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Load and Antibiotic Susceptibility Pattern of Microorganisms in Muscle Foods Sold in Akure, Southwest Nigeria

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HIGHLIGHTS

- Low fungal counts were recorded as 1.0×10^2 to 1.30×10^2 spore forming unit/g.
- The multidrug resistant microorganisms, ranged 33.3 to 100% in muscle foods, can be a risk factor to public health.
- Microbial contamination of the samples could be considered as result of poor hygiene of the retailers or handlers.

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Acronyms and abbreviations
CFU=Colony Forming Unit
SFU=Spore Forming Unit
MAR=Multiple Antibiotic Resistance

ABSTRACT

Background: Muscle foods, notably red meat, poultry meat, and fish are the first choice of animal source food with adequate protein for human. The present study was undertaken to analyze the load and antibiotic susceptibility pattern of microorganisms in muscle foods sold in Akure, Southwest Nigeria.

Methods: Hundred muscle food samples, including meat and fish were collected from different locations (A-E) of Akure, Nigeria and examined microbiologically using cultural techniques, biochemical tests, and analytical profile index. Antibiotic susceptibility patterns were also determined in isolated microorganisms from muscle foods against different antibiotics. Data were analyzed using SPSS software version 17.0.

Results: The highest (p<0.05) total viable bacterial count (8.3×10^6 CFU/g) were obtained from pork, including with 6.0×10^5 CFU/g for *Staphylococcus* and 5.8×10^5 CFU/g for *Salmonella-Shigella*. Mackerel collected from location D (Kings market) had the highest (p<0.05) bacterial count of 9.97×10^5 CFU/g, followed by 8.57×10^5 CFU/g, and 7.03×10^5 CFU/g in locations C and E, respectively. Low fungal counts were recorded ranged from 1.0×10^2 to 1.30×10^2 spore forming unit/g. The highest (p<0.05) occurrence of 26.50% was observed for *Escherichia coli*. The isolated microorganisms displayed varying degree of resistance (33.3 to 100%) to commonly used antibiotics.

Conclusion: The microorganisms found in muscle foods from Akure, Nigeria could be considered as result of poor hygiene of the retailers or handlers. Also, presence of the multidrug resistant bacteria in muscle foods distributed in this region could pose a serious risk factor to public health.

Introduction

Muscle foods, notably red meat, poultry meat, and fish are the first choice of animal source food with adequate protein for human. Muscle foods are nutritionally important as derivation of quality protein with all essential amino acids, thiamin (B_1), riboflavin (B_2), niacin (B_3), pyridoxine (B_6), and bioavailable minerals like cal-

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cium, phosphorous, and potassium (Lawrie and Ledward, 2006). These nutrients are essential for human to improve their digestive system, healthy growth of nerves, muscles, bone, heart, and red blood cell production. Fishes also provide essential unsaturated fats (Omega-3 fatty acids), help to reduce cholesterol level, blood pressure, and risk of developing cardiovascular disease as well as Alzheimer (Pereira and Vicente, 2013; Swanson et al., 2012).

Foods of animal origin are often spoiled quickly if they are not preserved properly. Certain species of bacteria utilize muscle foods as a growth medium due to its nutritional composition. Meat and fish have been found not only susceptible to microbial spoilage but also they are frequently implicated as potential vehicles for spreading food-borne pathogens (Datta et al., 2012). Some bacteria which may show Multiple Antibiotic Resistance (MAR) can typically cause severe food-borne diseases in meat consumers (Dhama et al., 2013). Nowadays, overuse of antibiotics in animal husbandry and consequent antibiotic residue in foods of animal can result in antibiotic resistance, which is an important public health concern (Done et al., 2015; Doyle, 2015; Economou and Gousia, 2015; Marshall and Levy, 2011).

The present study was undertaken to analyze the presence, number, type of microorganisms, as well as to reveal the antibiotic susceptibility pattern of isolated microorganisms from meat and fish sold in different places in Akure, Southwestern Nigeria.

Materials and methods

Sample collection

During July 2016 to April 2017, a total of 100 muscle food samples, including meat and fish were collected from Akure, the capital of Ondo State in Southwestern Nigeria. Ten samples were collected from different places at commercial areas of Akure, Nigeria, including beef (*Bos taurus*), chicken (*Gallus gallus domesticus*), turkey (*Meleagris gallopavo*), pork (*Sus scrofa domesticus*), chevon (*Capra aegagrus hircus*), mackerel (*Scomber scombrus*), horse mackerel (*Trachurus trachurus*), herrings (*Clupea pallasii*), blue whiting (*Merluccius merluccius*), and croaker (*Micropogonias undulatus*). There were five sampling points, including location A (meat from abattoir or fish from cold room), location B (The Federal University of Technology, Akure zone), location C (Isinkan market zone), location D (King's market zone), as well as location E (Shasha market zone).

