Original Research Article

ASSESSING FOOD SAFETY IMPLICATIONS OF MULTI ANTIBIOTIC RESISTANT FERMENTED-FOOD-CONDIMENT-ENVIRONMENT-ADAPTED BACTERIAL SPECIES

ABSTRACT

Food safety implications of the condiment-adapted bacterial strains, regarding their intrinsic, acquired and transferable antibiotic resistance potentials are yet to be reportedly fully ascertained. Using the Kirby-Bauer agar disc-diffusion method, phenotypic multi-antibiotic-drug-in-disc resistance (MADIDR) profiles of 138 condiment-borne (Gram-positive = 71; Gram-negative = 67) bacterial strains from *iru*, *ogiri* and *okpehe* were evaluated. None of the condiment-adapted bacterial strains was totally susceptible to the test antibiotics; just five (3.62%: n = 0.7%: Gram-positive: n = 2.9% Gram-negative) strains were mono-resistant, while six (4.37%) were totally or pandrug-resistant (PDR). Of the remaining 92.03% condiment-adapted bacterial strains, 6.57% exhibited co-antibiotic drug resistance (CDR); 43.8% (Gram-positive = 17.52%; Gram-negative = 26.28%) were multi-drug resistant (MDR); and 41.55% (Gram-positive = 25.55%: Gram-negative = 16.0%) displayed extensive-drug resistance (XDR). A total of 43.48% Gram-positive and 36.96% Gram-negative bacterial strains were multi-resistant to between four and eight of the test in-discs antibiotics. Overall, augmentin (95.8%), cloxacillin (94.4%) cotrimoxazole (71.8%) and erythromycin (71.8%) were the most-resisted in-discs-antibiotics by the condiment-adapted Gram-positive bacteria, while cloxacillin (93.8%), ciprofloxacin (80.0%) and augmentin (76.9%) were the most-resisted in-discs antibiotics by Gram-negative bacteria. In conclusion, tremendous multi and extensive resistance were recorded among the fermented-food-condiment-environment-adapted bacteria to in-discs-antibiotics that are commonly administered in human and animal prophylaxis and therapy, indicating a serious food safety challenge in the ethnic cottage-food industries, food chain, and the community. Food safety during cottage-production of nutritious, indigenous fermented foods, as well as consumers‘protection must be of utmost priority.

Keywords: Consumer health protection, fermented-food-condiment-environment-adapted bacteria (FFCEAB), foodborne pathogens and diseases, food safety, *ogiri* Ijebu.

1.0 INTRODUCTION

The cottage-produced Nigerian indigenous fermented food condiments (NIIFFCs) from leguminous (vegetative) seeds, prepared mostly by traditional fermentation methods, are a variety of popular strong-smelling food culinary products, with consistently appealing, unique organoleptic qualities, which enhance soups, sauces and other prepared dishes. By giving distinctively pleasant aroma, peculiar taste, flavour, and overall food delicacy characteristics to soups, sauces and prepared dishes, the indigenous fermented food condiments, such as, *ogiri*, *iru* / *dawadawa* / *dadawa*, *okpehe*, *ugba*, etc., are undeniably incomparable, which is responsible for their massive consumption rates in Africa, Asia and other parts of the world [1-9].

It is well known that indigenous fermented foods are strongly linked to culture and tradition [10], and thus, each indigenous community in the world has its distinct food culture [11], which includes fermented foods and alcoholic / non-alcoholic beverages that symbolise the heritage and socio-cultural aspects of the ethnicity [12], even beyond rural households and village communities. Furthermore, ethnic foods have in-built systems, both as foods to meet up with hunger, and also as medicine [12-14]. So, traditional fermented foods being staple foods for most of the developing countries, and also key healthy foods for developed countries, as well as impart some health benefits to consumers [15,16]. All these have led to gradual discovery of their healthy food functions, through production of antioxidant and antimicrobial compounds and bio-availability of nutrients; stimulation of probiotic functions, as well as, fortification with some health-promoting bioactive compounds [16-21]. Connections between human resident microbes and many aspects of physiology have also been reported [22,23].

