coli*, *Klebsiella pneumoniae*, and multidrug-resistant *Serratia* producing β-lactamases are included in this list and have been repeatedly cited in articles over the past decade across multiple continents (24).

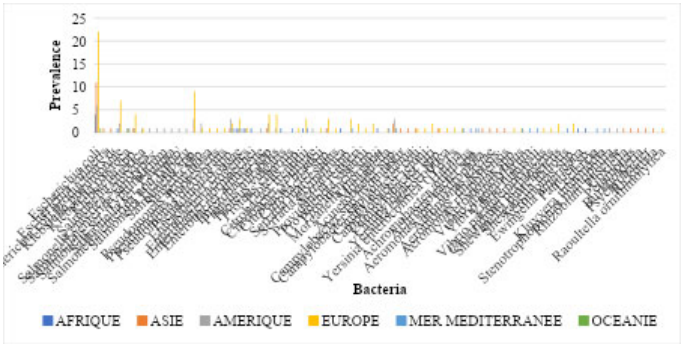


Figure 4. Representation of Antibiotic-Resistant Bacteria in Unprotected Areas in Africa, Asia, the Americas, Europe, the Mediterranean Sea, and Oceania. The prevalence on the y-axis is relative to the total number of times a resistant bacterium was mentioned across all the articles collected in the respective area

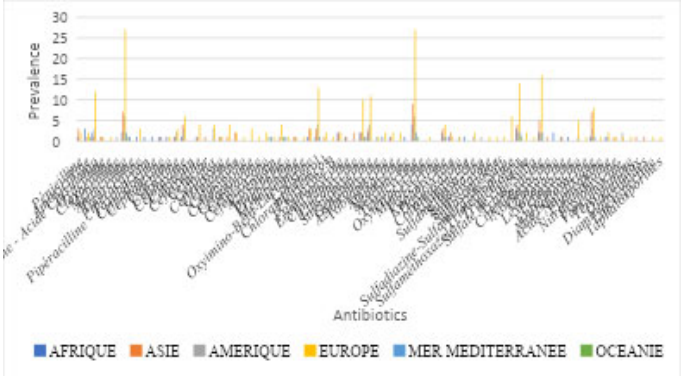


Figure 5. Antibiotic Resistance Profiles in Unprotected Areas in Africa, Asia, the Americas, Europe, the Mediterranean Sea, and Oceania. The prevalence on the y-axis is relative to the total number of times a resistant bacterium was mentioned across all the articles collected in the respective area

Pseudomonas spp. (*P. aeruginosa*) is present in a wide range of wild animals across various continents in our study: Peruvian boobies (*Sula variegata*), wild birds (*Columba livia*, *Buteo buteo*, etc.), bats, howler monkeys (*Alouatta palliata*), spider monkeys (*Ateles geoffroyi*), felids (jaguars, *Panthera onca*), pumas (*Puma concolor*), jaguars (*Puma yagouarundi*), Mediterranean loggerhead turtles (*Caretta caretta*), mammals, tortoises, marsh turtles, birds, and reptiles, among others. It is worth noting that *Pseudomonas aeruginosa* is rarely part of the normal microbial flora in healthy humans or animals (40). The presence of antimicrobial-resistant *Pseudomonas spp.* poses a significant therapeutic challenge for the treatment of bacterial diseases caused by this pathogen, due to its ability to develop resistance to multiple classes of antibiotics (40). Similarly, cases of multidrug resistance in *Acinetobacter spp.*, and *Enterobacteriaceae* (such as *E. coli* and *K. pneumoniae*) producing extended-spectrum beta-lactamases (ESBLs) fall within the same context as *Pseudomonas spp.*. Indeed, these bacteria are found in the microbiomes of a diversity of wild hosts across all continents, and these wild animals may come into contact with humans and/or be consumed by them (11, 41). According to Figures 2 and 3, Europe is the continent where the most antibiotic-resistant bacteria and antibiotics are observed in wildlife from unprotected areas. In contrast, Africa is the most affected continent in protected areas. This difference may be explained by the number of published articles (which we have collected for this review) between these two types of areas (protected and unprotected), as well as by the number of species identified and found in each of these areas. Environmental and anthropological factors are equally cited in both protected and unprotected areas. Wildlife living close to human settlements or livestock raised for food, or drinking from waterways derived from wastewater, tends to exhibit more antibiotic-resistant bacteria clinically relevant to humans than wildlife in less anthropized habitats (4, 6). This scenario is observable in both areas. However, environmental factors or seasonality are not sufficiently prominent in our articles as factors that could potentially justify this difference between Europe and Africa.

