Prevalence of multi-drug resistant bacteria associated with foods and drinks in Nigeria (2015-2020): A systematic review

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Abstract

Foods are essential vehicles in human exposure to antibiotic resistant bacteria which serve as reservoirs for resistance genes and a rising food safety concern. Antimicrobial resistance, including multi-drug resistance (MDR), is an increasing problem globally and poses a serious concern to human health. This study was designed to synthesize data regarding the prevalence of MDR bacteria associated with foods and drinks sold within Nigeria in order to contribute to the existing findings in this area. A comprehensive literature search on the prevalence of multi-drug resistant bacteria associated with foods and drinks in Nigeria from 2015 to 2020 was conducted using three databases; PubMed, Science Direct and Scopus. After screening and selection, 26 out of 82 articles were used for the qualitative data synthesis. Of the total of one thousand three hundred and twenty-six MDR bacteria reportedly isolated in all twenty-six articles, the highest prevalence (660) was observed in drinks, including water, while the lowest (20) was observed in the article which combined results for both protein and vegetable-based foods. *Escherichia sp.* had the most frequency of occurrence, appearing as MDR bacteria in ten out of the twenty-six articles. *Salmonella sp.* appeared as MDR in seven out of the twenty-six articles included in this study, in all seven articles where it was reported, it had the highest percentage (85.4%) prevalence as MDR bacteria. Public health personnel need to ensure critical control during the production and handling of foods and drinks, as well as create more awareness on proper hygienic practices to combat the spread of MDR bacteria

Introduction

Foods are essential in the exposure of humans to resistant bacteria and this is becoming a growing food safety issue (Zurfluh *et al*., 2019; Mesbah *et al*., 2017; Campos *et al*., 2019). Foods can be contaminated by different means, including exposure to irrigation water, manure, feces or soil with pathogenic bacteria. Foods can also become contaminated as they are harvested, handled after harvest or during processing if food safety standards are not correctly applied (Meshbah *et al*., 2017). Food-borne diseases caused by resistant organisms are one of the most important public health problems as they contribute to the risk of development of antibiotic resistance in the food production chain (Hehempour-Baltork *et al*., 2019). Apart from pathogenic bacteria causing food-borne diseases, foods that are raw or not processed following standard procedures can introduce several antibiotic-resistant bacteria (ARB) to consumers (Gekemidis *et al*., 2018). Antibiotic resistance, though harbored in non-pathogenic bacteria, can potentially be spread through horizontal gene transfer to other species including opportunistic pathogens that are present in the environment or after consumption of ARB-contaminated foods. When ARB-contaminated foods are consumed, the spread of antibiotic resistant genes may affect the gut microbiome thereby contributing to the pool of antibiotic-resistance genes (ARG) in the human gut (Gekemidis *et al*, 2018). MDR bacteria have been defined as bacteria that are resistant to at least one antimicrobial agent present in three or more antimicrobial classes (Sweeny *et al*., 2018). There has been an increase in drug resistance in pathogens isolated from food for human consumption with species of *Escherichia coli* and *Salmonella enterica* being considered among the most important pathogens due to their ability to effect zoonotic transfer of resistant genes (Canton *et al*., 2018; Maneilla-Becerra *et al*., 2019). However, other pathogens, such as *Vibrio* spp., some species of *Aeromonas*, spores of *Clostridium botulinum* type F, and *Campylobacter*, have been linked to food-borne diseases in humans who have consumed seafood or other animal foods (Maneilla-Becerra *et al*., 2019). Some other resistant bacteria associated with foods include *Staphylococcus aureus, Listeria* spp.*, and Shigella* spp. (Maneilla-Becerra *et al*., 2019)

This study was therefore designed to synthesize data (2015-2020) regarding the prevalence of MDR bacteria associated with foods and drinks sold within Nigeria in order to contribute to the existing findings in this area.

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Materials and Methods

Search strategy

A comprehensive literature search was conducted on the prevalence of multi-drug resistant bacteria associated with foods and drinks in Nigeria within five years (2015 to 2020). Three databases including Science Direct, PubMed and Scopus were utilized to search for relevant data. The search terms employed combinations of the following: antibiotics, multi-drug, resistant bacteria, foods and drinks without narrowing or restricting search items (Table 1).

Search terms

The mentioned databases were searched using the search terms *antibiotic resistance;*

multi-drug resistance; antibiotic resistant bacteria in foods; antibiotic resistant bacteria in drinks; multi-drug resistant bacteria in foods and multi-drug resistant bacteria in drinks. Articles published in English between 2015 and 2020 that observed bacteria isolated from drinks including juices, water as well as soft drinks which showed resistance to at least one agent in three or more antimicrobial classes were considered for the screening process.

Study selection

Studies included in this review were selected based on their alignment with the search terms earlier reported. Full length research papers of studies conducted within Nigeria were screened according to the inclusion and exclusion criteria defined below.

Inclusion criteria

Inclusion criteria were research articles with cross-sectional designs that were carried out in Nigeria and published in English which reported the prevalence of multi-drug resistant bacteria associated with foods and drinks within the study period. The data synthesis focused only on articles whose full text were freely available online.

Exclusion criteria

Studies whose full texts were inaccessible were excluded as their quality could not be assessed as well as studies that were not carried out between 2015 and 2020. Abstracts, conference proceedings, and review articles and letters to editors were also excluded. Full length articles that did not have direct links with the inclusion criteria above were not included in this systematic review.

Data extraction

Relevant data were extracted from each of the full-text articles into Microsoft Excel. Data extracted included first author's name, year of sample collection, sampling point, type of samples collected, number of samples collected, class of samples collected, antibiotics used, isolated bacteria, method of antibiotic sensitivity testing, bacterial species isolated, number of antibiotic resistant bacteria, number of multi-drug resistant bacteria, specific antibiotics tested for resistance and percentage of multi-drug resistant bacteria. All data were analyzed and presented in the form of a flowchart, charts, tables, and figures.

