Bacteriological Assessment and Multidrug Resistance Profile of Bacteria Associated with Food from different Cafeterias in a Tertiary Institution within Ibadan, Oyo State, Nigeria

***Joseph, O.J., Oyinlola, K.A., Ogunleye, G.E., Balogun, A.I. and Adesuntola, O.**
Department of Biological Sciences, KolaDaisi University, Ibadan. Nigeria
***Corresponding Author -** *oluwarotimi.joseph@koladaisiuniversity.edu.ng*

Abstract
Food is an important commodity and is required for survival and healthy living in humans. However, poor hygiene and unsanitary practices by food handlers tend to expose the foods to microbial contamination thereby predisposing consumers to different diseases. This study aimed at determining the antibiogram and multidrug resistance profile of bacteria isolated from food samples purchased from two different cafeterias within a Tertiary Institution in Ibadan, Nigeria. Microorganisms were isolated from food samples using appropriate agar media following standard microbiological procedures. Pure cultures were obtained and identified using different morphological and biochemical tests and thereafter subjected to different antibiotics such as Ciprofloxacin, Sulfamethoxazole/Trimethoprim, Amoxicillin, Tigecycline and Imipinem. The total heterotrophic, coliform and Salmonella-Shigella counts ranged between 0.46×10^4 CFU/mL, 2.56×10^4 CFU/mL and 6.10×10^4 CFU/mL respectively, for both cafeterias. A total of 14 bacterial species were isolated and they belonged to the species *E. coli*, *Staphylococcus aureus*, *Salmonella* spp., *Pseudomonas aeruginosa*, *Proteus* sp. and *Klebsiella* sp. The antibiotics susceptibility revealed that 7.1%, 21.4% and 71.4% of the isolates showed resistance to Imipenem, Ciprofloxacin and Trimethoprim/Sulfamethoxazole respectively, while all of the isolates were resistant to Tigecycline and Amoxicillin. However, 78.6% of the isolates were multidrug-resistant. The result of this study has shown that the food samples were contaminated with pathogenic microorganisms which also exhibited antibiotic resistance to some antibiotics used in medicine and this could pose a serious health risk to humans when consumed.

Keywords: Food, antibiotics resistance, multi-drug resistance, *Escherichia coli*, *Proteus* spp.

Introduction

Food intake is quite a significant factor in human survival. However, during food consumption, oftentimes humans ingest harmful pathogens as well as their toxins [1]. There has been a long and fascinating relationship between humans and foodborne microbes, even from pre-historic times. Besides offering nutrition to humans, food is also a rich medium for microbial growth [2]. Usually, bacteria alongside other microbes contaminate food and the reason for this is not far-fetched since microbes are ubiquitous and they readily colonize even the human habitat and environment.

According to Sinclair and Gerba [3], a number of factors predispose food to contamination by microorganisms; food vendors' hands, service tables or counters, eating tables, chopping boards, blenders, wetness of work surfaces, inadequate cleaning of cooking utensils and containers such as coolers, plates, chopping boards and even washing materials such as sponges, bowls as well as the use of unclean water during washing. More so, many cafeterias within tertiary institutions operate a cash exchange system in which students immediately pay by cash once they are served their foods and thus is an avenue of exchange of microorganisms as little or no caution is given to sanitary practices during these times [2], [4].

One major group of microorganisms that have been implicated as contaminants of food and causative agents of gastroenteritis due to food ingestion in humans are the enteric bacteria. Significantly, this group of bacteria inhabits a wide range of habitats while utilizing several animals as potential reservoirs, hence their transmission from these reservoirs to food is very much easy [5]. Enteric pathogens can be transmitted when these animals pollute the soil, air or water and consequentially transmitted to food substances during food preparation especially when the food handler does not practice good personal hygiene. Additionally, flies and other domestic animals may serve as a vehicle of transmission when they come in contact with these foods [5].

