Prevalence and antimicrobial resistance of *Salmonella* and *Yersinia* in the feces of hunted wildlife in Abeokuta, Nigeria

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Summary

Meat from wildlife contributes significantly to food security and income generation in many African communities. Salmonellae and yersiniae are important causes of foodborne infections. This study investigated the presence and antimicrobial resistance of salmonellae and yersiniae in the fecal contents of hunted wild rodents and ruminants at a wildlife meat-processing center in Abeokuta, Nigeria. Bacteria were isolated and identified by selective culture methods and biochemical characterization. Antimicrobial susceptibility was determined by the Kirby Bauer disk diffusion method. Salmonellae were isolated from 15 (9.8%) and yersiniae from 11 (7.2%) samples out of 153. Salmonellae were detected in nine cane rats (*Thryonomys swinderianus*), five royal antelopes (*Neotragus pygmaeus*) and one African giant rat (*Cricetomys gambianus*). Yersiniae were detected in eight cane rats, two royal antelopes and one waterbuck (*Kobus ellipsiprymnus*). The levels of resistance in *Salmonella* isolates were 100% for ampicillin and ceftiofur, 93.3% for tetracycline, 33.3% for cefotaxime, 26.7% for ceftazidime, 13.3% for amoxicillin/clavulanic acid, nalidixic acid and sulfamethoxazole/trimethoprim, and 6.7% for gentamicin, streptomycin and norfloxacin. The levels of resistance in yersiniae isolates were 81.8% for ampicillin, 72.7% for ceftiofur, 63.6% for nalidixic acid, 54.5% for cefotaxime, ceftazidime and sulfamethoxazole/trimethoprim, 36.4% for tetracycline, 27.3% for amoxicillin/clavulanic acid and streptomycin, 18.2% for ciprofloxacin, and 9.1% for chloramphenicol and gentamicin. All the isolates showed multiresistance to antimicrobials from at least three different classes. The detection of antimicrobial resistant salmonellae and yersiniae in wildlife is of veterinary and public health significance as these organisms can be transmitted to domestic animals and humans.

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■ INTRODUCTION

Hunted wildlife is a major source of animal protein to support families in many rural African communities. In some rural communities, game is people's main source of meat. In addition, game meats are considered special delicacies in the diet of people of all social statuses across Africa. Hunters also sell game to generate income. Therefore, wildlife hunting contributes to the food security and socioeconomic viability of many countries in Africa (Schulte-Herbrüggen et al., 2013).

Processing and consuming game meat can expose people to a similar risk of foodborne infection to that originating from processed livestock meat. Game meat consumption may pose a higher risk of disease transmission because processing of hunted game is not subjected to routine meat inspection. *Salmonella* spp. and *Yersinia* spp. are important human pathogens transmissible directly or indirectly from animal sources (Saraka et al., 2017; Uche et al., 2017). *Salmonella* in particular is a leading cause of foodborne infection all over the world

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(Majowicz et al., 2010). An earlier study has reported a higher prevalence of *Salmonella enterica* serovars (2.9%) than *Escherichia coli* O157:H7 (0.2%) in samples from wild rodents (Kilonzo et al., 2013). Contact with animals and consumption of food of animal origin are risk factors in the transmission of salmonellae and yersiniae. Infections are characterized by gastroenteritis, septicemia and other complications that can sometimes be fatal (Uche et al., 2017). In order to limit the fatal consequences of infections, physicians prescribe antimicrobial agents. However, the involvement of antimicrobial resistant strains could lead to therapy failure with protracted illness, high medical care costs, increased spread of infection, and high fatality rates, among other problems. Multidrug resistant non-typhoidal *Salmonella* poses a threat in sub-Saharan Africa with the possibility of zoonotic transmission from animal reservoirs (Balasubramanian et al., 2018).