Results

Antibiotic resistance

The search term 'antibiotic resistance' resulted in a total of one hundred and forty-eight thousand, eight hundred and eighty-three (148,883) articles which comprised research articles, articles published within the study period and generally articles covered within the inclusion criteria for this search with Scopus hosting the largest number of articles (58,879) related to this search term (Table 2).

Multi-drug resistance

The search term 'multidrug-resistance' resulted in a total of forty-seven thousand and sixty-one, (47,061) articles which comprised research articles, articles published within the study period covered in this research and generally articles which matched the inclusion criteria for this search with Science direct hosting the largest number of articles (21, 662) related to this search term (Table 2).

Antibiotic resistant bacteria in foods in Nigeria

The search term 'antibiotic resistant bacteria in foods in Nigeria' resulted in a total of three hundred and eleven (311) articles which comprised research articles, articles published within the study period covered in this research and generally articles which matched the inclusion criteria for this search with Science direct hosting the largest number of articles (210) related to this search term (Table 2).

Antibiotic resistant bacteria in drinks in Nigeria

The search term 'multidrug-resistance bacteria in drinks in Nigeria' resulted in a total of forty-seven (47) articles which comprised research articles, articles published within the period covered in this research and generally articles which matched the inclusion criteria for this search with Science direct hosting the largest number of articles (39) related to this search term. Scopus database hosted no article related to this search term (Table 2).

Multi-drug resistant bacteria in foods in Nigeria

The search term 'multidrug-resistant bacteria in food in Nigeria' resulted in a total of one-hundred and fifty-three (153) articles which comprised research articles, articles published within the period covered in this research and generally articles which matched the inclusion criteria for this search with Scopus hosting the largest num-

Table 1. Search terms used for databases.

S/N	*Search erms
1	Antibiotic resistance
2	Multi-drug resistance
3	Antibiotic resistant bacteria in foods in Nigeria
4	Antibiotic resistant bacteria in drinks in Nigeria
5	Multi-drug resistant bacteria in foods in Nigeria
6	Multi-drug resistant bacteria in drinks in Nigeria
7	3 or 4
8	5 or 6
9	7 and 8

*Search terms were repeated in the same pattern in all three databases employed for this study.

Table 2. Search result for each search item in Scopus, Science Direct and PubMed.

Search term	Scopus	Science Direct	PubMed	Total
AR	56879	46904	45100	148883
MDR	4053	21662	21346	47061
ARB in foods in Nigeria	32	210	69	311
ARB in drinks in Nigeria	0	39	8	47
MDRB in foods in Nigeria	84	58	11	153
MDRB in drinks in Nigeria	4	20	3	27
3 or 4	32	217	75	324
5 or 6	84	63	13	160
7 and 8	17	55	10	82

AR-Antibiotic resistance, MDR-Multidrug resistant, ARB- Antibiotic resistant bacteria, MDRB-Multi-drug resistant bacteria, 3-8 (Refer to Table 1).

ber of articles (84) related to this search term (Table 2).

Multi-drug resistant bacteria in drinks in Nigeria

The search term ‘multidrug-resistant bacteria in drinks in Nigeria’ resulted in a total of twenty-seven (27) articles which comprised research articles, articles published within the period covered in this research and generally articles which matched the inclusion criteria for this search with Science direct hosting the largest number of articles (20) related to this search term (Table 2).

Data extraction

After careful searches of databases using the combined search terms in item 9 of Table 1, twenty-six out of a total of eighty-two articles that matched the selection criteria, were identified and selected. From the eighty-two articles, three articles which were duplicated in two or more databases were excluded leaving a total of seventy-nine articles. Following the defined inclusion and exclusion criteria, twenty-six published articles were carefully selected for data extraction in order to address the

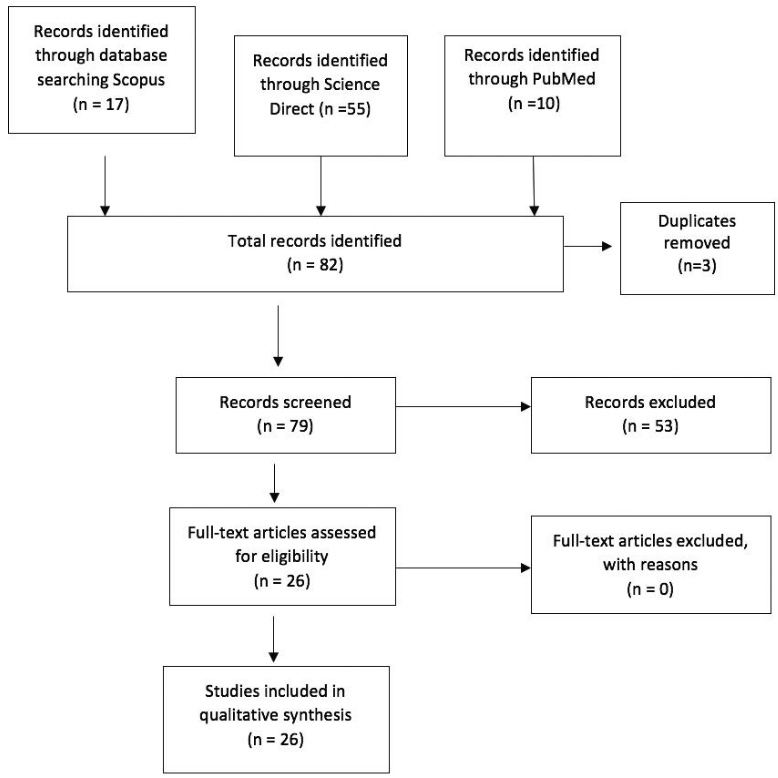

Figure 1. Number of studies selected and included in data synthesis.