Preparation of inoculum

Each sample was aseptically cut into smaller pieces with the weight of 10 g using sterile knife and placed into 90 ml of sterile peptone water, and then the serial dilutions were obtained (Ogidi et al., 2016).

Isolation of microorganisms

Bacterial isolation was done using nutrient agar (Oxoid Basingstoke, UK) for viable bacterial count, mannitol salt agar (Oxoid Basingstoke, UK) for *Staphylococcus* count, *Salmonella-Shigella* agar (Biomark, Pune, India) for *Salmonella-Shigella* count, and violet red bile agar (Axiom Medical Ltd, Berkshire, UK) for total coliform count. The potato dextrose agar (Oxoid, Basingstoke UK) was used for fungi isolation. The media were prepared according to manufactures' instructions. One ml of diluted samples was inoculated onto the plates, incubated at 37 °C for 24 h for bacteria and 28 °C for 48 h for fungi. Colonies were counted using colony counter (TT-20, Techmel and Techmel, USA). The microbial counts obtained from each plate were expressed as Colony Forming Unit per gram (CFU/g) for bacteria and Spore Forming Unit per gram (SFU/g) for fungi.

Identification of microorganisms

After morphological examinations and biochemical tests based on Cappuccino and Sherman (1999), the bacteria and fungi were identified according to Cowan and Steel (1993) and Samson et al. (2010), respectively.

Antibiotic susceptibility of isolated microorganisms

Antibiotic susceptibility of the isolated microorganisms was carried out using agar disk diffusion method according to CLSI (2012) protocol. The microbial isolates were cultivated in sterile Mueller-Hinton broth (Merck, Germany) at 37 °C for 24 h. A sterile swab stick was immersed into bacterial suspension and spread on surface of Muller-Hinton agar (Merck, Germany) in Petri dish. Commercially available antibiotic disks (Abtek Biological Ltd, Liverpool, L9 7AR, UK) were used, including erythromycin (15 µg), pefloxacin (5 µg), gentamycin (10 µg), ampicillin (10 µg), nitrofurantoin (300 µg), amoxicillin (30 µg), rifampicin (5 µg), ciprofloxacin (5 µg), streptomycin (10 µg), trimethoprim-sulfamethoxazole (25 µg), ofloxacin (5 µg), augmentin (amoxicillin/clavulanate potassium; 30 µg), tetracycline (30 µg), and chloramphenicol (30 µg). After incubation of Petri dishes at 37 °C for 18 h, inhibition zones were measured in millimeter according to the guideline of CLSI (2012).

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Statistical analysis

Data were analyzed using Statistical Package for Social Sciences (SPSS) software version 17.0 (SPSS Inc., Chicago, IL, USA) by one-way Analysis of Variance (ANOVA).

Results

The bacterial count of meat samples are summarized in Table 1. The highest (p<0.05) total viable bacterial count (8.3×10^6 CFU/g), *Staphylococcus* count (6.0×10^5 CFU/g) and *Salmonella-Shigella* count (5.8×10^5 CFU/g**)** were obtained from pork in location B. Beef collected from market zones (C, D, and E) had the highest (p<0.05) total bacterial count of 2.53×10^6, 4.08×10^6, and 4.20×10^6 CFU/g, respectively. Turkey meat from locations B, C, D, and E had the highest bacterial count ranged from 1.04×10^6 to 2.70×10^6 CFU/g. A relatively higher (p<0.05) *Staphylococci* count of 1.30×10^5 to 1.87×10^5 CFU/g was observed in turkey collected from locations C, D, and E. The highest (p<0.05) total bacterial count of 2.70×10^6 CFU/g was seen in chicken collected from location D. Chevon has the lowest range of total bacterial count ranging from 1.90×10^5 to 7.30×10^5 CFU/g.