Meanwhile, a wide range of infections are caused by these pathogens and some of them have specific environmental or food sources. Infections caused by species of *Campylobacter* and *Salmonella* are often related to consumption of uncooked or undercooked poultry products, whereas gastroenteritis due to *Yersinia* spp. arises from ingestion of undercooked vegetables and pork [6], [7]. Enteropathogenic and enterohemorrhagic *Escherichia coli* and *Shigella* infections have been associated with the ingestion of water and food that are contaminated. It is interesting to mention that several areas within the gastrointestinal tracts are colonized by these pathogens with *Vibrio cholerae* having more affinity for the small intestine while the cecum and colon are often colonized by enterohemorrhagic *E. coli* and *Campylobacter jejunii* [8].

Foodborne disease is a global burden especially in developing nations such as Nigeria and the poor handling of food substances in restaurants has predisposed consumers of these foods to ingestion of contaminated foods, hence they become ill. As a result, it has therefore become important to ascertain the microbiological quality of these restaurants and the foods they cook especially within tertiary institutions. This study aimed at determining the antibiogram and multidrug resistance profile of bacteria isolated from food samples purchased from two different cafeterias within a tertiary institution in Ibadan, Nigeria. The need to ascertain the microbiological quality of these restaurants within the University has necessitated this research.

Materials and Methods

Sample Collection

Freshly prepared food samples (composite) were purchased into sterile re-sealable disposable bags twice weekly for a period of two weeks from two commonly patronized cafeterias within a Tertiary Institution in Ibadan, Oyo State, Nigeria. Samples were immediately transferred in ice-packs to the Microbiology laboratory of KolaDaisi University, Ibadan for analysis.

Sample Preparation and Isolation of Bacteria

Samples were serially diluted and 1 mL from dilutions 10^{-2} were aseptically inoculated into labeled sterile petri dishes using the pour plate method. Thereafter, different media (Nutrient agar, MacConkey agar and Salmonella Shigella agar ([LabM, UK]) were prepared following manufacturers' instructions and autoclaved at 121°C for 15 minutes. They were allowed to cool and dispensed into the appropriate petri dishes, swirled to allow even distribution and upon solidification, the plates were incubated inversely at 37°C for 24 hours and then observed for growth. The resulting colonies were counted and the respective microbial load was calculated as shown below;

$$\text{CFU/g} = \frac{\text{Number of clonies} \times 1/\text{dilution factor}}{\text{Volume of inoculum}}$$

Furthermore, distinct colonies obtained were subsequently subcultured using the streak-plate technique of isolation in order to obtain pure cultures of the isolates [9], and were stored in agar slants under refrigerating conditions.

Characterization of Bacterial Isolates

Pure cultures of isolates were characterized via different morphological (pigment production, Gram staining, motility), biochemical (catalase, oxidase, indole, urease, etc.) and sugar fermentation tests following standard microbiological guidelines [10].

Antibiotics Susceptibility Test

The antibiotics susceptibility patterns of the isolates were determined using the Kirby-Bauer Disc diffusion technique following CLSI guidelines [11]. One millilitre of 0.5M McFarland equivalent of each isolate was dispensed and evenly spread on Mueller-Hinton agar with a sterile swab stick. Thereafter, using a sterile forcep, impregnation of the antibiotic discs was done on the agar plates which were thereafter incubated at 37°C for 24 hours and the diameters of inhibition were measured using a ruler [12]. The antibiotics used were Tigecycline (15µg), Ciprofloxacin (10µg), Imipenem (10µg), Amoxicillin (20µg) and Trimethoprim-sulfamethoxazole (25µg). Isolates showing resistance to three or more antibiotics from different classes were considered to exhibit multidrug resistance (MDR) [13].

Results

The mean total heterotrophic bacterial count of the food samples was 0.46×10^4 CFU/mL and 5.23×10^4 CFU/mL from restaurant 1 and 2 respectively. Meanwhile, for the coliform count on MacConkey agar, the mean bacterial count was 1.57×10^4 CFU/mL and 2.56×10^4 CFU/mL for restaurant 1 and 2 respectively. However, Salmonella-Shigella count was 0.91×10^4 CFU/mL in food sample from cafeteria 1 and 6.10×10^4 CFU/mL for cafeteria 2 (Table 1).