Table 3. Frequency of MDR bacteria in foods and drinks.

MDR bacteria	Frequency	Total no. of isolates	Number of MDR bacteria	% MDR Bacteria
Escherichia sp.	10	860	272	31.6
Staphylococcus sp.	9	286	131	45.8
Salmonella sp.	7	158	135	85.4
Bacillus sp.	5	90	14	15.6
Pseudomonas sp.	4	441	41	9.3
Shigella sp.	3	18	6	33.3
Proteus sp.	3	91	6	6.6
Klebsiella sp.	2	28	NA	–
Enterobacter sp.	2	51	18	35.3
Clostridium sp.	1	NA	NA	–
Alcaligens sp.	1	NA	NA	–
Lactobacillus sp.	1	NA	NA	–
Pleisomonas sp.	1	66	66	100
Serratia sp.	1	12	NA	–
Vibrio sp.	1	NA	NA	–
Photobacterium sp.	1	NA	NA	–
Campylobacter sp.	1	NA	NA	–
Neisseria sp.	1	NA	NA	–
Propionibacterium sp.	1	NA	NA	–
Amycolatopsis sp.	1	NA	NA	–
Eubacterium sp.	1	NA	NA	–
Chromobacterium sp.	1	NA	NA	–
Tropheryma sp.	1	NA	NA	–
Enterococcus sp.	1	268	129	48
Total	61	2369	818	34.5

NA, Numbers of specific genera of the MDR bacteria were not specified in the searched articles.

objectives of this research (Figure 1). Amongst the twenty-six articles searched, *Escherichia sp.* had the most frequency of occurrence, appearing as MDR bacteria in ten out of the twenty-six articles while *Clostridium sp., Alcaligens sp., Lactobacillus sp., Pleisomonas sp., Serratia sp., Vibrio sp., Photobacterium sp., Campylobacter sp., Neisseria sp., Propionibacterium sp., Amycolatopsis sp., Eubacterium sp., Chromobacterium sp., Tropheryma sp., Enterococcus sp.* had the least occurrence recorded only in one article (Tables 3 and 4). Of the eight hundred and sixty *Escherichia sp.* isolated from various food and drink samples in all twenty-six articles, two hundred and seventy-two (272) were multi-drug resistant, giving a percentage prevalence of 31.6% MDR bacteria. *Salmonella sp.,* although reported as MDR in only seven of the twenty-six articles had the highest prevalence of 135 MDR out of 158 total isolated (85.4%) while *Shigella sp.* and *Proteus sp.* had an occurrence of six (6) MDR bacteria out of 18 and 91 respectively amounting to percentage of 6.7 and 33.3 respectively in both isolates (Table 3). When observed according to different geopolitical zones of Nigeria, in all cases of MDR bacteria, the Southwest had the most occurrence with the exception of *Staphylococcus sp* and *Salmonella sp* whereas the South-South had the highest occurrence and an equal distribution for Southwest and North central respectively (Table 5). Based on major food groups, of the twenty-six articles, fourteen (14) of them reported isolating MDR bacteria from proteins, eight (8) from drinks, two (2) from vegetables, one (1) from carbohydrates, another one (1) reported isolating from both proteins and vegetables (Figure 2, Table 4). Of the total one thousand three hundred and twenty-six MDR bacteria reportedly isolated in all twenty-six articles included in this search, the highest (660) was observed in drinks, including water, while the least (20) was observed in the article which combined results for both protein and vegetables (Figure 3). In all sixty-five antibiotics screened in the twenty-six articles, one hundred percent (100%) resistance was observed in Methycillin (MET), Penicillin (PEN), Augmentin (AUG), Cefprozil (CPR), Ticarcillin (TIC), Cefazolin (CFZ), Ampicillin-Sulbactam (SAM), Enrofloxacin (ENR), Levofloxacin (LVX), Doxycycline (DOX), Sulphamethoxazole (SMT), Florfenicol (FLO), Cephalothin (CEF), Pefloxacin (PFX), Sparfloxacin (SPX), Ampiclox (AX), Carbenicillin (CAR), Metronidazole (MTX), Clarithromycin (CLR), Aztreonam (ATM), Ticarcillin-Clavulanic acid (TIM), Piperacillin (PIP) and Ceftiofur (CTF). However, six out of the total twenty-six articles reported one hundred percent resistance to penicillin (Table 6).

Discussion

Multi-drug resistant (MDR) bacteria isolates

From this systematic review, of all the MDR bacteria reported to be associated with foods and drinks, those with high percentages of occurrence include *Escherichia* sp., *Staphylococcus* sp., *Salmonella* sp., *Bacillus* sp., *Pseudomonas* sp., *Shigella* sp., *Proteus* sp., *Klebsiella* sp., *Enterobacter* sp., with *E. coli* showing the highest case of occurrence. In 2015, Adenipekun *et al.* (2015) reported isolating 211 *E. coli* from cattle, chicken and swine out of which 26 were multi-drug resistant to tetracycline (124/211;58.8%), trimethoprim/sulfamethoxazole (84/211;39.8%), and ampicillin (72/211;34.1%). Adesoji *et al.* (2019a) also reported the presence of MDR bacteria which were resistant to Ceftazidime, Cefuroxime, Gentamicine, Ciprofloxacin, Ofloxacin, Amoxycillin clavulanate, Nitrofurantoin, Ampicillin, Erythromycin, Cloxacillin (5μg),