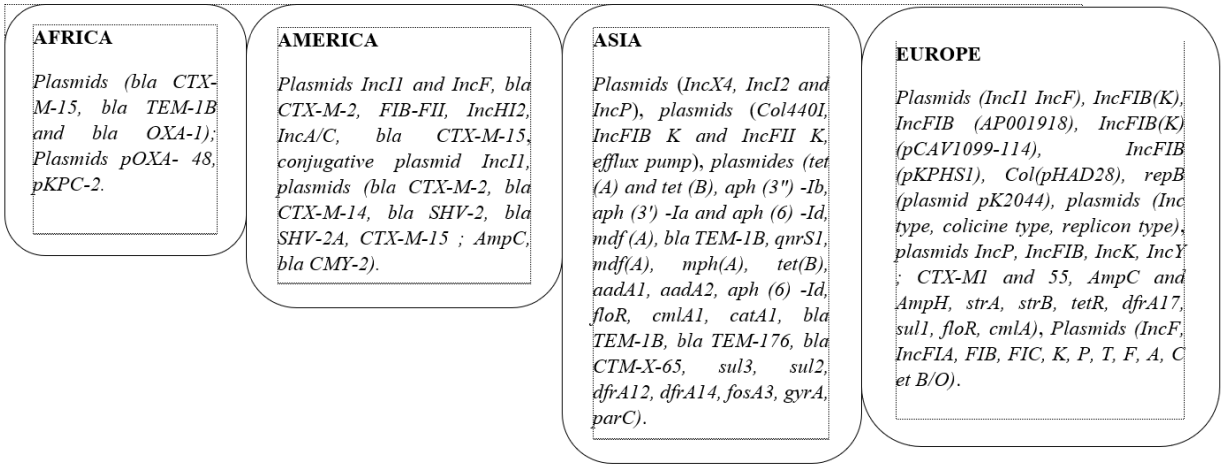
Figure 5 presents several peaks of antimicrobial resistance in Europe. Two antibiotics stand out with the highest peaks: ampicillin and tetracycline. Other antimicrobials are also significant, including amoxicillin + clavulanic acid, chloramphenicol, gentamicin, streptomycin, sulfamethoxazole + trimethoprim, and ciprofloxacin. These antibiotics are most frequently associated with resistance in wildlife from unprotected areas in Europe, but also in comparison to other regions. The amoxicillin + clavulanic acid (AMC) combination is commonly used in clinical medicine to address beta-lactamases. It is prescribed in cases of resistance to beta-lactam antibiotics (42, 43). Additionally, it is also used in the breeding of domestic animals raised for food (44). Amoxicillin alone is a group A penicillin with broad-spectrum activity against both Gram-positive and Gram-negative bacteria, including anaerobes and spirochetes (45). Therefore, in cases of resistance to group A penicillins, the amoxicillin + clavulanic acid combination (AMC) is commonly used in both clinical and veterinary practice (44). The significant presence of AMC resistance in wildlife therefore suggests potential anthropogenic and/or veterinary contamination (11, 14). This observation also applies to other antibiotics previously mentioned, such as chloramphenicol, gentamicin, streptomycin, and the sulfamethoxazole + trimethoprim combination (11, 14). All these antibiotics are used in both human and veterinary medicine, and show high resistance rates in wildlife (46, 47). Cases of ampicillin, tetracycline, and ciprofloxacin are also noteworthy. Ampicillin is a group A penicillin effective against Gram-positive aerobic bacteria, Gram-negative aerobic bacteria, and anaerobes. It is inhibited by penicillinases (48). In clinical practice, this antibiotic is used to treat various infections, such as skin infections, renal, urogenital, and digestive infections (48). It is also used in veterinary medicine. Tetracycline, on the other hand, is a broad-spectrum antibiotic widely used in clinical and veterinary medicine. The detection of these antibiotics in wildlife is concerning, particularly as antimicrobial resistance is observed in all regions studied, within a rich biodiversity (41). In response to this resistance, other antibiotics, such as the amoxicillin + sulbactam combination, are used in clinical settings to circumvent ampicillin resistance (49). As for ciprofloxacin, it plays a crucial role in the treatment of certain clinical infections, such as pyelonephritis, prostatitis, and digestive infections (50). This medication is typically administered for severe infections where other antibiotics are less suitable or cannot be used (50). Ciprofloxacin, a fluoroquinolone, acts on Gram-positive aerobic bacteria, Gram-negative aerobic bacteria, and other bacteria, including mycoplasmas (50). The abundant presence of these antibiotics in wildlife could result from likely anthropogenic pollution, but it may also be linked to horizontal gene transfer between bacterial populations within the same microbiome, as well as between animal populations sharing the same environment and infectious agents (4). It is now established that the presence of antibiotic-resistant bacteria in wild animals is more closely linked to anthropogenic pollution than to natural selection of resistance (4). However, wildlife can contribute to the spread of these bacteria and their resistance genes across various ecosystems (4). Local transmission of resistant bacteria can occur between animals sharing the same environment (living sympatrically), particularly in non-migratory animals. Additionally, the geographic spread of antimicrobial resistance can also occur through migratory animals, such as birds, bats, fish, and turtles (4, 46).