The challenge of antimicrobial resistance is worldwide. The increasing report of antimicrobial resistance in commensal and pathogenic bacteria has reached an alarming state indicating that the end of the antibiotic era is probably nearer than envisaged (Harrison and Svec, 1998a; 1998b). Although every form of antimicrobial usage could lead to the selection of resistant strains, overdependence on antimicrobial agents for therapeutic, prophylactic and growth promotion purposes in livestock production favors the accelerated emergence and widespread dissemination of resistance traits in bacteria. Food animals are recognized as major sources for the distribution of antimicrobial resistant bacteria that could be transmitted to humans through the food chain. Similarly, the presence of antimicrobial resistant bacterium strains has been reported in wildlife (Literak et al., 2010). Therefore, the role of wildlife in the dissemination of antimicrobial resistance in the environment cannot be ignored (Furness et al., 2017). The present study investigated the presence and antimicrobial resistance of salmonellae and yersiniae in the feces of hunted wildlife, while being processed for public consumption in Abeokuta, Nigeria.

■ MATERIALS AND METHODS

Sample collection

Fecal contents were collected from the rectum of hunted wildlife during evisceration at a processing center in Abeokuta, Nigeria. Abeokuta is the capital and largest city of Ogun State with a population of about 450,000 inhabitants. It is located at 7º 10' N, 3º 21' E, about 77 kilometers north of Lagos. The processing center is a point of collection, dressing and sale of game meat. Processing involved evisceration, singeing for hair removal and thorough washing of the carcasses. Sometimes, the carcasses were roasted before sale. There was no form of meat inspection of the game before, during and after processing. Carcasses of hunted game were brought to the processing center very early in the morning (4:00–6:00) after overnight hunting. This corresponded to about four to eight hours after the death of the animals. Carcasses were transported in sacks, bowls or hand-woven baskets. There was no official documentation on the activities of game meat processing in the center. During the period of sample collection, it was observed that at least 20 carcasses were processed daily. All animals included in the study were fresh carcasses without obvious signs of autolysis. The animals were hunted in the vegetation of immediate rural communities around Abeokuta. However, the specific origin of individual animals could not be ascertained.

A total of 153 samples were collected that represented four categories of game: 108 cane rats (*Thryonomys swinderianus*), 40 royal antelopes (*Neotragus pygmaeus*), 3 African giant rats (*Cricetomys gambianus*), and 2 waterbucks (*Kobus ellipsiprymnus*). Visits were made to the processing center once a week between January and May 2013. The samples were labeled, preserved in icepacks and transported to the Veterinary Microbiology Laboratory of the Department of Veterinary Microbiology and Parasitology, Federal University of Agriculture, Abeokuta, Nigeria, for microbiological analysis. They were analyzed within 24 hours of collection.

Isolation and identification of salmonellae

Ten grams of each fecal content was homogenized and inoculated into 90 ml of buffered peptone water (BPW CM0509, Oxoid, Basingstoke, UK) for pre-enrichment. They were incubated at 37°C for 18–24 hours. Subsequently, 0.1 ml of the pre-enrichment culture was transferred onto modified semisolid Rappaport Vassiliadis broth (MSRV CM0910, Oxoid) with novobiocin supplement (Oxoid SR0161) for enhanced selective isolation of *Salmonella* at 42°C. After 24 hours of incubation, the MSRV culture was observed for growth of motile *Salmonella* as indicated by the presence of migrating opaque halo larger than 20-mm circumference around the point of inoculation. Subcultures were made from the periphery of the spreading growth on MRSV onto xylose-lysine desoxycholate agar (XLD CM0469, Oxoid) and modified brilliant green agar (mBGA CM0329, Oxoid) containing sulphamandelate supplement (Oxoid SR0087). Both XLD and mBGA cultures were incubated at 37°C for 24 hours. Suspected *Salmonella* colonies (pink colonies with black centers on XLD, and red to pink-white opaque colonies surrounded by red zones on mBGA) were selected for biochemical characterization using a biochemical test kit (Oxoid Microbact GNB 24E). Isolates identified as *Salmonella* were tested serologically for the detection of *Salmonella* somatic (O) and flagellum (H) antigens by slide agglutination using *Salmonella* polyvalent O (BD Difco Salmonella O Antiserum) and H (Oxoid Salmonella Test Kit, DR1108) antisera, according to the manufacturer's instruction.