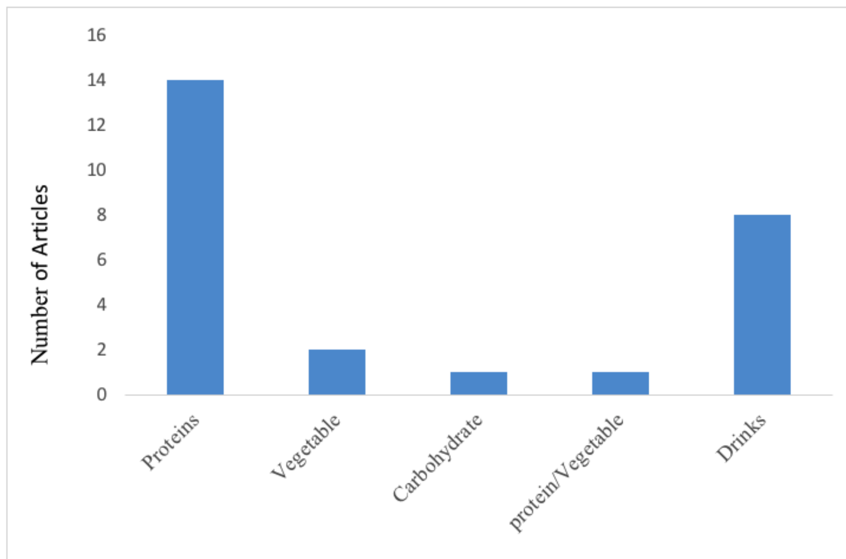

Figure 2. Frequency of occurrence of MDR bacteria among different food groups in articles included in data synthesis. NB: The result for drinks presented includes water.

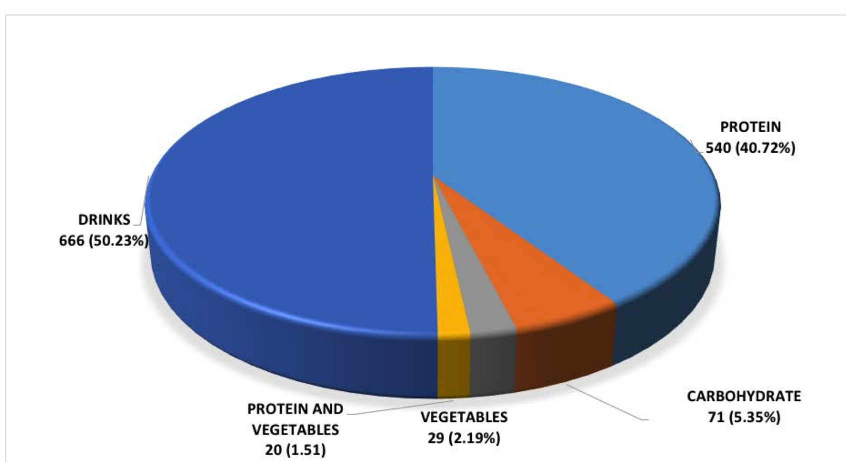

Figure 3. Number of MDR bacteria isolated from each food group. NB: The result for drinks presented includes water.

Table 4. Frequency of isolation of MDR from different food groups in the selected articles.

Authors	Food type	Type of antibiotics used	Method of testing	Mdr bacteria/resistotypes	Resistance pattern
Igbinosa et al., 2016a	Beef, pork, chicken	MET, CXC, PEN, AMX, ERY, GEN, KAN, CLI, VAN, CHL, SXT	Disc diffusion	*Staphylococcus* sp.	Resistant to ≥1 antimicrobial agent in ≥3 classes of antimicrobial agents)
Musa et al., 2020	Raw meat	CHL, CRO, AMP, TET,NAL, ERY, CIP, COT	Disc diffusion	*Salmonella* sp.	Resistant to > 2 class of antimicrobial agent
Uzeh et al., 2017	Beef, chicken	AMX, NIT, GEN, NAL, OFX, AMC, TET,SXT	Disc diffusion	*S. enteritidis, S.* typhimurum	Resistant to ≥5 antibiotics
Ifeanyichukwu et al., 2016	Chicken, meat, Egg, Poultry egg contents	CRO, PEN, GEN, AMX,NIT, TET, AMC, SXT,OFX, CTX, TOB, CAZ, IPM, ETP, NAL	Disc diffusion	*Salmonella* sp.	Resistant to greater than 50% of antibiotics testes
Kwoji et al., 2019	Poultry	FOX, ERY, VAN, NAL,TET, COT, STR, CHL, CIP	Disc diffusion	*Staphylococcus aureus*	Resistant to > 2 class of antimicrobial agent
Adesoji et al., 2019a	Suya, Smoked fish	CAZ, GEN, OFX, AUG, CXM, NIT, AMP, ERY, CPR, CXC, CRO	Disc diffusion	*Staphylococcus* sp., *E. coli, Pseudomonas* sp. *Enterobacter* sp., *Klebsiella* sp. *Shigella* sp., *Bacillus* sp.,*Salmonella* sp. and *Proteus* sp.	Resistant to ≥ 3 class of antimicrobial agent.
Olowe et al., 2019	Milk, cheese, beef, chicken, yoghurt	AMP, TIC, CFZ, LEX, CXM,FOX, CAZ, CTX, IPM, MEM, AMC, SAM, TZP, AMK, KAN, GEN, TOB, SPT, CIP, ENR, LVX, DOX, TET, SMT, SXT, TMP, CST, CHL	Disc diffusion	*E .coli (biofilm forming)*	Resistant to > 2 classes of antimicrobial agent
Amaeze et al., 2016	Suya	AMX, NAL, TET, VAN,GEN, STR,CHL, ERY, ERY, CXM, NIT, CIP	Disc diffusion	*Staphylococcus* sp., *Bacillus* sp, *S.* typhi and *E. coli*	Resistant to at least three antibiotics
Ahmed et al., 2019	Poultry	TET, STR, NAL, NEO, CTX, CAZ, CHL, FOX, GEN, AMP, Complex sulfonamides	Disc diffusion	*Salmonella agama, S. albany, S. colindale, S. enterica ser. 4.5.12:i, S. enterica ser. 4.12.27:z:, S. enterica ser. 6.7:d:-, S. enterica ser. 45:d: 1.7, S. istanbul, S. larochelle, S. muenster, S. nigeria, S. orion and S. typhimurium. Salmonella enterica ser. 6.7:d:*	Mostly resistant to fluoroquinolone and cephalosporins
Adesoji et al., 2015	Water	FLO, TET, GEN, KAN,CHL, NAL, AMC, SMT, SXT, CEF, STR	Breakpoint assay	*Pseudomonas* sp.	Resistant to > 3 classes of antimicrobial agent
Odumosu et al., 2016	Vegetables, Cow and Poultry	TZP, FEP, IPM, AMK, CIP, CAR, CAZ	Disc diffusion	*Pseudomonas* sp.	Mostly resistant carbenicillin and ceftazidime
Ogu et al., 2017	Water	GEN, AMP, OFX, CHL, FOX, TET, NOR, CXM, AMX, LEX, CXC,AMC, COT, ERY, CLI, CIP	Disc diffusion	*S. aureus Bacillus* sp., *Escherichia coli, Pseudomonas* sp. *Enterobacter* sp. *Proteus* sp. and *Klebsiella* sp.	Resistant to at least three antimicrobial classes
Ayandiran and Dahunsi, 2017	Catfish	ERY, CIP, NOR, OFX, GEN, KAN, CRO, LEX, CXM, CHL, AMP, AMX,AUG, NIT, TET, CLI, COT	Disc diffusion	*Bacillus* sp., *Clostridium* sp., *Alcaligens faecalis, Flavobacterium aquatile, Enterobacter dissolvens and Corynebacterium striatum*	Resistant to between four to nine types of antibiotics
Lateef and Ojo, 2015	Dried lafun Fermenting broth, Water for steeping cassava	AUG, GEN, PFX, OFX, SPX, STR, COT, CHL, CIP, AMX, AX, CXM, CRO, CIP, ERY	Disc diffusion	*S. aureus, Salmonella* typhimurum and *E.coli, Lactobacillus* sp.	Resistant to between two to ten types of antibiotics
Adesoji et al., 2019b	Water	GEN, CXM, OFX, CXC, CAZ, CRO, ERY, AUG	Disc diffusion	*S. aureus*	Resistant to four or more antimicrobial agents