Genetic supports of antimicrobial resistance in game species in protected and unprotected areas

Antimicrobial resistance, a global health challenge, is a global issue with no geographic boundaries (51). It involves genetic and biochemical mechanisms, including horizontal gene transfer (HGT) (52). HGT allows bacteria to rapidly become resistant to antibiotics, integrating new genetic material into their DNA. These resistance genes can spread globally, with some remaining confined to specific regions and others spreading worldwide, particularly against beta-lactams, tetracyclines, and sulfonamides (1, 53). The distribution of these genes, according to our data, is summarized in figure 4 below.

Genes affecting antimicrobial resistance (AMR) and multidrug-resistant (MDR) *E. coli* resistance vary across continents, with tetracycline resistance found on all continents. High molecular weight plasmids are associated with resistance to various antibiotic classes. The potential relationship between genes and plasmids in wild avifauna, including *E. coli* isolates, suggests a potential link between multidrug resistance and plasmid loss, potentially leading to the spread of these resistant bacteria to humans, livestock, and the environment (54).

Table 4. Distribution of Plasmids Worldwide in the Two Areas



In Africa, the majority of observed phenotypic resistances are attributed to the genetic resistance determinants of the bacterial chromosome (55, 56). The majority of plasmid-derived resistances are caused by extended-spectrum beta-lactamases, with the blaKPC-2 gene being the most prevalent globally (55). Vancomycin resistance genes (*vanA* and *vanB*) have only been found in Africa. In Asia and on other continents, phenotypic resistance is primarily due to the expression of genes, whether carried on plasmids or the bacterial chromosome. Plasmids *IncX4, IncI2*, and *IncP*, which carry the *mcr-1* gene responsible for colistin resistance, have only been found in Asia (46). IncX4 plasmids are involved in the intercontinental spread of the mcr-1 gene, which is responsible for resistance to colistin (46). IncX4 plasmids are ubiquitous and promiscuous (46). *IncX4* and *IncI2* plasmids may share similar plasmid backbones with isolates acquired from humans, animals, and the environment. This indicates the plasmid-driven spread of these elements in the environment, animals, and humans (46). Additionally, in the horizontal transfer of the *mcr-1* gene*, IncP* plasmids also play a role in its widespread dissemination across various hosts. The presence of IncX4, IncI2, and IncP plasmids has also been associated with resistance genes such as *aad, aph, cmlA, dfrA, floR, mdf, mcr-1, qnrs, oqx, sul,* and *tet* (46). *Col440I, IncFIB K*, and *IncFII K* plasmids have also been reported in Asia, carried by *K. pneumoniae* K85, resistant to sixteen antimicrobials (57). Whole genome sequencing predicted genes for efflux pumps, antimicrobial inactivation enzymes, genes involved in protection and target replacement, and genes for reducing permeability to