With billions to feed worldwide, the need to produce adequate amounts of safe food, unadulterated by bacterial, viral and protozoan pathogens, etc., remains one of the major challenges in modern times [24]. Most documented studies on the distinct indigenous fermented food condiments have usually been on their processing, nutritional, physicochemical, acceptability, storage or shelf-life characteristics, as well as their fermenting microbial flora [11,25,26]; with only few studies actually reporting the effect of their microbial quality and food safety [27-30]. Whereas, the presence and potential ablility of the fermenting microbes, which are likely to cause health problems, as a consequence of their survival, and consumption of the end products [30,31] call for adequately screening of such mostly uncontrolled, traditional fermented nutritional foods.

The purpose of this study therefore, is to evaluate the implications of antibiotic-in-disc-multi--resistance (AIDMR) of easily-culturable bacterial flora isolated from market samples of three most popular Nigerian fermented food condiments, *iru*, *ogiri* and *okpehe*.

2.0 MATERIALS AND METHODS

2.1 Traditional preparations of the condiments

The traditional preparations and fermentations of the test condiments in this study, *ogiri* Ijebu, from melon seeds (*Citrilus lanatus*); *iru /dawadawa /daddawa*, from African locust bean seeds (*Parkia biglobosa*) and *okpehe / afiyo* from mesquite (*Prosopis africana*), are as shown in figures 1-3.

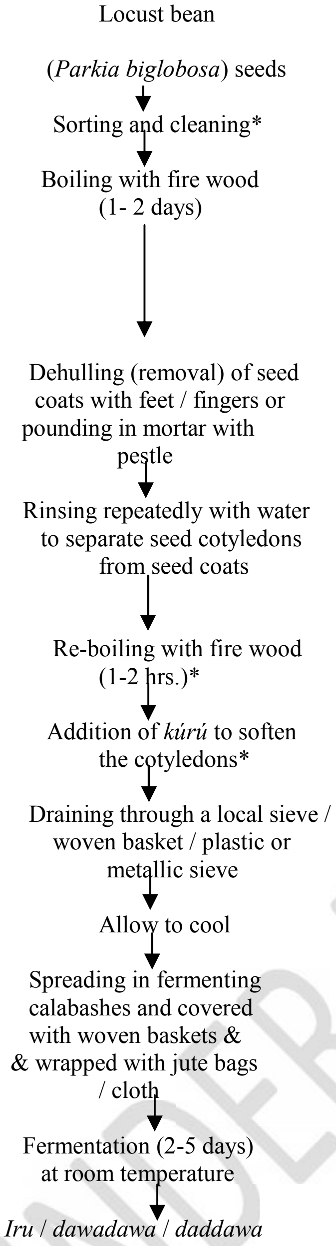

Fig. 1: Flow chart for traditional preparation of *irú / dawadawa / daddawa* (Oyeyiola, 1988)

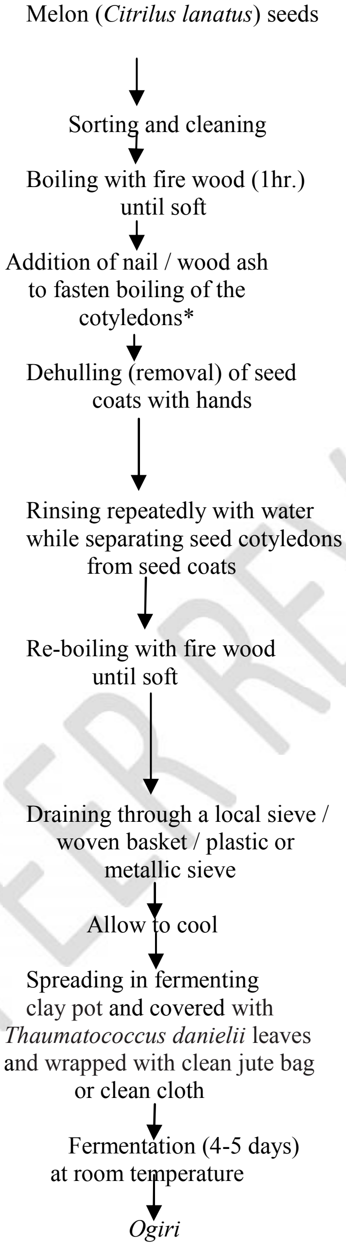

Fig. 2: Flow chart for traditional preparation of *Ogiri* (Ogunshe Pers. Comm.)