Table 4. Frequency of isolation of MDR from different food groups in the selected articles.

Authors	Food type	Type of antibiotics used	Method of testing	Mdr bacteria/resistotypes	Resistance pattern
Okiki et al., 2018	Nono	AUG, OFX, AMP, CIP, GEN, CAZ, NIT, CXM, STR, LEX, TET, CHL, ERY, PEN		*Vibrio natiensis, Photobacterium damselae, Campylobacter gracilis Neisseria spp, Moraxella catarrhalis, Tropheryma whipplei, Propionibacterium acnes, Amycolatopsis benzoatilytica, Eubacterium nodatum, Bacillus subtilis and Chromobacterium violaceum*	Resistant to between five to eight antimicrobial drugs
Igbinosa et al., 2016b	Milk, cattle	MET, PEN, CLX, AMX, ERY, GEN, KAN, CLN, CHL, SXT, VAN	Disc diffusion	methylin-resistant *Staphylococcus sp: S. aureus, S. epidermidis , S. haemolyticus, S. saprophyticus, S. chromogenes, S. simulans, S. pseudintermedius and S. xylosus*	Resistant to all the antimicrobial agents tested
Titilawo et al., 2015	Water	AMK, STR, KAN, NEO, GEN, FEP, CEF,CXM, MEM, IPM, CIP, GAT, NAL, SMT, NIT, CHL, TET, DOX, AMX, AMP	Disc diffusion	*E. coli*	Resistant to three to ten antimicrobials, but mostly sulfonamides, β-lactams and tetracyclines
Chigor et al., 2020	Vegetables	AMX, AMP, PEN, CXA, CXM, STR, RIF, MTZ, SMT, TMP, VAN, ERY, CLR, CHL, CIP, NOR, TET, IPM	Disc diffusion	*E. coli*	Resistant to ≥ 3 class of antimicrobial agent.
Adesiyan et al., 2019	Water	AMK, NEO, STR, TMP, GEN, NET, CEF, CTX, CIP, MEM, IPM, CAZ, SMT, ERY, CHL, TET, SXT, AMX, AMP	Disc diffusion	*Pleisomonas shiggeloides*	Resistant to four to thirteen antimicrobials
Fakayode et al., 2018	Water	AMP, AMC, GEN, KAN,STR, TET, NAL, CIP, SXT,CHL, ERY, VAN, RIF	Disc diffusion	*β-proteobacteria, γ-proteobacteria, Firmicutes, Actinobacter , Pseudomonas, Enterobacter, Escherichia and Klebsiella*	Resistant to ≥ 3 class of antimicrobial agent.
Adenipekun et al., 2015	Cattle, chicken, swine	AMK, AMP, SAM, ATMCFZ, FEP, FOX, CPD,CAZ, CRO, CXM, CEF,CIP, ETP, GEN, MEM,TZP, TET, TIM, TOB,SXT,TGC	Broth microdilution with the Sensititre™ system.	*E. coli* (genetically diverse based on PFGE)	Resistant to three to five antimicrobial agent
Beshiru et al., 2017	Pig	PIP, PEN, ERY, GEN, KAN, CLI, IPM, MEM, CIP, TET	Disc diffusion	*Enterococcus* faecalis and *Enterococcus faecium*	Resistant to two to eight antimicrobial agents
Bamigboye et al., 2020	Water	LEX, OFX, NAL, PFX, CIP, SXT, STR, GEN, AUG, AX, AMP, CRO, CXM, ERY, AMX	EUCAST, Disc diffusion	*Klebsiella pneumoniae, Proteus vulgaris, E.coli, Shigella dysenteriae, Pseudomonas aeruginosa, Serratia marcescens and Stpahylococcus aureus*	Resistant to three to ten antimicrobials
Nwinyi and Nduchukwuka, 2016	Vegetables	ERY, CLX, COT, AUG, TET, GEN, CHL, STR, OFX,NAL, AMX, NIT	Disc diffusion	*Salmonella* sp., *Shigella* sp., *E.coli, Chromobacterium violaceum, Micrococcus luteus*	Not stated
Adesoji et al., 2019c	Water	FLO, TET, STR, GEN, KAN, CHL, NAL, AMC, CTF, SMT, SXT, AMP, ERY, RIF, LCM, CIP	Disc diffusion	*Chromobacterium violaceum, Alcaligenes sp, Proteus mirabilis, Morganella sp, Klebsiella pneumoniae, Bacillus sp., Proteus vulgaris, Morganella morganii and Escherichia coli*	Resistant to ≥4 antimicrobial agents