antimicrobials, as well as genes for aminoglycoside-modifying enzymes (*aadA16*, *aph*(3′)-Ia, and *acc*(6′)-*Ib-cr*) (Wang et al., 2022). Other genes conferring resistance to beta-lactams (*blaCTX-M-3, blaSHV-93*, and *blaTEM-1*), general resistance mechanisms for fluoroquinolones (*qnrB2* and *qnrS1*), sulfonamides (*sul1* and *sul3*), and tetracyclines (*tet34* and *tetT*) were also detected (57). In Europe, plasmids (*IncFIA, FIB, FIC, K, P, T, F, A, C,* and *B/O*) were all carriers of ESBLs and isolated from *Escherichia coli* producers of extended-spectrum beta-lactamases from wild ungulates in Portugal (58). Antibiotic resistance genes such as *blaTEM, blaSHV, blaOXA, blaCTX-M* (beta-lactams), *qnrA, qnrB, qnrS, aac(6')-Ib-cr* (fluoroquinolones), *aac3'-II, aac3'-IV, ant2", strA, strB* (aminoglycosides), tetA, tetB (tetracycline), *sul1, sul2, sul3* (sulfamethoxazole), *dfrA1, dfrA12* (trimethoprim), *fosA3, fosA5, fosC2* (fosfomycin), *cmlA1, catA*, and *floR* (chloramphenicol) are ubiquitous and have been found on nearly every continent (58). *IncP, IncFIB, IncK*, and *IncY* plasmids have been detected in more than one *E. coli* isolate resistant to colistin (mcr-1), and have been associated with several resistance genes including *blaTEM, tetA, tetB, sul2, sul3, dfrA1, dfrA12, cmlA1*, and *floR*, conferring resistance to beta-lactams, tetracyclines, sulfonamides, trimethoprim, and chloramphenicol, respectively (58).

Conclusion

This study highlights the significant diversity of phenotypes and antibiotics resistance gnes in bushmeat. This raises concerns about the potential consequences of consuming wild animals for the spread of antimicrobial resistance genes in the human population, which could lead to therapeutic dead ends.

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REFERENCES

1. Van den Honert, M.S., Gouws, P.A., Hoffman, L.C. A preliminary study: Antibiotic resistance of *Escherichia coli* and *Staphylococcus aureus* from the meat and feces of various South African wildlife species. Food Sci. Anim. Resour. 2021, 41(1), 135.
2. Olaru, I.D., Walther, B., Schaumburg, F. Zoonotic sources and the spread of antimicrobial resistance from the perspective of low and middle-income countries. Infect. Dis. Poverty. 2023, 12(03), 73-87.
3. Tanga, C.T.F., Makouloutou-Nzassi, P., Mbehang Nguema, P.P., Düx, A., Lendzele Sevidzem, S., Mavoungou, J.F., et al. Antimicrobial Resistance in African Great Apes. Antibiotics. 2024, 13(12), 1140.
4. Laborda, P., Sanz-García, F., Ochoa-Sánchez, L.E., Gil-Gil, T., Hernando-Amado, S., Martínez, J.L. Wildlife and antibiotic resistance. Front. Cell. Infect. Microbiol. 2022, 12, 873989.
5. Tang, K.W.K., Millar, B.C., Moore, J.E. Antimicrobial resistance (AMR). Br. J. Biomed. Sci. 2023, 80,11387.
6. Dolejska, M., Literak, I. Wildlife Is Overlooked in the Epidemiology of Medically Important Antibiotic-Resistant Bacteria. Antimicrob. Agents Chemother. 2019, 63(8), e01167- 19.
7. Albrechtova, K., Papousek, I., De Nys, H., Pauly, M., Anoh, E., Mossoun, A., et al. Low rates of antimicrobial-