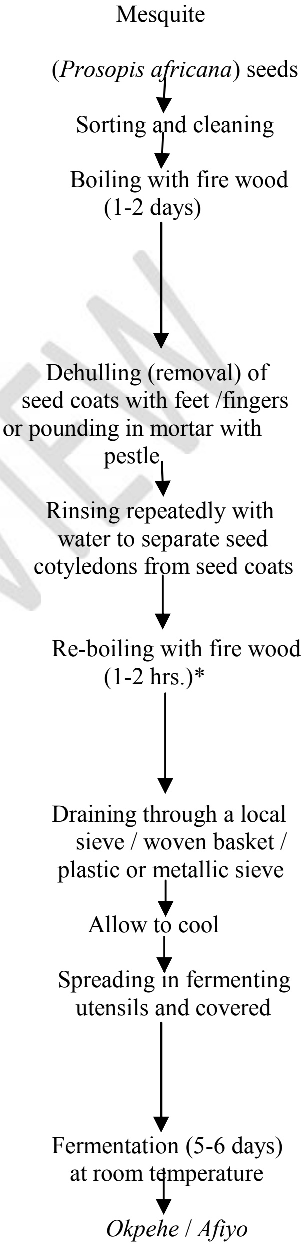

Fig. 3: Flow chart for traditional preparation of *Okpehe / Afiyo* (Ogunshe *et al*., 2007)

2.2 Test bacterial flora

The test bacterial flora screened for phenotypic antibiotic profiles included some of those earlier isolated from indigenous Nigerian fermented food condiments *iru*, *ogiri* and *okpehe* (Figs. 1-3), obtained from local markets in Ijebu Ode, Abeokuta, Ibadan, Lokoja, Gboko, Ondo, Akungba and Lagos in Nigeria [27-30].

2.3 Antibiotic susceptibility / resistance determination (discs)

In determining the antibiotic-in-disc-multi-resistance (AIDMR) of easily-culturable bacterial flora from three most popular Nigerian fermented food condiments, *iru*, *ogiri* and *okpehe*, phenotypic antibiotic susceptibility and resistance of the Gram-positive and Gram-negative condiment-borne bacterial species to various antibiotics, was according to Bauer *et al*. [32]. and NCCLS [33] agar disc-diffusion methods. Test antibiotics (discs) used for the Gram-positive bacteria screening were, tetracycline (TET; 30µg), streptomycin (STR; 10mg), augmentin (AUG; 30µg), gentamicin (GEN; 10µg), erythromycin (ERY; 5µg), cloxacillin (CXC; 30µg), chloramphenicol (CHL; 30µg), cotrimoxazole (COT / CTX; 25µg). Test antibiotics (discs) used for Gram-negative bacteria screening were, fortum (CAZ; 30mg), ciprofloxacin (CPX; 10 µg), gentamicin (GEN; 10µg), claforan (CTX; 30 µg), ofloxacillin (OFL; 30 µg), augmentin (AUG; 30µg), nitrofurantoin (NIT; 250µg) and cloxacillin (CXC; 30µg).

The entire surface of each sterile Mueller-Hinton agar plate was seeded with each bacterial isolate using sterile wab sticks. The plates were left for about 15 minutes before aseptically placing the antibiotic multi-discs on the agar surfaces with sterile forceps, followed by incubation at 32-35^{0}C for 24-36 hours. Zones of inhibition were measured and recorded in millimetre diameter, while zones of inhibition less than 10.0mm in diameter or absence of zones of inhibition were recorded as resistant (negative) [30].

3.0 RESULTS

Identified fermenting and associated bacterial flora of the sampled Nigerian fermented condiments in this study were reported as, *Micrococcus*, *Staphylococcus aureus*, *Streptococcus*, *E. coli*, *Enterobacter aerogenes*, *Klebsiella pneumoniae*, *Proteus mirabilis*, *Pseudomonas aeruginosa*, *Salmonella* and *Shigella dysenteriae*, in addition to *Bacillus* species.