Isolation and identification of yersiniae

Ten grams of each fecal content was inoculated into 90 ml of buffered peptone water and kept in the refrigerator at 4°C for three weeks for cold enrichment. Subcultures were made weekly from BPW onto yersinia selective agar base (Oxoid CM0653) containing yersinia selective supplement (Oxoid SR0109: cefsulodin, irgasan and novobiocin). The subcultures were incubated at 35°C for 24 hours. They were examined for colonies with deep red centers and transparent margins (bull's eye). Presumptive *Yersinia* colonies were identified by biochemical characterization using a test kit for the identification of Gram-negative, oxidase-negative bacilli (Oxoid Microbact GNB 24E). The results of biochemical reactions were interpreted according to the manufacturer's instruction using the accompanying computer software package (Oxoid Microbact 2000 vers. 2.03).

Antimicrobial susceptibility testing

All identified isolates were tested for susceptibility to ampicillin (10 µg), amoxicillin/clavulanic acid (30 µg), cefotaxime (30 µg), ceftazidime (30 µg), ceftiofur (30 µg), chloramphenicol (30 µg), ciprofloxacin (5 µg), nalidixic acid (30 µg), norfloxacin (10 µg), gentamicin (30 µg), streptomycin (10 µg), sulfamethoxazole/trimethoprim (25 µg) and tetracycline (30 µg) by the Kirby Bauer disk diffusion method. Results were interpreted according to the guideline of the Clinical and Laboratory Standards Institute (CLSI, 2012) (Table I). *Escherichia coli* ATCC25922 was tested along with the isolates for quality control.

■ RESULTS

Salmonellae were isolated from 15 (9.8%) samples out of 153 (Table II). The positive samples were from cane rats (9/108, 8.3%), royal antelopes (5/40, 12.5%) and an African giant rat (1/3, 33.3%).

Table I

Interpretative breakpoints according to CLSI (2012) for the determination of antimicrobial susceptibility of salmonellae and yersiniae isolated from hunted wildlife in Abeokuta, Nigeria

Antimicrobial agent	Zone diameter breakpoints for disk diffusion test (mm)		
	Susceptible	Intermediate	Resistant
Ampicillin	≥ 17	14–16	≤ 13
Amoxicillin / clavulanic acid	≥ 18	14–17	≤ 13
Cefotaxime	≥ 26	23–25	≤ 22
Ceftiofur	≥ 21	18–20	≤ 17
Ceftazidime	≥ 21	18–20	≤ 17
Chloramphenicol	≥ 18	13–17	≤ 12
Ciprofloxacin	≥ 21	16–20	≤ 15
Gentamicin	≥ 15	13–14	≤ 12
Nalidixic acid	≥ 19	14–18	≤ 13
Norfloxacin	≥ 17	13–16	≤ 12
Streptomycin	≥ 15	12–14	≤ 11
Sulfamethoxazole/ trimethoprim	≥ 16	11–15	≤ 10
Tetracycline	≥ 15	12–14	≤ 11

Yersiniae were isolated from 11 (7.2%) samples out of 153. *Yersinia pseudotuberculosis* was isolated from nine (5.9%) samples out of 153, whereas *Y. aldovae* was isolated from two (1.3%) samples. *Y. pseudotuberculosis* was detected in cane rats (8/108, 7.4%) and a royal antelope (1/40, 2.5%). *Y. aldovae* was isolated from a royal antelope (1/40, 2.5%) and a waterbuck (1/2, 50%).