resistant Enterobacteriaceae in wildlife in Taï National Park, Côte d'Ivoire, surrounded by villages with high prevalence of multiresistant ESBL- producing *Escherichia coli* in people and domestic animals. PLoS One. 2014, 9(12), e113548.
8. Benavides, J., Shiva, C., Virhuez, M., Tello, C., Appelgren, A., Vendrell, J., et al. Extended- spectrumbeta-l actamase-producing *Escherichia coli* in common vampire bats *Desmodus rotundus* and livestock in Peru. Zoonoses Public Health. 2018, 65(4), 454-8.
9. Mbehang Nguema, P.P., Okubo, T., Tsuchida, S., Fujita, S., Yamagiwa ,J., Tamura, Y., Ushida, K. Isolation of multiple drug-resistant enteric bacteria from feces of wild Western Lowland Gorilla (*Gorilla gorilla gorilla*) in Gabon. J. Vet. Med. Sci. 2015b, 77(5), 619.
10. Mbehang Nguema, P.P., Onanga, R., Ndong Atome, G.R., Obague Mbeang, J.C., Mabika Mabika, A., Yaro, M., et al. Characterization of ESBL-producing enterobacteria from fruit bats in an unprotected area of Makokou, Gabon. Microorganisms. 2020, 8(1),138.
11. Mbehang Nguema PP, Onanga R, Ndong Atome GR, Tewa JJ, Mabika Mabika A, Muandze Nzambe JU, et al. High level of intrinsic phenotypic antimicrobial resistance in enterobacteria from terrestrial wildlife in Gabonese national parks. PLoS One. 2021;16(10):e0257994.
12. Guenther, S., Ewers, C., Wieler, L.H. Extended-spectrum beta-lactamases producing *E. coli* in wildlife, yet another form of environmental pollution? Front. Microbiol. 2011, 2, 246.
13. Atterby, C., Börjesson, S., Ny, S., Järhult, J.D., Byfors, S., Bonnedahl, J. ESBL-producing *Escherichia coli* in Swedish gulls—a case of environmental pollution from humans? PloS one. 2017, 12(12), e0190380.
14. Oyaba Yinda, L.E.D., Onanga, R., Mbehang Nguema, P.P., Akomo-Okoue, E.F., Nsi Akoue G., Longo Pendy, N.M., et al. Phylogenetic groups, Pathotypes and antimicrobial resistance of *Escherichia coli* isolated from Western lowland Gorilla Faeces (*Gorilla gorilla gorilla*) of Moukalaba-Doudou National Park (MDNP). Pathogens. 2022, 11(10), 1082.
15. Menu, E., Davoust, B., Mediannikov, O., Akiana, J., Mulot, B., Diatta, G., Levasseur, A., Ranque, S., Raoult, D. and Bittar, F. Occurrence of ten protozoan enteric pathogens in three non-human primate populations. Pathogens. 2021, 10(3), 280.
16. Patouillat, L., Hambuckers, A., Adi Subrata, S., Garigliany, M., Brotcorne, F. Zoonotic pathogens in wild Asian primates: a systematic review highlighting research gaps. Front. Vet. Sci. 2024,11,1386180.
17. Parmanik, A., Das, S., Kar, B., Bose, A., Dwivedi, G.R., Pandey, M.M. Current treatment strategies against multidrug-resistant bacteria: a review. Current microbiology. 2022, 79(12), 388.
18. Mbehang Nguema, P.P., Okubo, T., Tsuchida, S., Fujita, S., Yamagiwa, J., Tamura, Y., Ushida, K. Isolation of multiple drug-resistant enteric bacteria from feces of wild Western Lowland Gorilla (*Gorilla gorilla gorilla*) in Gabon. J. Vet. Med. Sci. 2015, 77(5), 619-23.
19. Glover, B., Wentzel, J., Jenkins, A., Van Vuuren, M. The first report of *Escherichia fergusonii* isolated from non-human primates, in Africa. One Health. 2017, 3, 70-5.
20. Benavides, J.A., Godreuil, S., Bodenham, R., Ratiarison, S., Devos, C., Petretto, M.O.;, Michel Raymond, M., and Escobar-Páramo, P. No evidence for transmission of antibiotic- resistant *Escherichia coli* strains from humans to wild western lowland gorillas in Lope National Park, Gabon. Appl. Environ. Microb 2012, 78(12), 4281-7.