The morphological, biochemical and sugar fermentation characteristics of the isolated bacteria identified them to belong to the species *Staphylococcus aureus*, *Escherichia coli*, *Pseudomonas aeruginosa*, *Salmonella* spp., *Proteus* sp. and *Klebsiella* sp. Of all 14 bacterial isolates, 5 (35.7%) were identified as *E. coli*, 3 (21.4%) as *Staphylococcus aureus*, 2 (14.3%) as *Salmonella* spp., 2 (14.3%) as *Pseudomonas aeruginosa* and 1 (7.1%) each as *Proteus* sp. and *Klebsiella* sp., respectively (Figure 1).

The antibiotics susceptibility test showed that 1 (7.1%), 6 (42.9%) and 7 (50%) of the isolates were resistant, intermediate and susceptible, respectively to Imipenem, while 3 (21.4%), 4 (28.6%) and 7 (50%) of the bacterial isolates were resistant, intermediate and susceptible, respectively to ciprofloxacin. Meanwhile, 10 (71.4%) of the bacteria isolated showed resistance to Trimethoprim/Sulfamethoxazole, while 3 (21.4%) were intermediate and just 1 (7.1%) was susceptible. However, all 14 (100%) of the bacteria isolated showed resistance to Tigecycline and Amoxicillin, that is, none was susceptible to both antibiotics (Table 2).

The phenotypic resistance profile and multidrug resistance (MDR) index of the isolates are shown in Table 3. Of all the isolates, 3 (21.4%) were not multidrug-resistant while 11 (78.6%) were multidrug-resistant, that is, showed resistance to more than two different antibiotics classes. Amongst the 11 MDR isolates, 9 had MDR index of 0.6 while 1 had MDR index of 0.8. Notably, one isolate had MDR index of 1.0, that is, it was resistant to the five different classes of antibiotics it was subjected to.

Discussion

Food is a substance consumed by all, it is therefore essential that it is prepared following strict hygienic processes. This is because food contains high nutritive substances and therefore can easily be colonized by microorganisms. This study focused on the bacteriological assessment of food samples purchased in two cafeterias within a Tertiary Institution in Ibadan, Nigeria.

The microbial load of the food samples purchased from the two restaurants showed a fairly high load of bacteria in the food samples. This observation of high contamination of food substances has been previously reported by a number of authors. Akpoka *et al*. [14] reported a fairly comparative bacterial load in different ready-to-eat cooked foods in selected restaurants in Okada, South-South, Nigeria; in their study, the total aerobic viable counts, total coliform counts and total *Staphylococcus* count ranges in the ready-to-eat cooked food from the six sampled restaurants were $1.15 \pm 0.03 \times 10^4$ CFU/g – $2.71 \pm 0.05 \times 10^4$ CFU/g, $0.33 \pm 0.33 \times 10^4$ CFU/g – $2.39 \pm \times 10^4$ CFU/g and $0.37 \pm \times 10^4$ CFU/g – $6.60 \pm \times 10^4$ CFU/g respectively and this is similar to the range of bacterial population reported from this study. Omorodion and Adesewa [15] also reported a high bacterial load in different ready-to-eat food samples obtained from three different restaurants within the University of Port Harcourt, Choba, Port Harcourt, Rivers State. Similarly, Kone *et al*. [16] in different food samples collected from different cafeterias within different universities in Abidjan, Côte d'Ivoire, reported a highest microbial load of ($2.3 \text{ X } 10^6$). This observation of high load of bacteria thereby renders the food bacteriologically unfit for consumption according to the standards set by the International Commission for Microbiological Specification for Food (ICMSF). The ICMSF reported in their guidelines that in food samples, the total heterotrophic bacterial count must not exceed 10^3 CFU/g to be acceptable for consumption. However, the body also mentioned that a bacterial load between 10^4 and 10^5 CFU/g is tolerable [17], meanwhile the bacterial load in the food samples from this study exceeded this limit. The high level of contamination observed in this study may be

attributed to poor personal hygiene and general hygiene practices by the food handlers in the restaurants. Additionally, some of these bacteria may have entered into the food samples as a result of the frequent opening of the food containers while serving the foods.