Salmonella isolates showed complete (100%) resistance to ampicillin and ceftiofur, and 93.3% to tetracycline (Table III). Other

Table II

Occurrence of salmonellae and yersiniae in hunted wildlife in Abeokuta, Nigeria

Wildlife species (n)	Number (%) of bacterial species		
	Salmonella	*Yersinia pseudotuberculosis*	*Y. aldovae*
Cane rat (108)	9 (8.3)	8 (7.4)	0
Royal antelope (40)	5 (12.5)	1 (2.5)	1 (2.5)
African giant rat (3)	1 (33.3)	0	0
Waterbuck (2)	0	0	1 (50.0)
Total (153)	15 (9.8)	9 (5.9)	2 (1.3)

antimicrobial resistance of *Salmonella* ranged from 33.3% for cefotaxime to zero for chloramphenicol and ciprofloxacin. *Yersinia* isolates showed 81.8% resistance to ampicillin, 72.7% to ceftiofur, 63.6% to nalidixic acid, and 54.5% to cefotaxime, ceftazidime and sulfamethoxazole/trimethoprim (Table III). Other antimicrobial resistance of *Yersinia* ranged from 45.5% for cephalexin to zero for norfloxacin. All the isolates in this study showed multiple antimicrobial resistance with resistance to antimicrobials from at least three different classes.

■ DISCUSSION

Oboegbulem and Okoronkwo (1990) reported a *Salmonella* prevalence of 32% from the intestine, spleen and liver of hunted greater cane rats (*Thryonomys swinderianus*) in Nssuka, Nigeria, which was higher than that of 8.3% observed in our study from the fecal contents of hunted games. To our knowledge, there is no previous report on the detection of *Salmonella* in the waterbuck and the African giant rat in Nigeria. The detection of *Salmonella* from these wildlife sources shows that wildlife species should be considered as important reservoirs of *Salmonella* that could be transmitted to domestic

Table III

Antimicrobial susceptibility profile (%) of salmonellae and yersiniae isolated from hunted wildlife in Abeokuta, Nigeria

Antimicrobial agent	Salmonellae			Yersiniae		
	Resistant	Intermediate	Susceptible	Resistant	Intermediate	Susceptible
Ampicillin	100	0	0	81.8	18.2	0
Amoxicillin / clavulanic acid	13.3	46.7	40	27.3	36.4	36.3
Cefotaxime	33.3	66.7	0	54.5	36.4	9.1
Ceftiofur	100	0	0	72.7	18.2	9.1
Ceftazidime	26.7	46.7	26.6	54.5	45.5	0
Cephalexin	53.3	20	26.7	45.5	9.1	45.4
Chloramphenicol	0	60	40	9.1	72.7	18.2
Gentamicin	6.7	0	93.3	9.1	18.2	72.7
Ciprofloxacin	0	20	80	18.2	54.5	27.3
Nalidixic acid	13.3	86.7	0	63.6	36.4	0
Norfloxacin	6.7	0	93.3	0	63.6	36.4
Streptomycin	6.7	66.7	26.6	27.3	27.3	45.4
Sulfamethoxazole/ trimethoprim	13.3	26.7	60	54.5	18.2	27.3
Tetracycline	93.3	6.7	0	36.4	54.5	9.1

animals and humans through direct and indirect contacts as well as through consumption of contaminated foods (including the meat of these animals) and water. Improper disposal of intestinal contents of hunted game especially during processing can also lead to environmental contamination and widespread dispersal of potentially zoonotic pathogens leading to possible disease outbreaks or sporadic infections. Hunters and processors of game meat are particularly at risk of acquiring *Salmonella* infections from hunted game. Wild animals may also be an important source of *Salmonella* transmission to domestic animals through contamination of farm environment as well as via fecal contamination of feed and water sources. The nomadic system of ruminant management in West Africa, whereby pastoralists and their livestock migrate from place to place through grasslands and forests, can increase livestock infectious contacts with wildlife and their fecal contaminants, thereby increasing the possibility of exchange of pathogenic microorganisms between wildlife and livestock.