21. Barnes, M.D., et al. *Klebsiella pneumonia*e carbapenemase-2 (KPC-2), substitutions at Ambler position Asp179, and resistance to ceftazidime-avibactam: unique antibiotic-resistant phenotypes emerge from β-lactamase protein engineering. MBio. 2017, 8 (5), 10-1128.
22. Mohamed Gandor, N.H., Amr, G.E.S., Eldin Algammal, S.M.S., Ahmed, A.A. Characterization of Carbapenem-Resistant *K. Pneumoniae* Isolated from Intensive Care Units of Zagazig University Hospitals. Antibiotics (2079-6382). 2022, 11(8).
23. Kebede, T., Bech, N., Allienne, J.F., Olivier, R., Erko, B., Boissier, J. Genetic evidence for the role of non-human primates as reservoir hosts for human schistosomiasis. Plos Neglect. Trop. Dis. 2020, 14(9), e0008538.
24. Tacconelli, E., Carrara, E., Savoldi, A., Harbarth, S., Mendelson, M., Monnet, D.L., et al. Discovery, research, and development of new antibiotics: the WHO priority list of antibiotic- resistant bacteria and tuberculosis. Lancet Infect. Dis. 2018, 18(3), 318-27.
25. Tamma, P.D., Simner, P.J. Phenotypic detection of carbapenemase-producing organisms from clinical isolates. J. Clin. Microbiol. 2018, 56(11), 10-1128.
26. Al-Tawfiq, J.A., Laxminarayan, R., Mendelson, M. How should we respond to the emergence of plasmid-mediated colistin resistance in humans and animals? Int. J. Infect. Dis 2017, 54, 77-84.
27. Morgan, D., Strindberg, S., McElmurray, P., Zambarda, A., Singono, I., Huskisson, S., Musgrave, S., Eyana Ayina, C., Funkhouser, J., Hellmuth, H., Joshi, P., Cassidy, R., & Sanz, C. Extending the conservation impact of great ape research: Flagship species sites facilitate biodiversity assessments and land preservation. Primates. 2024, 65(6), 571-591.
28. Abensperg-Traun, M. CITES, sustainable use of wild species and incentive-driven conservation in developing countries, with an emphasis on southern Africa. Biol. Conserv. 2009, 142(5), 948-63.
29. Scalbert, M., Vermeulen, C., Tossens, S., Holvoet, J., d'Aspremont Lynden, M., & Doucet, J. L. Interactions between forest elephants (*Loxodonta cyclotis*) and selective logging in central Africa. In European Conference of Tropical Ecology. 2022
30. Xie, H-B., Yan, C., Adeola, A.C., Wang, K., Huang, C.P., Xu, M.M, et al. African suid genomes provide insights into the local adaptation to diverse African environments. Mol. Biol. Evol. 2022, 39(12), msac256.
31. Scaccia, N., Vaz-Moreira, I., Manaia, C.M. The risk of transmitting antibiotic resistance through endophytic bacteria. Trends Plant Sci. 2021, 26(12), 1213-26.
32. Shwailiya, S., Mahdi, A., Mohammed, Q. The efficacy of anti-microbial agents against Actinomyces species isolated from patients with dental caries. J. Stomatol. 2024, 77(1), 47- 54.
33. Perles, L., Martins, T.F., Barreto, W.T.G., Carvalho de Macedo, G., Herrera, H.M., Mathias, L.A., et al. Diversity and seasonal dynamics of ticks on ring-tailed coatis Nasua nasua (Carnivora: Procyonidae) in two urban areas from Midwestern Brazil. Animals. 2022, 12(3), 293.
34. Iovine, R.D.O., Dejuste, C., Miranda, F., Filoni, C., Bueno, M.G., Carvalho, V.M.D. Isolation of *Escherichia coli* and *Salmonella spp.* from free-ranging wild animals. Braz. J. Microbiol. 2015, 46(4),1257-63.