The narrow-spectrum or broad-spectrum test antibiotics (belonging to the aminoglycosides, macrolides, penicillins, tetracyclines, quinolones, etc.), are mostly bactericidal (bacterial death), and few bacteriostatic (growth inhibiting) towards the condiment-adapted bacterial strains. Results of the antibiotic susceptibility and resistance rates and profiles of condiment-adapted bacterial strains recorded in this study expressed that, with the exception of gentamicin (4.68%-26.7%), tremendously high antibiotic resistance rates of between ≥50.0% and 100% were exhibited by the Gram-positive bacteria. Generally, augmentin vs. cloxacillin antibiotics (discs) were the most-resisted antibiotics by the Gram-positive bacterial species [*Bacillus* / *Micrococcus* spp. 100% vs. 100%; *Staphylococcus aureus* 87.0% vs. 100%; *Streptococcus* 100% vs. 90.9%] (Table 1). But overall, antibiotics mostly resisted by ≥50.0% of the Gram-positive bacterial strains were erythromycin / cotrimoxazole (71.8%), chloramphenicol (66.2%), tetracycline (63.3%) and streptomycin (50.7%) (Figure 4a).

The Gram-negative bacteria isolated from the indigenous fermented food condiments exhibited between 53.8% and 93.8% overall resistance rates, with the exception of ofloxacillin (4.6%) and gentamicin (20.0%) (Figure 4b) but higher resistance towards the two antibiotics were recorded for *Klebsiella* (ofloxacillin = 50.0%) and *Proteus* (gentamicin = 50.0%). More significant resistance rates were also exhibited by *Klebsiella*, *Proteus* and *Pseudomonas* species (Table 1). No resistance was exhibited by *Enterobacter* towards ofloxacillin but all the strains were resistant to augmentin and cloxacillin (100%), while 75.0% of *Enterobacter* strains exhibited resistance towards nitrofurantoin, claforan, ciprofloxacillin and fortum (Table 2). All the *E. coli* strains were resistant to fortum, 93.3% and 80.0% of the *E. coli* strains were resistant to cloxacillin and augmentin respectively, while 66.7% of the strains were resistant to ciprofloxacillin and claforan but the lowest resistance was recorded for ofloxacin (13.3%).

The two *Klebsiella pneumoniae* strains were totally resistant (100%) to augmentin, ciprofloxacin, claforan, fortum, ofloxacillin, nitrofurantoin and cloxacillin but no resistance was exhibited towards gentamicin. *Salmonella* strains exhibited highest antibiotic resistance rates towards cloxacillin (93.1%), fortum and ciprofloxacin (72.4%) but lowest resistance was recorded for gentamicin (20.7%), while no resistance (0.0%) was recorded for ofloxacin. The most resisted antibiotics by *Shigella dysenteriae* were ciprofloxacin, cloxacillin (83.3%), fortum and augmentin (66.7%), while no resistance was exhibited against gentamicin (0.0%). Total resistance (100%) were also exhibited by *Proteus mirabilis* against fortum, ciprofloxacin, augmentin and cloxacillin; no resistance was recorded against ofloxacillin, while 50.0% resistance were recorded against gentamicin. *Pseudomonas aeruginosa* strains were all susceptible to ofloxacillin but total antibiotic resistance (100%) were recorded for cloxacillin, augmentin, ciprofloxacin and fortum, while 71.4% and 85.7% antibiotic resistance were recorded for nitrofurantoin and claforan respectively. Lowest resistance of 14.3% was recorded for gentamicin.

The overall percentage multiple antibiotic resistance (%MAR) rates of 25.0%-100%, and respective %MAR for the condiment-borne bacteria were 25.0 - 75.0% (*Salmonella*), 25.0 - 87.5% (*Bacillus*, *E. coli*), 25.0 - 100% (*Micrococcus*), 37.5 - 100% (*Staphylococcus*), 50.0 - 87.5% (*Streptococcus*, *Pseudomonas*), 62.5 - 75.0% (*Enterobacter*, *Proteus*, *Shigella*), and 75.0% - 87.5% (*Klebsiella*). A total of 80.8% (n = 43.9% Gram-positive: n = 36.9% Gram-negative) of the condiment-borne bacterial strains displayed ≥50.0% MAR. More of the Gram-positive bacteria had 50.0-87.5%, while the Gram-negative bacteria had more 62.5-75.0% MAR (Table 2).