In the present study, *Y. pseudotuberculosis* was isolated from cane rats and royal antelopes. Previous studies have established the reservoirs of *Y. pseudotuberculosis* in wildlife and its zoonotic transmission to humans (Fukushima et al., 1988; Welsh et al., 1992). *Y. pseudotuberculosis* is a zoonotic bacterial pathogen associated with acute gastroenteritis and mesenteric lymphadenitis (Long et al., 2010). The involvement of *Y. pseudotuberculosis* in outbreaks of foodborne infections has been documented (Jalava et al., 2004). Unfortunately, *Y. pseudotuberculosis* is often overlooked leading to misdiagnosis and underestimation of its role as an etiology of gastrointestinal infections (Long et al., 2010). *Y. aldovae* was isolated from a royal antelope and a waterbuck. It is usually isolated from aquatic environments and from fish (Bercovier et al., 1984) but it rarely causes clinical infection. The animals that harbored *Y. aldovae* in this study could have acquired the organism from drinking contaminated water.

There is a dearth of information on the prevalence and antimicrobial resistance of bacteria in Nigerian wildlife populations. Most epidemiological surveillance and antimicrobial monitoring programs do not much address the possible role of wildlife as reservoirs in the emergence, environmental dissemination and food contamination of antimicrobial resistant pathogens. Nevertheless, high rates of antimicrobial resistance have been reported among bacteria isolated from food animal species.

In our study, salmonellae and yersiniae from hunted wildlife showed resistance to a wide range of antimicrobial agents from different classes including the β-lactams (cefotaxime, ceftazidime, ceftiofur), aminoglycosides (streptomycin, gentamicin), quinolones (nalidixic acid, ciprofloxacin, norfloxacin), phenicols (chloramphenicol), and folic acid inhibitors (sulfamethoxazole/trimethoprim combination), and tetracycline. In our study salmonellae and yersiniae also showed a very high degree of resistance to ampicillin and tetracycline, which are the most commonly used antimicrobial agents in veterinary and human medical practices (Ojo et al., 2017). This is similar to other reports where *Salmonella* isolates from chickens and Japanese quails showed a high level of resistance to ampicillin (80.0% to 100%) and tetracycline (35% to 100%) (Ojo et al., 2012; Omoshaba et al., 2017). The rates of resistance to gentamicin (6.7% in *Salmonella* and 9.1% in *Yersinia*) observed in this study were lower than that of 21.4% reported in *Salmonella* in Japanese quails (Omoshaba et al., 2017). Similarly, *Salmonella* and *Yersinia* isolates from this study showed a lower level of resistance to streptomycin (6.7% and 27.3, respectively) than the 57.2% resistance reported in *Salmonella* in Japanese quails (Omoshaba et al., 2017). *Salmonella* and *Yersinia* isolates showed a low resistance below 20.0% to fluoroquinolones (ciprofloxacin and norfloxacin) similar to those reported by Ojo et al. (2012) and Omoshaba et al. (2017). The 26.7% resistance to ceftazidime among *Salmonella* isolates in this study was lower than the 78.6% reported by Omoshaba et al. (2017). In the present study, *Salmonella* showed 100% and *Yersinia* 72.7% resistance to ceftiofur. Previous studies on antimicrobial resistance in *Salmonella* of livestock origin in Nigeria did not include ceftiofur among the antimicrobial agents tested. However, the ceftiofur resistance rates observed here were higher than the 6.0% to 62.0% rates reported in *S. enterica* serovar Heidelberg from chicken meat and humans in Canada (Dutil et al., 2010), 18.1% in *S.* Typhimurium from poultry in Brazil (Biffi et al., 2014), and 30.7% to 36.7% in *Salmonella* from swine and cattle in Minnesota, United States (Hong et al., 2016).

Differences in antimicrobial resistance profiles of bacterium strains between countries may be caused by differences in antimicrobial usage and related practices. Resistance to third-generation cephalosporins and fluoroquinolones is particularly worrisome because of the importance of these drugs as last-resort antimicrobial agents in the treatment of infections that are refractory to treatment by the older generation of antimicrobial agents (Chen et al., 2013; Lunguya et al., 2013). The fluoroquinolones are particularly useful in the treatment of human salmonellosis (Chen et al., 2013). Salmonellae showing resistance to fluoroquinolones are probably more invasive and capable of causing more fulminating infections in humans (Kariuki et al., 2015).