MET: Methycillin, CXC: Cloxacillin, PEN: Penicillin, AMX: Amoxicillin, ERY: Erythromycin, GEN: Gentamycin, KAN: Kanamycin, VAN: Vancomycin, CHL: Chloramphenicol, SXT: Sulphamethoxazole/Trimethoprim, CRO: Ceftriaxone, AMP: Ampicillin, TET: Tetracycline, NAL: Nalidixic Acid, CIP: Ciprofloxacin, COT: Cotrimoxazole, NIT: Nitrofurantoin, OFX: Ofloxacin, AMC: Amoxicillin- Clavulanic Acid, TOB: Tobramycin, CAZ: Ceftazidime, IPM: Imipenem, ETP: Ertapenem, FOX: Cefoxitin, STR: Streptomycin, AUG: Augmentin, CXM: Cefuroxime, CPR: Cefprozil, TIC: Ticarcillin, CFZ: Cefazolin, LEX: Cephalexin, CTX: Cefotaxime, MEM: Meropenem, SAM: Ampicillin-Sulbactam, TZP: Piperacillin-Tazobactam, AMK: Amikacin, SPT: Spectinomycin, ENR: Enrofloxacin, LVX: Levofloxacin, DOX: Doxycycline, SMT: Sulphamethoxazole, TMP: Trimethoprim, CST: Colistin, NEO: Neomycin, FLO: Florfenicol, CEF: Cephalothin, FEP: Cefepime, CLI: Clindamycin, NOR: Norfloxacin, PFX: Pefloxacin, SPX: Sparfloxacin, AX: Ampiclox, CAR: Carbenicillin, GAT: Gatifloxacin, RIF: Rifampin, MTZ: Metronidazole, CLR: Clarithromycin, NET: Netilmicin, ATM: Aztreonam, CPD: Cefpodoxime, TIM: Ticarcillin-Clavulanic Acid, TGC: Tigecycline, PIP: Piperacillin, CTF: Ceftiofur, LCM: Lincomycin

Augmentin and Ceftriaxone in both smoked fish and suya sampled, including *Staphylococcus* sp., *Escherichia* sp., *Enterobacter* sp., *Shigella* sp., *Bacillus* sp., *Salmonella* sp. and *Proteus* sp. with *Escherichia* sp. having the highest prevalence of 13 out of 35 (37.1%) in smoked fish and 10 out of 46 (21.7%) in suya. Previous research by Odonkor and Addo (2018) reported the prevalence of MDR *Escherichia coli* which were resistant to penicillin (32) representing 32.99%, followed by cefuroxime (28) representing 28%, erythromycin (23) representing 23.71%, tetracycline (21) representing 21.45%, chloramphenicol (18) representing 18.65%, pipemidic acid (13) representing 13.40%, and ampicillin (11) representing 11.32% in drinking water samples to be 48 (positive as MDR) out of a total 97 isolates (49.48%). Although in a lower percentage, Olowe *et al*. (2018) reported a prevalence of 37 MDR out of 216 (17.1%) of MDR *Escherichia coli* resistant to ticarcillin, tetracycline, trimethoprim, ampicillin, doxycycline, sulfamethoxazole and sulfamethoxazole/trimethoprim, levofloxacin, enrofloxacin, ciprofloxacin, ampicillin/sulbactam, cefuroxime, cefotaxime, cefazolin, cephalexin, ceftazidime, tobramycin, gentamicin, amoxicillin/clavulanic acid and kanamycin in foods of animal origin. However, in their own reports Ifeanyichukwu *et al*. (2016); Uzeh *et al*. (2017); Ahmed *et al*. (2019); Musa *et al*. (2020). *Salmonella* sp. was identified as having a prevalence of 31 MDR out of 31 isolates (100) in foods. Meanwhile, Ayandiran and Dahunsi (2017) reported the highest prevalence of MDR *in Bacillus* and *Clostridium* sp. Both were resistant to ofloxacin, cotrimoxazole, ceftriaxone, erythromycin, ciprofloxacin, gentamicin, cephalexin, ampicillin and augmentine. The prevalence of multi-drug resistance among *E. coli* isolates were also supported by Bamigboye *et al*. (2020). They reported isolating an *E. coli* that showed one hundred percent resistance to all the tested antibiotics. The reason for the high prevalence of MDR *Escherichia sp*. could be the development of biofilms which would offer protection against antimicrobial agents which may lead to chronic infections and treatment problems (Olowe *et al*., 2018). Also, as *E. coli* is a normal flora of humans, the handling of food during processing may have contributed to its spread (Rasheed *et al*., 2014). Considering that most of the sampled food were animal-based proteins and vegetables, *E. coli* inhabiting the gut of the animals (Maneilla-Becerra *et al*., 2019) may have migrated to the meat of the animals during slaughter and processing. The use of contaminated water in vegetable farms may also result in the spread of MDR *E. coli.* Industrial and household effluents dumped directly into rivers, which are primary sources of water in vegetable farms, may contribute to the MDR patterns (Titilawo *et al*., 2015). Chigor *et al*. (2020) corroborated this when they reported MDR bacteria from wastewater samples. Once accumulated in the environment, bacteria species may begin to transmit antibiotics resistance genes amongst themselves posing serious public health concerns.