In this study, the 14 isolates eventually recovered were identified to belong to 5 different species namely *Escherichia coli*, *Staphylococcus aureus*, *Pseudomonas aeruginosa*, *Salmonella* sp. and *Proteus* sp. These species of bacteria have been earlier reported as the frequent bacterial isolates recovered from different food samples obtained from several restaurants. In a microbiological survey of food samples obtained from cafeteria from different public sector universities in Karachi, Pakistan, Giwa *et al*. [18] reported *E. coli*, *Staphylococcus aureus*, *Pseudomonas aeruginosa*, *Shigella*, *Klebsiella* as the most prevalent bacterial isolates. Similarly, Iroha *et al*. [19] identified the bacteria isolated from food samples around PRESCO campus of Ebonyi State University, Abakaliki as *Escherichia coli*, *Pseudomonas aeruginosa* and *Klebsiella pneumoniae*; in the above-mentioned study however, the frequency of occurrence for these isolates in the food samples were very much higher than what was obtained from this study and this may be due to the higher number of samples collected from the study as compared to the very low number collected in this present study.

The presence of *E. coli*, *Salmonella* sp. and other enteric bacteria is an indication of faecal contamination that may have resulted from contaminated water, raw foods as well as poor practice of hygiene by the food handlers. It is even more worrisome as these isolates have been reported by a number of studies as the causative agents in numerous cases of food poisoning and other gastrointestinal disorders [14], [19], [20]. In a study, Oranusi *et al*. [21] isolated these bacteria from different food samples sold in different student cafeteria around Sango Ota, Ogun state, Nigeria.

Meanwhile, the presence of other species of bacteria such as *Staphylococcus aureus* is an indication of human contact or contamination as well as poor sanitary and hygiene practices because *Staphylococcus aureus* is regarded as a normal flora of the human skin, that is, they reside permanently on the human skin and also in the nasal passage [21], [22].

Pseudomonas aeruginosa is also a notorious bacterial species as strains from this species have been found to be responsible for a number of diseases including foodborne diseases, Urinary tract infections and in some cases, pneumonia [21].

From this study, there was very low percentage of resistance to imipenem and ciprofloxacin, whereas a very large percentage of the isolates showed resistance to Sulfamethoxazole/trimethoprim, Amoxicillin and Tigecycline. In this study, all the *Salmonella* species were entirely susceptible to imipenem and this agrees with the reports by Karikari *et al*. [23] that less than 5% of all the *Salmonella* species isolated from different food sources in Tamale, Ghana were resistant to imipenem. Likewise, in the above-mentioned study [23], less than 3% of the *Salmonella* isolates were resistant to ciprofloxacin and this is in line with what was obtained in this study as all the *Salmonella* spp. isolated in the present study were susceptible to ciprofloxacin. Also, in a study by Majolagbe *et al*. [24], a very low percentage (10%) of the test bacteria isolated from ready-to-eat foods in popular eateries along Ogbomoso-Oyo road was resistant to ciprofloxacin.

Meanwhile, high percentage of resistance to tigecycline, amoxicillin and sulfamethoxazole/

trimethoprim exhibited by the isolates in this study corroborates with the reports by Vijayalakshmi *et al*. [25] in which less than 21% of bacteria isolated from different food sources in India were susceptible to tigecycline, amoxicillin and sulfamethoxazole/trimethoprim. The high resistance to these antibiotics exhibited by the test isolates may be due to a number of antibiotic resistance mechanisms; according to Kraemer *et al*. [26], antibiotic resistance may be naturally acquired and can be acquired via horizontal gene transfer (conjugation or transformation). More so, the development of resistance to tigecycline, amoxicillin and sulfamethoxazole/trimethoprim by the isolates from this study may also be attributed to changes in its genetic makeup, that is, via mutations that may have caused the antibiotics to be unable to recognize the target point in order to destroy the bacteria [27], [28].