Exposure to antimicrobial agents is a major factor in the emergence, persistence and spread of antimicrobial resistant bacteria. Unlike livestock that are usually exposed to antimicrobial agents through therapeutic, prophylactic and growth promotion applications, wildlife is mainly exposed to antimicrobial agents through environmental pollution (Radhouani et al., 2014; Singer et al., 2016). Improper disposal of antimicrobial packages, migration of wildlife (searching for food) to dwelling areas and farms, discharge of animal effluents from commercial livestock farms and abattoirs into water bodies, discharge of antimicrobial waste from pharmaceutical factories into water bodies are among the various factors that influence exposure of wildlife to antimicrobial residues as well as acquisition of resistant bacteria or resistance genes (Kümmerer, 2004; Radhouani et al., 2014). Antimicrobial usage is a very common practice in Nigerian food animal production (Ojo et al., 2016; 2017). Farmers depend heavily on antimicrobials for growth promotion as well as for the prevention and treatment of infections. Ogun State is the largest producer of poultry. It has clusters of large, medium and small-scale commercial poultry farms. Wastes from these farms and from abattoirs are washed into Ogun River, which serves as the main source of drinking water for wildlife and nomadic livestock during the dry season.

■ CONCLUSION

The emergence of multidrug-resistant bacteria in wildlife observed in the present study is of public health significance. Avoiding contact with wildlife may prevent the transmission of pathogens from these animals to humans. Adherence to the principles of hygiene during processing and marketing of wildlife meat could help limit meat contamination, and cooking meat before consumption may destroy foodborne pathogens. However, cooking may not destroy the antimicrobial resistance genes. Responsible antimicrobial stewardship as well as proper treatment of human and animal wastes before disposal may limit contamination of the environment and thus the transfer of resistance from humans and livestock to wildlife. This study is a preliminary assessment of the role of wildlife as reservoirs of antimicrobial resistant foodborne pathogens. Further studies on antimicrobial resistance in wildlife involving larger collections of samples across wider geographical locations are needed for better understanding of the role of wildlife in the emergence and spread of antimicrobial resistant pathogens.

Author contributions statement

OEO and MAO conceptualized and designed the study. OEO and OOO were responsible for sample collection and laboratory works. OEO, OOO and MAO participated in data analysis and result interpretation. OEO and OOO prepared the draft manuscript. MAO, MAD and EBO critically reviewed the manuscript.

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Résumé

Ojo O.E., Ogunjobi O.O., Oyekunle M.A., Dipeolu M.A., Otesile E.B. Prévalence et résistance antimicrobienne de salmonelles et de yersinias dans les fèces d'animaux sauvages issus de la chasse à Abeokuta, Nigeria

La viande de brousse contribue de manière significative à la sécurité alimentaire et à la génération de revenus de nombreuses communautés africaines. Les salmonelles et les yersinias sont des causes importantes d'infections alimentaires. Cette étude a porté sur la présence et la résistance antimicrobienne de salmonelles et de yersinias dans les fèces de rongeurs et de ruminants sauvages issus de la chasse dans un centre de traitement de viande de brousse à Abeokuta, au Nigeria. Les bactéries ont été isolées et identifiées par culture sélective et caractérisation biochimique. La sensibilité aux antimicrobiens a été déterminée par la méthode de diffusion sur disque Kirby Bauer. Des salmonelles ont été isolées dans 15 (9,8 %) échantillons sur 153 et des yersinias dans 11 (7,2 %). Des salmonelles ont été détectées chez neuf aulacodes (*Thryonomys swinderianus*), cinq antilopes royales (*Neotragus pygmaeus*) et un cricétome des savanes (*Cricetomys gambianus*). Des yersinias ont été détectées chez huit aulacodes, deux antilopes royales et un cobe (*Kobus ellipsiprymnus*). Les isolats de salmonelles ont présenté des taux de résistance de 100 % à l'ampicilline et au ceftiofur, de 93,3 % à la tétracycline, de 33,3 % à la céfotaxime, de 26,7 % à la ceftazidime, de 13,3 % à l'amoxicilline / acide clavulanique, à l'acide nalidixique et au sulfaméthoxazole/triméthoprime, et de 6,7 % à la gentamicine, à la streptomycine et à la norfloxacine. Les isolats de yersinias ont révélé des taux de résistance de 81,8 % à l'ampicilline, de 72,7 % au ceftiofur, de 63,6 % à l'acide nalidixique, de 54,5 % à la céfotaxime, à la ceftazidime et au sulfaméthoxazole/triméthoprime, de 36,4 % à la tétracycline, de 27,3 % à l'amoxicilline / acide clavulanique et à la streptomycine, de 18,2 % à la ciprofloxacine, et de 9,1 % au chloramphénicol et à la gentamicine. Tous les isolats ont présenté une multirésistance à au moins trois classes différentes d'antimicrobiens. La détection de salmonelles et de yersinias résistantes aux antimicrobiens chez les animaux sauvages révèle un problème de santé publique et vétérinaire, car ces organismes peuvent être transmis aux humains et aux animaux domestiques.