As shown in Table 3, most of the condiment-borne bacterial species were multi drug resistant (MDR) (Gram-positive = 17.52% Gram-negative = 26.28%) and extensively drug resistant (XDR)

(Gram-positive = 25.55% Gram-negative = 16.0%), while just 6.57% exhibited co-drug resistance (CDR). Only five (3.62%) strains of the condiment-borne bacterial strains (n = 0.7% Gram-positive: n = 2.9% Gram-negative) exhibited mono-resistance but six (Gram-positive = 4.37%) were totally (100%) resistant, i.e., pandrug-resistant (PDR).

4.0 DISCUSSION

As earlier suggested by Abriouel *et al.* [34], using all types of guidelines to perform risk assessments, there is need for closer investigations on the antibiotics-in-food safety. So, in this study, narrow and broad-spectrum test antibiotics (belonging to the aminoglycosides, macrolides, penicillins, tetracyclines, quinolones, etc.), which are the classes of antibiotics commonly administered as prophylactic or /and therapeutic agents in human clinical cases, were incorporated into discs, ideally for antibiotic susceptibility testing. Tremendous resistance to the test antibiotics, by both the fermenting and other associated bacterial flora of the ethnic fermented food condiments were also indicated in this study. In an earlier related study [35-38], which was the first study that ascertained massive multi-resistance by condiment-borne bacterial flora to commonly administered antibiotic medications in human and animal prophylaxis and therapy, significant multi resistance to 2-15 of 18 antibiotic drugs were recorded. Only 2.9% of the bacterial strains were totally susceptible to the 18 antibiotic medications, and even, the bacterial strains that were susceptible had more of minimal (narrow zones of inhibition) susceptibility values.

Only 3.62% of the condiment-adapted bacterial strains were mono-resistant, while none of the strains was totally susceptible to the test antibiotics. In spite of their special link to cultural socio-nutrirional profiles, consumers unknowingly and inadvertently ingest large viable populations of multi-antibiotic resistant bacteria along with the fermented foodcondiments. Food as means of vehicle can considerably play significant role in facilitating infection, by protecting the foodborne pathogens from the effects of the stomach's acidity [39-40]. So, contrary to the findings of Salminen *et al*. [41], antibiotic resistance in fermenting and associated condiment-borne bacterial cannot be beneficial in these regards. Preservation and safeguarding of food are still the major objectives of food fermentation [42], which is typically carried out by the performance of each single microbial strain or mixed cultures, consisting of multiple microbial species or strains, in isolation and in synergy or antagonism with other strains, as the microbial consortia ultimately determine the final fermented food products, especially from cottage and industrial fermentation perspectives.

Nowadays, terms such as, extensive drug resistance (XDR), and pan drug resistance (PDR) are commonly used to exhibit the depth of bacterial resistance [43]. Co-resistance refers to the presence of resistance to more than one class of antibiotics in the same bacterial strain. MDR was defined as acquired resistance to at least one antibiotic in three or more antibiotic classes, XDR was defined as resistance to at least one antibiotic in all but two or fewer antimicrobial classes (i.e., bacterial isolates is susceptible to only one or two classes of antibiotics), while PDR was defined as resistance to all antibiotics in all antibiotic classes [43, 44]. In the era of multidrug-resistant (MDR), extensively drug-resistant (XDR) and even pandrug-resistant (PDR) bacteria, the medical community is facing the threat of untreatable infections [44, 45]. According to Zwietering *et al*. [46], if a hazardous microorganism is found in a finished food product, it means something but, absence of microbes in a limited number of food samples is no guarantee of safety of a whole production batch.

Dietary habits have been found to affect the composition of human faeces, and even linked to colon cancers through faecal water genotoxicity [47], since evidence suggested that intestinal microbiota highly contributes to the balance by induction of chronic inflammation, due to bacterial infections and /or production of toxic bacterial metabolites [48-52]. Transfer of antimicrobial resistance genes between bacteria after ingestion by humans may occur, and under minimal processing or preservation treatment conditions, sublethally damaged or stressed cells can be maintained in the food, inducing antimicrobial resistance build-up, which can enhance the risk of antimicrobial resistance transfer [53]. Furthermore, indicator bacterial species belonging to the Enterobacteriaceae had been reportedly diverse in water used for cottage-production of the ethnic fermented food condiments, and the fermented condiments [29].