Antibiotics resistance is a complex problem globally and resistance to antibiotics lower effectiveness thereby becoming an economic burden to individuals, public health and the community as a whole [29], [30]. In this study, 78.6% of the isolates were multidrug-resistant as they showed resistance to more than two different classes of antibiotics. This observation of high MDR isolates corroborates with the study of Vijayalakshmi *et al*. [25] in which around 60% of bacteria isolated from food sources such as animal products in different food markets in India were multidrug-resistant. This is a major concern for public health as these isolates when ingested with food may pose a serious health risk to unsuspecting individuals and this may cause a medical burden on individuals and other clinical setups. In addition, should these bacteria find their way into the guts of humans, even if they were non-pathogenic, genes conferring antibiotic resistance to them may become transferred via different processes to other pathogenic bacteria, thereby increasing the spread of antibiotic-resistant bacteria and genes coding for such resistance. Notably, the species of *Salmonella* isolated in this study were MDR and this is in line with previous studies by Vijayalakshmi *et al*. [25]. Should these MDR *Salmonella* spp. be ingested, a case of salmonellosis may arise and this demands antibiotic treatment which may even become compromised as a result of the resistant strain [31]. More so, non-pathogenic resistant bacteria can become ingested by humans via consumption of foods contaminated with these bacteria. Thus, there is transfer of genes conferring antibiotics resistance to other gut-residing bacteria through mobile genetic elements such as transposon, integrons, plasmid, gene cassette, and insertion sequence [32].

Conclusions

Reports from this study have shown that the different food samples purchased from the two restaurants within the institution are highly contaminated by pathogenic bacteria. More importantly, a number of these isolates showed resistance to majority of the antibiotics and this is a grave concern to the health of the students because should they become ill as a result of consumption of these foods, the illness may be quite difficult to treat.

Table 1: Microbial Load of Food Samples from the Two Restaurants (× 10^4 CFU/mL)

Restaurant	Total heterotrophic bacterial count	Coliform count	Salmonella/Shigella count
1	0.46 ± 0.03	1.57 ± 0.01	0.91 ± 0.04
2	5.23 ± 0.04	2.56 ± 0.06	6.10 ± 0.14

Values are Means± Standard deviations of quadruplicate samplings

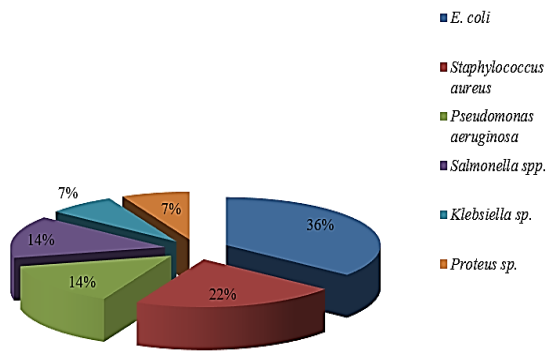

Figure 1: Frequency (%) of occurrence of bacteria isolated from food samples.

Table 2: Antibiotics Sensitivity Profile of Bacteria Isolated from the different Food Samples