Table 2 shows the bacterial count from fishes. Mackerel collected from location D (Kings market) had the highest (p<0.05) bacterial count of 9.97×10^5 CFU/g, followed by 8.57×10^5 CFU/g and 7.03×10^5 CFU/g in locations C and E, respectively. Horse mackerel from location D (Kings market) had the highest values (p<0.05) of 4.80×10^6 CFU/g, 4.20×10^5 CFU/g, and 2.75×10^5 CFU/g for total bacterial, staphylococi, and *Salmonella-Shigella* count, respectively. Blue whiting from location D and Croaker from locations B, C, D, and E had the highest (p<0.05) coliform count ranged from 2.20×10^5 CFU/g to 6.70×10^5 CFU/g. No *Salmonalla-Shigella* count recorded for markerel, herrings, and blue whiting in location A.

Low fungal counts were recorded for pork, horse mackerel, and croaker sampled from locations D and E, ranged from 1.0×10^2 to 1.30×10^2 SFU/g. No fungal growth was found in muscle food samples from the locations A, B, and C. Table 3 shows the occurrence of microbial isolates from different muscle foods in Akure, Southwestern Nigeria. The most predominant bacteria isolated from muscle foods were *Escherichia coli* with value of 26.50%, followed by *S. aureus* (20.30%), *S. epidermidis* (15.60%), *Sh. dysenteriae* (7.80%), *Bacillus cereus* (7.03%), *Pseudomonas aeruginosa* (5.4%), and *Salmonella* spp. (5.4%).

Table 4 shows the occurrence of antibiotic resistant bacteria isolated from muscle foods. *E. coli*, *S. aureus, S. epidermidis, Sh. dysenteriae, B. cereus, P. aeruginosa*, and *Salmonella* spp. were highly resistant (ranged from 33.3 to 100%) to one, two or more examined antibiotics.

Table 1: Bacterial count (Colony Forming Unit/g) in sampled raw meat from different locations in Akure, Nigeria

Samples	Sample size	Microbial count	A	B	C	D	E
Beef	10	TVBC	7.77×10^5	2.12×10^5	2.53×10^6	4.08×10^6	4.20×10^6
		SSC	1.90×10^4	1.63×10^5	1.37×10^5	2.57×10^5	2.20×10^5
		SC	1.13×10^5	3.60×10^5	3.57×10^5	4.80×10^5	1.03×10^6
		CC	6.00×10^4	2.20×10^5	1.01×10^6	1.65×10^6	1.30×10^6
Turkey	10	TVBC	5.57×10^5	1.04×10^6	2.50×10^6	2.70×10^6	2.48×10^6
		SSC	4.00×10^4	1.07×10^5	7.30×10^4	1.10×10^5	1.57×10^5
		SC	6.00×10^4	8.00×10^4	1.37×10^5	1.87×10^5	1.30×10^5
		CC	2.30×10^4	1.07×10^5	1.27×10^5	2.53×10^5	2.10×10^5
Chicken	10	TVBC	1.60×10^5	8.90×10^5	9.83×10^5	2.70×10^6	1.24×10^6
		SSC	7.00×10^3	3.00×10^3	3.70×10^4	1.03×10^5	1.40×10^5
		SC	6.00×10^4	1.53×10^5	1.67×10^5	2.07×10^5	4.73×10^5
		CC	1.80×10^4	6.70×10^4	1.07×10^5	1.53×10^5	1.50×10^5
Pork	10	TVBC	1.06×10^6	8.30×10^6	5.00×10^6	9.30×10^5	6.00×10^6
		SSC	5.10×10^4	5.80×10^5	3.90×10^4	2.70×10^4	4.20×10^5
		SC	3.70×10^4	6.00×10^5	4.70×10^4	4.80×10^4	3.00×10^4
		CC	5.30×10^5	2.00×10^5	1.00×10^6	3.20×10^5	3.00×10^5
Chevon	10	TVBC	1.90×10^5	3.20×10^5	2.00×10^5	7.30×10^5	2.60×10^5
		SSC	1.90×10^4	1.30×10^4	1.50×10^4	1.70×10^4	5.00×10^4
		SC	3.30×10^4	6.00×10^4	1.70×10^4	4.00×10^4	3.00×10^4
		CC	7.00×10^4	2.00×10^5	1.30×10^5	6.50×10^5	1.00×10^5

Values are mean of replicates (n=3)
TVBC: Total viable bacterial count
SSC: *Salmonella-Shigella* count
SC: *Staphylococcus* count
CC: Coliform count
A: abbatoir; B: The Federal University of Technology, Akure zone; C: Isinkan market zone; D: King's market zone; E: Shasha market zone