35. Depta, J., Niedźwiedzka-Rystwej, P. The phenomenon of antibiotic resistance in the polar regions: an overview of the global problem. Infect. Drug Resist. 2023, 1979-95.
36. Dolejska, M. Antibiotic-resistant bacteria in wildlife. Antibiotic Resistance in the Environment: A Worldwide Overview. 2020, 19-70.
37. Zeballos-Gross, D., Rojas-Sereno, Z., Salgado-Caxito, M., Poeta, P., Torres, C., Benavides J.A. The role of gulls as reservoirs of antibiotic resistance in aquatic environments: a scoping review. Front. Microbiol. 2021, 12, 703886.
38. Kaboré, M., Konaté, I., Cissoko, Y., Guindo, I., Coulibaly, B., Hermine, M., et al. Microbiological assessment and antimicrobials' use in an infectious diseases department in Mali. Adv. Microbiol. 2021, 11(8), 384-98.
39. Lalaoui, R., Javelle, E., Bakour, S., Ubeda, C., Rolain, J.M. Infections due to carbapenem- resistant bacteria in patients with hematologic malignancies. Front. Microbiol. 2020, 11,1422.
40. Mena, K.D., Gerba, C.P. Risk assessment of *Pseudomonas aeruginosa* in water. Rev. Environ. Contam. Toxicol. 2009, 201, 71-115.
41. Blasi, M.F., Migliore, L., Mattei ,D., Rotini, A., Thaller, M.C., Alduina, R. Antibiotic resistance of gram-negative bacteria from wild captured loggerhead sea turtles. Antibiotics. 2020, 9(4), 162.
42. Banik, B.K., Das, A. Antibacterial Effects of Beta-Lactam Antibiotics with Nanoparticles. Chemistry and Biology of Beta-Lactams. 2024, 304.
43. Vliegenthart-Jongbloed, K., Jacobs, J. Not recommended fixed-dose antibiotic combinations in low-and middle-income countries–the example of Tanzania. Antimicrob. Resist. Infect. Control. 2023,12(1), 37.
44. Belmar-Liberato, R., Gonzalez-Canga, A., Tamame-Martin, P., Escribano-Salazar, M. Amoxicillin and amoxicillin-clavulanic acid resistance in veterinary medicine–the situation in Europe: a review. Vet. Med. 2011, 56(10), 473.
45. Gambo, S., Mukhtar, A., Labaran, H., Labaran, H., Mustapha, A., Ibrahim, S., Ali, M. Chemistry, mode of action, bacterial resistance, classification and adverse effects of Beta- lactam antibiotics: a review. Int. J.Dermatol. Res. 2023, 5, 11-6.
46. Zhang, Y., Kuang, X., Liu, J., Sun, R.Y., Li, X.P., Sun, J., Liao, X.P., Liu, Y.H., and Yu, Y. Identification of the plasmid-mediated colistin resistance gene mcr-1 in *Escherichia coli* isolates from migratory birds in Guangdong, China. Front. Microbiol. 2021, 12, 755233.
47. Ong, K.H., Khor, W.C., Quek, J.Y., Low, Z.X., Arivalan, S., M., Humaidi, M., Chua, C., Seow, K.L.G., Guo, S., Tay, M.Y.F., Schlundt, J., Ching Ng, L., and Aung, K.T. Occurrence and antimicrobial resistance traits of *Escherichia coli* from wild birds and rodents in Singapore. Int. J. Environ. Res. Public Health. 2020, 17(15), 5606.