S/N	Probable Identity	IPM	CIP	TGC	AMC	SXT
1.	*Escherichia coli*	24 (S)	26 (S)	0 (R)	2 (R)	12 (I)
2.	*Pseudomonas aeruginosa*	18 (I)	30 (S)	0 (R)	0 (R)	8 (R)
3.	*Pseudomonas aeruginosa*	22 (S)	28 (S)	0 (R)	6 (R)	8 (R)
4.	*Proteus* sp.	20 (I)	22 (I)	0 (R)	0 (R)	10 (R)
5.	*Staphylococcus aureus*	20 (I)	16 (I)	0 (R)	0 (R)	6 (R)
6.	*Staphylococcus aureus*	32 (S)	28 (S)	0 (R)	4 (R)	32 (S)
7.	*Escherichia coli*	22 (I)	34 (S)	0 (R)	0 (R)	8 (R)
8.	*Klebsiella* sp.	22 (I)	24 (I)	0 (R)	6 (R)	8 (R)
9.	*Staphylococcus aureus*	18 (R)	18 (R)	0 (R)	0 (R)	0 (R)
10.	*Escherichia coli*	16 (R)	18 (R)	0 (R)	0 (R)	0 (R)
11.	*Salmonella* sp.	24 (S)	28 (S)	8 (R)	0 (R)	2 (R)
12.	*Escherichia coli*	26 (S)	24 (I)	0 (R)	8 (R)	12 (I)
13.	*Escherichia coli*	22 (I)	20 (R)	0 (R)	8 (R)	12 (I)
14.	*Salmonella* sp.	36 (S)	30 (S)	10 R)	0 (R)	6 (R)
Resistant n (%)		1 (7.1)	3 (21.4)	14 (100)	14 (100)	10 (71.4)
Intermediate n (%)		6 (42.9)	4 (28.6)	0	0	3 (21.4)
Susceptible n (%)		7 (50)	7 (50)	0	0	1 (7.1)

KEY: IPM; Imipinem, CIP; Ciprofloxacin, TGC: Tigecycline, AMC; Amoxicillin, SXT: Sulfamethoxazole-Trimethoprim
R= Resistant, I= Intermediate, S= Susceptible

Table 3: Phenotypic Resistance Pattern of Isolates and their MDR Index

S/N	Isolate Code	Probable identity	Phenotypic resistance pattern	MDR index
1.	R1^{1ST}	*Escherichia coli*	TGC-AMC	-
2.	R1^{2}ST	*Pseudomonas aeruginosa*	TGC-AMC-SXT	0.6
3.	R1^{2}FS	*Pseudomonas aeruginosa*	TGC-AMC-SXT	0.6
4.	R2^{1ST}	*Proteus* sp.	TGC-AMC-SXT	0.6
5.	R2^{1}FS	*Staphylococcus aureus*	TGC-AMC-SXT	0.6
6.	R2^{2}ET	*Staphylococcus aureus*	TGC-AMC	-
7.	R2^{2}ST	*Escherichia coli*	TGC-AMC-SXT	0.6
8.	R2^{2}FS	*Klebsiella* sp.	TGC-AMC-SXT	0.6
9.	R1^{3}FS	*Staphylococcus aureus*	CIP-TGC-AMC-SXT	0.8
10.	R2ET3	*Escherichia coli*	IPM-TGC-AMC-SXT	1.0
11.	R1^{2}ET	*Salmonella* sp.	TGC-AMC-SXT	0.6
12.	R2^{1}ET2	*Escherichia coli*	TGC-AMC	-
13.	R2^{1}ET	*Escherichia coli*	CIP-TGC-AMC	0.6
14.	R2^{3}ST	*Salmonella* sp.	TGC-AMC-SXT	0.6

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References

[1] Zarei, S., Ehrampoush, M.H., Mazloomi, S.M., Ghaneian, M.T., & Hajimohammadi, B.D. (2014). Evaluation of microbial quality of sausage slicers at food retail food stores in Shiraz, Iran. *Journal of Toloo-e-Behdasht*, *13*(3), 54-63.

[2] Anyanwu, N.C.J., John, W.C., & Idoko, M.O. (2016). Bacteriological examination of the Cafetria equipment in Karu L.G.A. Cafeterias, Nasaraw State, Nigeria. *Journal of Applied Life Science International*, *5*(2), 1-8.

[3] Sinclair, R.G., & Gerba, C.P. (2011). Microbial contamination in kitchens and bathrooms of rural Cambodian village households. *Journal of Microbiology*, *52*, 142-149.