The quality, safety and acceptability of the traditional fermented food condiments have been reportedly significantly improved by the use of starter cultures [54, 55], selected on the basis of multifunctional considerations [42], as well as being natural food products that appeal to the consumers, who often doubt the safety of synthetic chemical food additives [38]. Thus, in the presence of multidrug-resistant (MDR), extensively drug-resistant (XDR), and even pandrug-resistant (PDR) fermenting and associated bacterial strains, dependence of traditionally fermented food condiments on inoculation from previous fermented batch, as starter cultures, can also lead to enhancement and transference of antibiotic resistance virulence, while growth-detrimental interactions on the fermenting bacterial species are also possible. Bacteria can transfer from food to the GIT microbiota, and antimicrobial resistance gene transfer can then occur between the GIT microbiota, in the favourable conditions of the GIT [56], and thus, present a public health risk of foodborne diseases [57]. Antibiotic resistance genes are then vertically passed to the next generation of microbes; while in some cases, they are acquired through horizontal transfer from one microbe to another, when thriving in the same microbial environment [58, 59].

Food safety and quality depend on many specific factors, including favourable or harmful microbial properties [60], one of which is, foodborne microbial flora habouring antimicrobials and transferable antimicrobial resistance genes that can be involved in antimicrobial residues in foods. As highly important and popular as ethnic fermented food condiments are world-wide, available data highlighted some notable exceptions where they have been associated with bacterial pathogens implicated in outbreaks of foodborne illnesses [28, 31, 61], most likely due to contaminations during processing. Some traditional products, especially in developing countries, represent a huge reservoir of antimicrobial resistance genes, and even, microbes used as probiotics are not exempted from acquiring antibiotic resistance genes [62-65]. These have prompted food safety concerns in the food industries, leading to regulatory interventions in some cases.

As the world is running out of antibiotics [66], and emergence of resistance to multiple antimicrobial agents in pathogenic bacteria has become a significant public health threat, as there are fewer, or even sometimes no, effective antimicrobial agents available for infections caused by these bacteria [43]. Assaying for antibiotics-profiles of condiment-adapted-bacterial species, especially those selected as starter and probiotic cultures are strongly suggested, based on the findings of this study.

5.0 CONCLUSION

This study clearly demonstrates that the indigenous fermenting and associated bacterial flora in easily contaminated samples of three Nigerian cottage-produced fermented condiments, *iru*, *ogiri* and *okpehe* (*afiyo*) have successfully adapted to antibacterial resistance properties. Screening of the finished products of Nigerian indigenous fermented food condiments by antibiotic susceptibility and resistance testing, as a control measure, provided information not only on the lack of bacterial safety status of the ethnic fermented vegetable food condiments, but also on the tremendous resistance of the condiment-adapted bacteria to antibiotics (commonly administered in human prophylaxis and therapy). This easy-to-adapt antibiotic resistance screening method in the current study for food-condiment-borne bacteria, can certainly serve as a fermented-food microbiological risk and safety assessment tool.

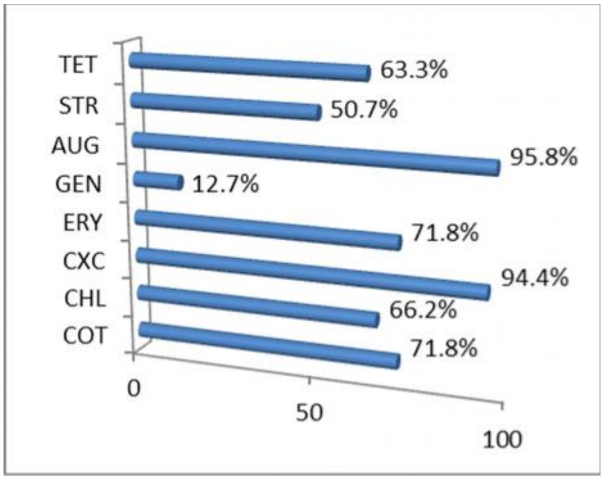

Fig. 4a: Overall percentage antibiotic resistance rates of Gram-positive bacterial species