MDR bacteria related to food groups

In the food groups, the highest percentage of MDR bacteria (666 out of 1326;

Table 5. Frequency of MDR bacteria in geo-political zones in Nigeria.

MDR Bacteria	S/West	S/East	S/South	N/West	N/East	N/Central	Total
Escherichia sp.	6	1	1	1	NIL	1	10
Staphylococcus sp.	2	NIL	3	2	1	1	9
Salmonella sp.	3	1	NIL	NIL	NIL	3	7
Pseudomonas sp	3	NIL	1	NIL	NIL	NIL	4
Bacillus sp.	2	NIL	1	1	NIL	1	5
Shigella sp.	2	NIL	NIL	1	NIL	NIL	3
Proteus sp.	1	NIL	1	1	NIL	NIL	3
Klebsiella sp.	1	NIL	1	NIL	NIL	NIL	2
Enterobacter sp.	NIL	NIL	1	1	NIL	NIL	2
Clostridium sp.	1	NIL	NIL	NIL	NIL	NIL	1
Alcaligens sp.	1	NIL	NIL	NIL	NIL	NIL	1
Lactobacillus sp.	1	NIL	NIL	NIL	NIL	NIL	1
Pleisomonas sp.	1	NIL	NIL	NIL	NIL	NIL	1
Serratia	1	NIL	NIL	NIL	NIL	NIL	1
Vibrio sp.	1	NIL	NIL	NIL	NIL	NIL	1
Photobacterium sp.	1	NIL	NIL	NIL	NIL	NIL	1
Campylobacter sp.	1	NIL	NIL	NIL	NIL	NIL	1
Neisseria sp.	1	NIL	NIL	NIL	NIL	NIL	1
Moraxella sp.	1	NIL	NIL	NIL	NIL	NIL	1
Propionibacterium sp.	1	NIL	NIL	NIL	NIL	NIL	1
Amycolatopsis sp.	1	NIL	NIL	NIL	NIL	NIL	1
Eubacterium sp.	1	NIL	NIL	NIL	NIL	NIL	1
Chromobacterium sp	1	NIL	NIL	NIL	NIL	NIL	1
Tropheryma sp.	1	NIL	NIL	NIL	NIL	NIL	1
Enterococcus sp.	1	NIL	NIL	NIL	NIL	NIL	1
	36	2	9	7	1	6	61

NIL: No organism recorded in region.

Table 6. Percentage Resistance/Susceptibility for each antibiotic used in all included articles.

Antibiotics	No. Used	No. Resistant	No. Susceptible	% Resistance	% Susceptibility
MET	2	2	0	100	0
CXC	2	0	2	0	100
PEN	6	6	0	100	0
AMX	13	9	4	69.2	30.78
ERY	18	12	6	66.7	33.3
GEN	22	12	10	54.5	45.5
KAN	9	4	5	44.4	55.6
VAN	6	4	2	66.7	33.3
CHL	18	8	10	44.4	55.6
SXT	12	9	3	75	25
CRO	8	5	3	62.5	37.5
AMP	14	13	1	92.9	7.1
TET	19	16	3	84.2	15.8
NAL	12	9	3	75	25
CIP	18	6	12	33.3	66.7
COT	7	5	2	71.4	28.6
NIT	8	7	1	87.5	12.5
OFX	10	2	8	20	80
AMC	7	5	2	71.4	28.6
TOB	3	2	1	66.7	33.3
CAZ	9	5	4	55.6	44.4
IPM	7	2	5	28.6	71.4
ETP	2	0	2	0	100
FOXN	5	2	3	40	60
STR	13	9	4	69.2	30.8
AUG	7	7	0	100	0
CXM	12	7	5	58.3	41.7
CPR	1	1	0	100	0
TIC	1	1	0	100	0
CFZ	2	2	0	100	0
LEX	6	3	3	50	50
CTX	4	3	1	75	25
MEM	5	1	4	20	80
SAM	2	2	0	100	0
TZP	3	2	1	66.7	33.3
AMK	5	0	5	0	100
SPT	1	0	1	0	100
ENR	1	1	0	100	0
LVX	1	1	0	100	0
DOX	2	2	0	100	0
SMT	6	6	0	100	0
TMP	3	2	1	66.7	33.3
CST	1	0	1	0	100
NEO	3	1	2	33.3	66.7
FLO	2	2	0	100	0
CEF	4	4	0	100	0
FEP	3	2	1	66.7	33.3
CLI	4	2	2	50	50
NOR	3	2	1	66.7	33.3
PFX	2	2	0	100	0
SPX	1	1	0	100	0
AX	2	2	0	100	0
CAR	1	1	0	100	0
GAT	1	0	1	0	100
RIF	3	1	2	33.3	66.7
MTZ	1	1	0	100	0
CLR	1	1	0	100	0
NET	1	0	1	0	100
ATM	1	1	0	100	0
CPD	1	0	1	0	100
TIM	1	1	0	100	0
TGC	1	0	1	0	100
PIP	1	1	0	100	0
CTF	1	1	0	100	0
LCM	1	0	1	0	100