[4] Rakhshkhorshid, M., Rakhshkhorshid, A., & Belarak, D. (2016). Survey of cooking utensils and dishes microbial contamination

rate in the cafeteria of Zahedan University of medical sciences, 2015. *International Journal of Biomedical and Healthcare Sci*ence, *6*(2), 187-193.

[5] Fredriksson-Ahomaa, M. (2012). Isolation of enteropathogenic *Yersinia* from non-human sources. Advances in Experimental Medicine and Biology, 954:97–105.

[6] Erhardt, M., & Dersch, P. (2015). Regulatory principles governing *Salmonella* and *Yersinia* virulence. *Frontiers in Microbiology*, *6*:949. https://doi.org/10.3389/fmicb.2015.00949

[7] García-Sánchez, L., Melero, B., Jaime, I., Hänninen, M.L., Rossi, M., & Rovira, J. (2017). *Campylobacter jejunii* survival in a poultry processing plant environment. *Food Microbiology*, *65*, 185–192. https://doi.org/10.1016/j.fm.2017.02.009.

[8] Nguyen, Y., & Sperandio, V. awol(2012). Enterohemorrhagic *E. coli* (EHEC) pathogenesis. *Frontiers in Cellular and Infectious Microbiology*, *2*, 90. https://doi.org/10.3389/fcimb.2012.00090

[9] Fawole, M.O., & Oso, B.A. (2004). Characterization of Bacteria: Laboratory Manual of Microbiology. 4th Edition, Spectrum Book Ltd., Ibadan, 24-33.

[10] Cheesebrough, M. (2006). District Laboratory Practices in Tropical Countries. Part II, 2nd Edition. Cambridge University Press.ISBN-10 0-511-34842-8.

[11] Clinical laboratory standard institute. (CLSI) (2020). Performance standards for antimicrobial susceptibility testing. Vol. 30th ed., CLSI supplement M100S.Wayne, PA: clinical and laboratory standards institute. 2020.

[12] Bauer, A.W., Kirby, W.M.M., Sherris, J.C., & Turck, M. (1966). Antibiotic susceptibility testing by a standard single disk method. Am. J. Clin. Pathol. 36, 493 – 496.

[13] Magiorakos, A., Srinivasan, A., Carey, R.B., Carmeli, Y., Falagas, M.E., & Giske, C.G. (2011). Multidrug-resistant, extensively drug-resistant and pandrug-resistant bacteria: an international expert proposal for interim standard definitions for acquired resistance. *Microbiology*, *18*(3), 268–81.

[14] Akpoka, A. O., Imade, O. S., Okwu, M. U., & Solanke, E. O. (2019). The Prevalence of foodborne pathogens recovered from ready-to-eat food from restaurants in Okada, Edo state, Nigeria. *Bacteria Empire*, *2*(2), 37-4.

[15] Omorodion, N. J. P. & Adesewa, O. (2012). Microbial and Physicochemical Screening of Ready to Eat Street Foods. *Asian Journal of Basic Science & Research*, *4*(1), 24-35.

[16] Kone, A., Sika, A.E., Adingra, A.A., Zamble, B.A>, Toule, A.C. & Koffi-Nevry, R. (2022). Microbiological contamination of cooked meals in collective and commercial catering of public universities of Abidjan in Côte d'Ivoire. *International Journal of Biological and Chemical Sciences*, *16*(1), 122-133.

[17] International Commission on Microbiological Specifications for Foods (ICMSF). (1996). *Microorganisms in Foods 5*: Microbiological Specifications of Pathogens.

[18] Giwa, A.S., Memon, A.G., Shaikh, A.A., Korai, R., Maitlo, I., Ali, S. & Ahmad, J. (2021). Microbiological survey of ready-to-eat foods and associated preparation surfaces in cafeterias of public sector universities. *Environmental Pollutants and Bioavailability*, *33*(1), 11-18.