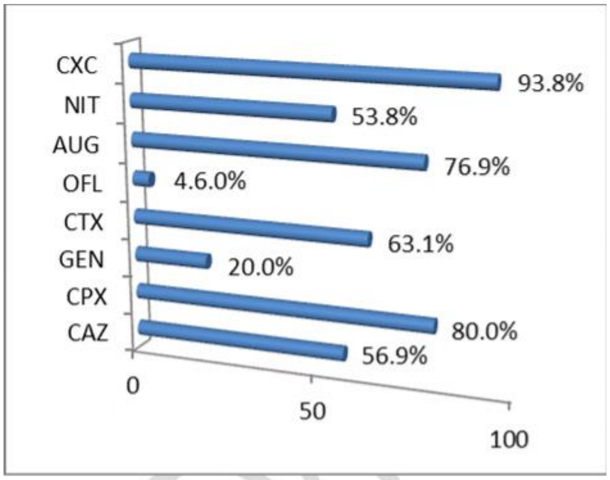

Fig. 4b: Overall percentage antibiotic resistance rates of Gram-negative bacterial species

Legends: COT = cotrimoxazole; CHL = chloramphenicol;CXC = cloxacillin; ERY = erythromycin; GEN = gentamicin;AUG = augmentin; STR = streptomycin;TET = tetracycline, CAZ = fortum; CPX = ciprofloxacillin; GEN = gentamicin; CTX = claforan; OFL = ofloxacillin; AUG = augmentin; NIT = nitrofurantoin; CXC = cloxacillin.

Table 1: Spatial distributions of percentage mono- and multi- antibiotic resistance rates among fermented-food-condiment-environment-adapted bacteria

Bacterial spp.	Percentage antibiotic resistance rates									
	0.0%	≥15.0%	≥25.0%	≥35.0%	≥50.0%	≥60.0%	≥70.0%	≥80.0%	≥90/0%	100%
Bacillus [12]			Gen (16.7%) Strep (25.0%)	Cot (41.7%)	Chl, Tet (50.0%)	Ery (66.7%)				Aug, Clx
Micrococcus [13]		Gen (14.3%)			Chl, Strep, Tet (57.4%)	Cot, (64.3%)	Ery, (71.4%)			Aug, Clx
Staphylococcus [23]			Gen (21.7%)			Chl, Cot, Str, Tet (69.6%)	Ery (73.9%)	Aug (87.0%)		Clx
Streptococcus [22]		Gen (4.68%)			Str (59.1%)	Ery (68.2%)	Chl (77.3%)	Tet, (81.8%)	Clx, Cot (90.9%)	Aug
Enterobacter [4]	Ofl (0.0%)		Gen (25.0%)				Caz, Cpx, Ctx, Nit (75.0%)			Aug, Cxc
E. coli [15]		Ofl (13.3%)	Gen (26.7%)	Nit (40.0%)		Cpx, Ctx (66.7%)		Aug (80.0%)	Cxc (93.3%)	Caz
Klebsiella [2]	Gen (0.0%)				Ofl (50.0%)					Aug, Caz, Cpx, Ctx, Nit
Salmonella [29]	Ofl (0.0%)		Gen (20.7%)	Nit (48.3%)	Ctx (55.2%)	Aug (62.1%)	Caz, Cpx (72.4%)		Cxc (93.1%)	
Shigella [6]	Gen (0.0%)	Ofl (16.7%)		Nit (33.3%)	Ctx (50.0%)	Aug, Caz (66.7%)		Ctx (85.7%)		Cxc, Cpx
Proteus [4]	Ofl (0.0%)				Ctx, Gen (50.0%)		Nit (75.0%)			Aug, Caz, Cpx, Cxc
Pseudomonas [7]	Ofl (0.0%)	Gen (14.3%)					Nit (71.4%)			Aug, Caz, Cpx, Cxc

Legends: Cot = cotrimoxazole; Chl = chloramphenicol;cxc = Cloxacillin; Ery = erythromycin; Gen = Gentamicin;aug = augmentin;
Str = streptomycin; Tet = tetracycline.
Caz = fortum; cpx = Ciprofloxacillin; Gen = gentamicin; Ctx = claforan; Ofl = ofloxacillin; Aug = augmentin; Nit = nitrofurantoin;
Cxc = cloxacillin.