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Table 2: Bacterial count (CFU/g) in fish sampled from different locations in Akure, Nigeria

Samples	Sample size	Microbial count	A	B	C	D	E
Mackerel	10	TVBC	6.30×10^4	6.60×10^5	8.57×10^5	9.97×10^5	7.03×10^5
		SSC	0.0	7.00×10^3	1.00×10^4	2.30×10^4	1.30×10^4
		SC	3.30×10^4	4.00×10^4	5.00×10^4	8.00×10^4	9.70×10^4
		CC	3.00×10^3	1.30×10^4	1.70×10^4	4.30×10^4	2.30×10^4
Horse mackerel	10	TVBC	7.00×10^4	2.40×10^4	3.90×10^4	4.80×10^6	1.00×10^5
		SSC	1.10×10^4	1.50×10^4	3.10×10^4	2.75×10^5	2.80×10^4
		SC	1.30×10^4	3.00×10^4	5.70×10^3	4.20×10^5	1.40×10^4
		CC	6.60×10^4	2.10×10^4	1.13×10^5	1.15×10^6	8.30×10^4
Herrings	10	TVBC	8.00×10^4	3.00×10^5	3.20×10^5	4.86×10^5	5.13×10^5
		SSC	0.0	1.30×10^4	3.00×10^3	2.30×10^4	2.00×10^4
		SC	4.30×10^4	8.60×10^4	9.00×10^4	1.50×10^4	2.20×10^4
		CC	1.60×10^4	4.00×10^4	6.00×10^4	9.00×10^4	5.60×10^4
Blue whiting	10	TVBC	9.30×10^4	3.83×10^5	4.70×10^5	5.30×10^5	5.00×10^5
		SSC	0.0	7.00×10^3	7.10×10^3	1.70×10^4	1.70×10^4
		SC	1.70×10^4	9.70×10^4	1.13×10^5	1.33×10^4	2.50×10^4
		CC	2.30×10^4	2.70×10^4	4.30×10^4	6.70×10^5	4.00×10^4
Croaker	10	TVBC	3.20×10^4	2.80×10^5	2.00×10^6	5.30×10^6	4.60×10^5
		SSC	2.10×10^3	1.30×10^4	1.70×10^5	4.70×10^5	1.00×10^4
		SC	3.10×10^3	6.00×10^3	5.70×10^4	8.00×10^4	1.00×10^4
		CC	2.50×10^4	2.20×10^5	3.50×10^5	4.80×10^5	3.00×10^5

Values are mean of replicates (n=3)
TVBC: Total viable bacterial count
SSC: *Salmonella-Shigella* count
SC: *Staphylococcus* count
CC: Coliform count
A: Cold room; B: The Federal University of Technology, Akure zone; C: Isinkan market zone; D: King's market zone; E: Shasha market zone

Table 3: Occurrence (%) of bacterial and fungal isolates from raw meats and fishes at different locations in Akure, Nigeria

Microbial isolates	Meat					Fish						N	Occurrence (%)
	Location	Beef	Chicken	Turkey	Pork	Chevon	Mackerel	Horse mackerel	Herrings	Blue whiting	Croaker		
Escherichia coli	A,B,C,D, E	+	+	+	+	+	+	+	+	+	+	34	26.50
Staphylococcus aureus	A,B,C,D, E	+	+	+	+	+	+	+	+	+	+	26	20.30
Staphylococcus epidermidis	A,B,C,D, E	+	+	+	+	-	+	+	+	+	-	20	15.60
Shigella dysenteriae	B,C,D,E	+	+	+	+	-	-	-	-	+	-	10	7.80
Bacillus cereus	A,B,C,D, E	+	+	+	+	-	+	+	+	+	-	9	7.03
Pseudomonas aeruginosa	A,B,C,D, E	+	+	+	+	-	-	+	-	-	-	7	5.40
Salmonella spp.	A,B,C,D	+	+	-	+	+	+	-	-	-	+	7	5.40
Aeromonas hydrophila	A,B,C,D, E	+	-	-	+	-	-	+	-	-	+	6	4.70
Micrococcus luteus	B,C,D,E	-	-		+	+	-	-	-	-	+	4	3.10
Penicillium notatum	D,E	-	-	-	+	-	-	+	-	-	-	2	1.50
Mucor mucedo	D,E	-	-	-	+	-	-	-	-	-	+	2	1.50
Geotrichum sp.	E	-	-	-	-	-	-	-	-	-	+	1	0.78