MET: Methycillin, CXC: Cloxacillin, PEN: Penicillin, AMX: Amoxicillin, ERY: Erythromycin, GEN: Gentamycin, KAN: Kanamycin, VAN: Vancomycin, CHL: Chloramphenicol, SXT: Sulphamethoxazole/Trimethoprim, CRO: Ceftriaxone, AMP: Ampicillin, TET: Tetracycline, NAL: Nalidixic Acid, CIP: Ciprofloxacin, COT: Cotrimoxazole, NIT: Nitrofurantoin, OFX: Ofloxacin, AMC: Amoxicillin- Clavulanic Acid, TOB: Tobramycin, CAZ: Ceftazidime, IPM: Imipenem, ETP: Ertapenem, FOX: Cefoxitin, STR: Streptomycin, AUG: Augmentin, CXM: Cefuroxime, CPR: Cefprozil, TIC: Ticarcillin, CFZ: Cefazolin, LEX: Cephalexin, CTX: Cefotaxime, MEM: Meropenem, SAM: Ampicillin-Sulbactam, TZP: Piperacillin-Tazobactam, AMK: Amikacin, SPT: Spectinomycin, ENR: Enrofloxacin, LVX: Levofloxacin, DOX: Doxycycline, SMT: Sulphamethoxazole, TMP: Trimethoprim, CST: Colistin, NEO: Neomycin, FLO: Florfenicol, CEF: Cephalothin, FEP: Cefepime, CLI: Clindamycin, NOR: Norfloxacin, PFX: Pefloxacin, SPX: Sparfloxacin, AX: Ampiclox, CAR: Carbenicillin, GAT: Gatifloxacin, RIF: Rifampin, MTZ: Metronidazole, CLR: Clarithromycin, NET: Netilmicin, ATM: Aztreonam, CPD: Cefpodoxime, TIM: Ticarcillin-Clavulanic Acid, TGC: Tigecycline, PIP: Piperacillin, CTF: Ceftiofur, LCM: Lincomycin

(50.23%) was observed in drinks which majorly includes water and nono; a local drink from cow's milk. Highest resistotype found in drinks was *E. coli* which accounted for 118 of the 666 (17%) MDR bacteria isolated from drinks. This result excludes Fakayode et al., (2018), where results for gram negative MDR was presented in group as higher 150 of 236 (63.6%) compared gram positive 27 of 94 (28.7%). In the gram-negative group occurrence of *E. coli* (39) was next only to Acetinobater (42), hence may have contributed most to the gram-negative bacteria MDR group. This result corroborated previous research which reported that all the organisms isolated from drinking water were multi-drug resistant (Ogu *et al*., 2017; Adesiyan *et al*., 2019; Adesoji *et al*., 2019; Bamigboye at al., 2020). This study also found protein-based foods such as beef, poultry and other animal food products to harbor the second highest percentage of MDR bacteria; 540 out of 1326 (40.72%). Highest resistotype found in protein-based food was Enterococcus; 129 out of 540 (23.9%) MDR bacteria, and Salmonella 128 out of 540 (23.7%) MDR bacteria This is in line with reports by Uzeh *et al*. (2017); Ahmed *et al*. (2019); Musa *et al*. (2020) that reported a high percentage of MDR bacteria in protein-based foods. Prevalence of MDR *E. coli* isolated from cattle, chicken and swine have also been reported by Adenipekun *et al*. (2015). The high prevalence of MDR bacteria in protein-based animal foods (predominantly chicken and poultry products) could be due to inappropriate use of antibiotics in treating livestock as resistant organisms present in the animal gut can contaminate the animal products during the slaughtering and processing of the animals for food (CDC, 2016).

Antibiotics related to MDR

In all the reports reviewed, the highest resistances observed in sulphamethoxazole (100%) (Adesiyan *et al*., 2019), cefuroxime, gentamicin, amoxillin/clavulanate and ciprofloxacin (66.7%) were observed among *E. coli* from "suya" (Adesoji *et al*., 2019), tetracycline, ceftiofur and sulphamethoxazole (40.9 -77.3 %) (Adesoji *et al*., 2015), ampicillin, cefotaxime and ceftazidime (100%) (Ahmed *et al*., 2019), erythromycin, ciprofloxacin, gentamicin, cephalexin, ceftriaxone, and ampicillin (100%) (Ayandiran and Dahunsi, 2017), clindamycin (99%) and (100%) in farms A and B respectively as reported in the article (Beshiru *et al*., 2017), penicillin, vancomycin and erythromycin (98%) (Chigor *et al*., 2020), ampicillin (80.9%) (Fakayode and Ogunjobi, 2028), methionine, penicillin, chloramphenicol, sulphamethoxazole/trimethoprim (Igbinosa *et al*., 2016), cefoxitin (100%) (Kwoji *et al*., 2019), ampicillin (100%) (Musa *et al*., 2020), cefuroxime (82%) (Amaeze *et al*., 2016), ceftazidime (91%) (Odumosu *et al*., 2016), sulphamethoxazole (100%) (Titilawo *et al*., 2015), amoxicillin and amoxicillin-clavulanate (100%) (Uzeh *et al*., 2017). It is not surprising that penicillin showed the highest prevalence in most of the articles included in this study. The high frequency of use of Beta lactams, which are characterized by low toxicity may have contributed to this result (Chigor *et al*., 2020). Similarly, thirteen articles reported resistance to ampicillin out of the fourteen articles which screened for MDR resistance to ampicillin. Titilawo *et al*. (2015), found ampicillin-resistant gene to be predominant in the environment, thus transfer of the resistant gene among bacteria isolate is possible. The result for ampicillin is also supported by Adenipekun *et al*. (2015) and Chigor *et al*. (2020).

Conclusions

This review has established the prevalence of multi-drug resistant bacteria in foods and drinks in Nigeria. The study has established that more MDR bacteria have been isolated from protein-based foods and from drinks. The study also reports a greater prevalence of *Escherichia sp.* among the species of MDR bacteria reportedly isolated. The presence of MDR bacteria in foods and drinks can lead to several public health issues, especially in Nigeria and therefore public health personnel need to ensure critical control during the production and handling of foods and drinks, as well as create more awareness as concerning proper hygienic practices to combat the spread of MDR bacteria.

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