Table 2: Overall percentage antibiotic resistance rates and patterns of fermented-food-condiment-environment-adapted bacterial flora

Condiment-borne bacterial species	% Antibiotic resistance rates								
	12.5*	25.0	37.5	**50.0**	**62.5**	**75.0**	**87.5**	**100**	**≥50.0**
Gram-positive spp.									
Bacillus [12]	-	3	-	**4**	**2**	-	**3**	-	[9] **6.52%**
Micrococcus [14]	-	1	1	**5**	**1**	**1**	**3**	**2**	[**12**] **8.70%**
Staphylococcus [23]	-	-	4	**1**	**4**	**4**	**7**	**3**	[**19**] **13.77%**
Streptococcus [22]	1	1	-	**2**	**3**	**6**	**8**	**1**	[**20**] **14.49%**
Total [**71**]	1	5	5	**12**	**10**	**11**	**21**	**6**	[**60**] **43.48%**
% Total	0.72%	3.62%	3.62%	**8.70%**	**7.25%**	**7.97%**	**15.22%**	**4.35%**	[51.39%]
Gram-negative spp.									
Enterobacter [4]		-	-	-	**3**	**1**	-	-	[4] **2.90%**
E. coli [15]	-	2	1	**1**	**8**	**2**	**1**	-	[12] **8.70%**
Klebsiella [2]	-	-	-	-	-	**1**	**1**	-	[2] **1.45%**
Salmonella [29]	2	2	7	**2**	**9**	**7**	-	-	[18] **13.0%**
Shigella [6]	2	-	-	-	**2**	**2**	-	-	[4] **2.90%**
Proteus [4]	-	-	-	-	**1**	**3**	-	-	[4] **2.90%**
Pseudomonas [7]	-	-	-	**1**	**2**	**3**	**1**	-	[7] **5.07%**
Total [**67**]	4	4	8	**4**	**25**	**19**	**3**	-	[**51**] **36.96%**
% Total	2.9%	2.9%	**5.8%**	2.9%	**18.1%**	**13.8 %**	2.17%	0.0%	[48.57%]

Legend: * = mono-resistance

Table 3: Percentage antibiotic resistance profiles of fermented-food-condiment-environment-adapted bacterial flora

Condiment-borne bacterial species	% Multiple antibiotic resistance profiles				Total ARP
	CDR (25.0%)	MDR (37.5-62.5%)	XDR (75.0-87.5)	PDR (100%)	Total
Gram-positive spp.					
Bacillus [12]	3	6	7	1	[17] 12.41%
Micrococcus [14]	1	6	4	2	[13] 9.49%
Staphylococcus [23]	-	8	10	2	[20] 14.6%
Streptococcus [22]	1	4	14	1	[20] 14.6%
Total [71]	5	24	35	6	[70] 51.1%
% Total	3.65%	17.52%	25.55%	4.38%	(51.1%)
Gram-negative spp.					
Enterobacter [4]	-	3	1	-	[4] 2.91%
E. coli [15]	2	10	3	-	[15] 10.95%
Klebsiella [2]	-	-	2	-	[2] 1.46%
Salmonella [29]	2	17	7	-	[26] 18.97%
Shigella [6]	-	2	2	-	[4] 2.91%
Proteus [4]	-	1	3	-	[4] 2.91%
Pseudomonas [7]	-	3	4	-	[7] 5.10%
Total [66]	4	36	22	-	[62] 45.21%
% Total	2.92%	26.28%	16.0%	0.0%	(45.2%)
Overall % Total	6.57%	43.80%	41.55%	4.38%	[132] **96.35%**

Legends: CDR = co-drug resistance; MDR = multi drug resistance XDR = extensive drug resistance; PDR = pan drug resistance.

Conflict of interest

Author declares no conflict of interest

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