-: organisms are absent
+: organisms are present
N: number of isolates
A: Meat from abattoir or fish from cold room; B: The Federal University of Technology, Akure zone; C: Isinkan market zone; D: King's market zone; E: Shasha market zone

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Table 4: Antibiotic resistance percentage (%) of bacteria isolated from muscle foods sold in Akure, Nigeria

Microbial isolates	No.	ERY	PEF	GEN	APX	NIT	AMX	RFA	CPX	STR	SXT	OFX	AUG	TET	CHL
Escherichia coli	34	NT	73.5	70.6	NT	NT	35.3	NT	50	61.8	52.9	61.7	67.6	44.1	85.3
Staphylococcus aureus	26	69.2	73.0	69.2	57.7	65.4	38.5	61.5	73.1	61.5	42.3	NT	NT	NT	NT
Staphylococcus epidermidis	20	50	80	75	65	60	75	55	70	40	45	NT	NT	NT	NT
Shigella dysenteriae	10	NT	70	40	NT	NT	80	NT	60	70	90	90	80	60	60
Bacillus cereus	9	77.8	77.8	55.6	100	77.8	0	44.4	77.8	44.4	66.7	NT	NT	NT	NT
Pseudomonas aeruginosa	7	NT	100	85.7	NT	NT	100	NT	100	71.4	71.4	100	85.7	100	100
Salmonella spp.	7	NT	71.4	100	NT	NT	85.7	NT	100	71.4	85.7	85.7	71.4	57.1	100
Aeromonas hydrophila	6	50	66.7	33.3	83.3	33.3	66.7	16.7	50	83.3	33.3	100	83.3	66.7	83.3
Micrococcus luteus	4	50	0	100	50	0	75	50	75	50	50	75	50	100	100

ERY: erythromycin (15 μg); PEF: pefloxacin (5 μg); GEN: gentamycin (10 µg); APX: ampicillin (10 μg); NIT: nitrofurantoin (300 µg); AMX: amoxicillin (30 μg); RFA: rifampicin ((5 μg); CPX: ciprofloxacin (5 μg); STR: streptomycin (10 µg); SXT: trimethoprim-sulfamethoxazole (25 µg); OFX: ofloxacin (5 μg); AUG: augmentin (30 μg); TET: tetracycline (30 μg); CHL: chloramphenicol (30 µg); NT: not tested

Discussion

Scientific approaches are required to safeguard food hazards and protect individuals from magnitude of health challenges associated with consumption of unsafe animal foods, which often led to different food-borne illnesses. In this study, higher microbial count was obtained from pork than the other kinds of meat samples. A survey carried out by Bohaychuk et al. (2011) showed the higher total aerobic bacteria, *Campylobacter* spp., coliform, and *E. coli* counts in pork carcass collected from Alberta, Canada. Datta et al. (2012) revealed microbial load of 3.65 to 8.65 log CFU/g for raw meat and meat products from different butcher shops in the commercial areas of Dhaka city, Bangladesh. Also, Ariyawansa et al. (2016) reported the high microbial count of 2.0×10^2 to 2.0×10^8 CFU/g for fish from Negombo, Western province of Sri Lanka. In this study, the number and type of microorganisms isolated from muscle foods (meat and fish) were varied that this could be associated with sanitary condition in the environment where the food samples were collected (Mrdovic et al., 2017; Sofos, 2008). The microorganisms that are primarily responsible for the microbial contamination are from knives, clothes, air, workers, carts, boxes, and equipment or processing facilities, water used in dressing, apron, paper used in packaging, trays, and unhygienic selling points (Bakhtiary et al., 2016).

The lower microbial load in meat and fish stored in cold rooms could be attributed to storage of muscle foods at the lower temperature. At lower temperature, the enzymatic activities and biochemical changes of lipids and proteins are minimized and thus, reduced microbial growth as well as deteriorative changes (Zhou et al., 2010). Lower fungal growth could be because of unfavorable conditions for their colonization due to higher water activity (a_w) and pH. Meat and fish have a_w of 60-65 and 70%, respectively with pH near neutrality. These are the main factors that influence better colonization of bacteria, but reduce the fungi growth. This conformed the findings by Thanigaivel and Anandhan (2015) who revealed that raw meat from retail outlets are highly contaminated with the bacteria and lower with fungi.