Mots-clés : *Salmonella*, *Yersinia*, résistance aux antimicrobiens, gibier, zoonose, Nigeria

Resumen

Ojo O.E., Ogunjobi O.O., Oyekunle M.A., Dipeolu M.A., Otesile E.B. Prevalencia y resistencia antimicrobiana a *Salmonella* y *Yersinia* en las heces de fauna cazada en Abeokuta, Nigeria

La carne de fauna silvestre contribuye significativamente a la seguridad alimenticia y a la generación de ingresos en muchas comunidades africanas. *Salmonella* y *Yersinia* son causas importantes de infecciones alimenticias. El presente estudio investigó la presencia y resistencia antimicrobiana a *Salmonella* y *Yersinia* en los contenidos fecales de roedores y rumiantes cazados, en una planta procesadora de carne de fauna silvestre en Abeokuta, Nigeria. Se aislaron e identificaron bacterias mediante medios de cultura selectivos y caracterización bioquímica. La susceptibilidad antimicrobiana se determinó mediante el método de difusión en disco de Kirby Bauer. *Salmonella* se aisló en 15 (9,8%) y *Yersinia* en 11 (7,2%) de las 153 muestras. *Salmonella* se detectó en nueve ratas de caña (*Thryonomys swinderianus*), cinco antílopes reales (*Neotragus pygmaeus*) y una rata gigante africana (*Cricetomys gambianus*). *Yersinia* se detectó en ocho ratas de caña, dos antílopes reales y un antílope acuático (*Kobus ellipsiprymnus*). Los niveles de resistencia en los aislamientos de *Salmonella* fueron de 100% para ampicilina y ceftiofur, 93,3% para tetraciclina, 33,3% para cefotaxima, 26,7% para ceftazidima, 13,3% para amoxicilina / ácido clavulánico, ácido nalidíxico y sulfametoxazol trimetroprima, y 6,7% para gentamicina, estrepnomicina y norfloxacina. Los niveles de resistencia en aislamientos de *Yersinia* fueron de 81,8% para ampicilina, 72,7% para ceftiofur, 63,6% para ácido nalidíxico, 54,5% para cefotaxima, ceftazidima y sulfametoxazol trimetroprima, 36,4% para tetraciclina, 27,3% para amoxicilina / ácido clavulánico y estrepnomicina, 18,2% para ciprofloxacina, y 9,1% para cloranfenicol y gentamicina. Todos los aislamientos mostraron resistencia múltiple a por lo menos tres clases diferentes de antimicrobianos. La detección de la resistencia antimicrobiana a *Salmonella* y *Yersinia* en fauna silvestre tiene un significado en salud pública y veterinaria, ya que estos organismos pueden transmitirse a animales domésticos y humanos.

Palabras clave: *Salmonella*, *Yersinia*, resistencia a los antimicrobianos, animales de caza, zoonosis, Nigeria