[19] Iroha, I., Afiukwa, N., Nwakaeze, E., Ejikeugwu, C., Oji, A., & Ilang, D. (2014). Antibiogram of food-borne pathogens isolated from ready-to-eat foods and Zobo Drinks Sold Within and Around PRESCO Campus of Ebonyi State University (EBSU), Abakaliki, Ebonyi State, Nigeria. *Journal of Toxicology and Environmental Health Sciences*, *6*(1), 1-4.

[20] Marwa, E.A., Aly, T., Essam, M.M., & Amin, A. (2012). Antibiotic resistance profile of *E. coli* strains isolated from clinical specimens and food samples in Egypt. International Journal of Microbiology Research, *3*(3), 176-182.

[21] Oranusi, S.U., Oguoma, O.I., & Agusi, E. (2013). Microbiological quality assessment of foods sold in student's cafeterias. *Global Research Journal of Microbiology*, *3*(1), 1-7.

[22] Monday, I.E., Francis, J.I., & Mohammed, S.U. (2014). Microbiological Quality of Ready-To-Eat Foods (Rice and Moi moi) Sold By Food Vendors in Federal Polytechnic Bali, Taraba State, Nigeria. *IOSR Journal of Environmental Science,*

Toxicology and Food Technology, *8*(2), 145-149.

[23] Karikari, A.B., Kpordze, S.W., Yamik, D.Y. & Saba, C.K.S. (2022). Ready-to-Eat Food as Sources of Extended-Spectrum β-Lactamase-Producing *Salmonella* and *E. coli* in Tamale, Ghana. *Frontiers in Tropical Diseases*, *3*, 834048. doi: 10.3389/fitd.2022.834048.

[24] Majolagbe, O.N., Idowu, S.A., Adebayo, E., Ola, I., Adewoyin, A.G., & Oladipo, E.K. (2011). Prevalence and antibiotic resistance of bacteria isolated from ready-to-eat (RTE) food samples of highly patronized eateries in Ogbomoso-Oyo state, Nigeria. *European Journal of Experimental Biology*, *1*(3), 70-78.

[25] Vijayalakshmi, P., Rajani Chowdary, A., Vidyullatha, P., & Sharon, S. M. (2021). Identification of bacteriological quality and antimicrobial resistance of microorganisms isolated from animal foods collected from the abattoir, butcher shops and local seafood market. *Food Research*, *5*(3), 144 – 151.

[26] Kraemer, S. A., Ramachandran, A., & Perron, G. G. (2019). Antibiotic pollution in the environment: from microbial ecology to public policy. *Microorganisms*, *7*(6), 180.

[27] Couvalin, P. (2016). Why is antibiotic resistance a deadly emerging disease? *European Society of Clinical Microbiology and Infectious Diseases*, *22*, 405–407.

[28] Munita, J. M., & Arias, C. A. (2016). Mechanisms of antibiotics resistance. *Microbiology Spectrum*, *4*(2). doi:10.1128/microbiolspec.VMBF-0016-2015

[29] Frieri, M., Kumar, K., & Boutin, A. (2017). Antibiotics resistance. *Journal of Infection and Public Health*. *10*, 369—378. https://doi.org/10.1007/978-1-4614-3561-7_12.

[30] Sharland, M., Saroey, P., & Berezin, E. N. (2015). The global threat of antimicrobial resistance -The need for standardized surveillance tools to define burden and develop interventions. *Journal of Pediatrics*, *91*, 410-422.

[31] Omololu-Aso, J., Omololu-Aso, O.O., Atiene, T.M., Adejuwon, A., Owolabi, A.T., & Shesha, A. (2017). Salmonellosis and shigellosis associated with cow dung contaminant from indigenous abattoir Osun State, Nigeria. *British Journal of Research*, *4*(1), 1-4. https://doi.org/10.21767/2394-3718.10002

[32] Bagudo, A.I., Tambuwal, F.M., Faleke, O.O., Egwu, O.O., & Aliero, A.A. (2014). Prevalence of Salmonella serotypes in Sokoto abattoir effluents and vegetables cultivated around the abattoir. *Microbiology Research International*, *2*(2), 13-17.