The isolated bacteria in this study are aerobic spoilage agents of meat and fish. Studies by Iroha et al. (2011) in Nigeria and Imarhiagbe et al. (2016) in Benin and Warri Metropolis showed similar microorganisms in beef, chicken, chevron, smoked and frozen fishes. Similarly, Kumar et al. (2014) isolated *Staphylococcus*, *Salmonella* spp., and *E. coli* from beef, chevon, mutton, pork, and chicken sold in Karnataka State, India. In another study by Wogu and Maduakor (2010), *S. aureus*, *Klebsiella* sp., *Salmonella* sp., *E. coli*, *Pseudomonas* sp., *Aspergillus*, *Geotrichum*, and *Penicillium* were isolated from fish. *E. coli*, *S. aureus*, and *Salmonella* were reported from frozen raw and undercooked *Oreochromis niloticus* in Ethiopia by Teka et al. (2017). *Salmonella* spp. are commonly associated with beef, pork, mutton, chicken, undercooked meat, raw eggs, milk, fish, and fresh products that is responsible for salmonellosis (Forshell and Wierup, 2006; Soltan Dallal et al., 2014). The presence of *S. aureus*, *Salmonella* spp., *E. coli*, *Bacillus* spp., and *Clostridium* spp. in food producing animals indicate the potential risk of food-borne illnesses. Ed-dra et al. (2017) revealed the varying degree of microbial load. They concluded that 80.7% of sausages in Meknes city,

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Morocco is out of the microbiological standards due to the lack of good hygiene practices. It is worthy to mention that muscle foods have appropriate matrices for colonization, growth, and reproduction of microorganisms. Many microorganisms grow in raw meat and fish since the growth factors present like a_w, pH, temperature, presence of simple sugars, free amino acids, protein, ammonia, peptides, lactate, and nitrate support their colonization and development (Jay et al., 2005). Growth of microorganisms on muscle foods makes unpleasant odor, flavor, color, appearance, and taste because of bioconversion of amino acids into amines, sulfides compounds, and organic acids (Lawrie and Ledward, 2006). This diminishes shelf life and quality of muscle foods and so unfit for consumption.

In this survey, the bacteria isolated from muscle foods showed different patterns of antibiotic resistance. Garedew et al. (2015) revealed the antibiotic resistance by *Salmonella* spp. isolated from meat, hand, knife, and chopping with 88.7, 62.3, 35.8, 32.1, and 30.2% resistance for ampicillin, amoxicillin, nitrofurantoin, tetracycline, and sulfamethoxazole-trimethoprim, respectively. Boss et al. (2016) reported the prevalence of MAR of *E. coli*, *Enterococci*, *P. aeruginosa*, and *S. aureus* isolated from raw fish and seafood imported to Switzerland. Wu et al. (2018) stated that *S. aureus* isolated from retail meat and meat products from China exhibited MAR to a variety of antimicrobials. Similarly, Mezali and Hamdi (2012) showed antimicrobial resistant of *Salmonella* spp. isolated from meat products sold in Algiers, Algeria. Also, 35 to 90% of *Salmonella* spp., isolated from meat sausages in Gaborone, Botswana, exhibited antimicrobial resistance (Samaxa et al., 2012). The microorganisms associated with facilities involved in livestock and fishery production could also contribute to MAR. Lee et al. (2016) showed that *Aeromonas veronii*, *A. jandaei*, *Plesiomonas shigelloides*, and *Pseudomonas alcaligene* isolated from water used for fish farming exhibited MAR towards some commonly used antibiotics, including ampicillin, penicillin, and gentamicin. Using antibiotics in animals may result in antibiotic residue in animal source food and thus making antibiotic-resistant bacteria. Therefore, it is necessary to provide baseline information on effective application of Hazard Analysis Critical Control Point (HACCP) and Good Manufacturing Practices (GMP) during animal production to minimize the use of antibiotics (Doménech et al., 2011).

Conclusion

The microorganisms found in muscle foods from Akure, Nigeria could be considered as result of poor hygiene of the retailers or handlers. Also, presence of the multidrug resistant bacteria in muscle foods distributed in this region could pose a serious risk factor to public health. Effective control programs are needed to reduce the microbial contaminations of muscle foods and to achieve the standard quality during production and distribution of these products.

Author contributions

R.S.B., C.O.O., and B.J.A. designed the concept and methodology and also conducted the experiments; R.S.B. and C.O.O. drafted the manuscript; C.O.O. and B.J.A. edited the manuscript; C.O.O. analyzed the data. All authors revised and approved the manuscript.

Conflicts of interest

Authors declare no conflict of interests.

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