48. Karunarathna, I., Hapuarachchi, T., Gunasena, P., & Gunathilake, S. Comprehensive review of amoxicillin: Indications, mechanism of action, and clinical application. 2024.
49. Ozma, M.A., Abbasi, A., Asgharzadeh, M., Pagliano, P., Guarino, A., Köse, Ş., Kafil, H.S. Antibiotic therapy for pan-drug-resistant infections. Le infezioni in medicina. 2022, 30(4), 525.
50. Junkert, A.M., Lazo, R.E.L., Deffert, F., Carneiro, J., Borba, H.L., de Campos, M.L., Pontarolo, R. Pharmacokinetics of oral ciprofloxacin in adult patients: A scoping review. Br. J. Clin. Pharmacol. 2024, 90(2), 528-47.
51. Sulis, G., Sayood, S., Gandra, S. Antimicrobial resistance in low-and middle-income countries: current status and future directions. Expert review of anti-infective therapy. 2022, 20(2),147- 60.
52. Belay, W.Y., Getachew, M., Tegegne, B.A., Teffera, Z.H., Dagne, A., Tirsit Ketsela Zeleke, T.Z., Abebe, R.B., Gedif, A.A., Fenta, A., Yirdaw, G., Tilahun, A., and Aschale, Y. Mechanism of antibacterial resistance, strategies and next-generation antimicrobials to contain antimicrobial resistance: A review. Front. Pharmacol. 2024, 15, 1444781.
53. Cornacchia, A., Centorotola, G., Tieri, E.E., Sulli, N., Del Matto, I., Iannitto, G., Petrone, D., Petrini, A., and Pomilio, F. Phenotypic and genetic characterization of *Klebsiella pneumoniae* isolates from wild animals in Central Italy. Animals. 2022, 12 (11), 1347.
54. Nairoukh, Y.R., Mahafzah, A.M., Irshaid, A., Shehabi, A.A. Molecular characterization of multidrug resistant uropathogenic *E. coli* isolates from Jordanian patients. Open Microbiol. J. 2018,12,1.
55. Baron, S.A., Mediannikov, O., Abdallah, R., Kuete Yimagou, E., Medkour, H., Dubourg, G., et al. Multidrug-resistant Klebsiella pneumoniae clones from wild chimpanzees and termites in Senegal. Antimicrob. Agents Chemother. 20216, 5(9), 10.1128/aac. 02557-20.
56. Abdallah, R., Kuete Yimagou, E., Hadjadj, L., Mediannikov, O., Ibrahim, BA., Davoust, E., Barciela, A., Hernandez-Aguilar, R.A., Diatta, G., Sokhna, C., Raoult, D., Jean-Marc Rolain, J.M., and Baron, S.A.Population diversity of antibiotic resistant Enterobacterales in samples from wildlife origin in Se negal: Identification of a multidrug resistance transposon carrying bla CTX–M–15 in *Escherichia coli*. Front. Microbiol. 2022, 13, 838392.
57. Wang X, Zhang Y, Li C, Li G, Wu D, Li T, et al. Antimicrobial resistance of *Escherichia coli, Enterobacter spp., Klebsiella pneumoniae* and *Enterococcus spp*. isolated from the feces of giant panda. BMC Microbiol. 2022, 22(1), 102.
58. Torres, R.T., Cunha, M.V., Araujo, D., Ferreira, H., Fonseca, C., Palmeira, J.D. A walk on the wild side: Wild ungulates as potential reservoirs of multi-drug resistant bacteria and genes, including *Escherichia coli* harbouring CTX-M beta-lactamases. Environ. Pollut. 2022, 306, 119367.

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