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Safety Assessment of Traditional Ready-to-Eat Meat Products Vended at Retail Outlets in Kebbi and Sokoto States, Nigeria

M. I. Ribah, M. Jibir, Y. A. Bashar, S. S. Manga

Abstract**—**Food safety is a significant and growing public health problem in the world and Nigeria as a developing country, since food-borne diseases are important contributors to the huge burden of sickness and death of humans. In Nigeria, traditional ready-to-eat meat products (RTE-MPs) like balangu, tsire, guru and dried meat products like kilishi, dambun nama, banda, were reported to be highly appreciated because of their eating qualities. The consumption of these products was considered as safe due to the treatments that are usually involved during their production process. However, during processing and handling, the products could be contaminated by pathogens that could cause food poisoning. Therefore, a hazard identification for pathogenic bacteria on some traditional RTE-MPs was conducted in Kebbi and Sokoto States, Nigeria. A total of 116 RTE-MPs (balangu-38, kilishi-39 and tsire-39) samples were obtained from retail outlets and analyzed using standard cultural microbiological procedures in general and selective enrichment media to isolate the target pathogens. A six-fold serial dilution was prepared and using the pour plating method, colonies were counted. Serial dilutions were selected based on the prepared pre-labeled Petri dishes for each sample. A volume of 10-12 ml of molten Nutrient agar cooled to 42-45°C was poured into each Petri dish and 1 ml each from dilutions of 102, 104 and 106 for every sample was respectively poured on a pre-labeled Petri plate after which colonies were counted. The isolated pathogens were identified and confirmed after series of biochemical tests. Frequencies and percentages were used to describe the presence of pathogens. The General Linear Model was used to analyze data on pathogen presence according to RTE-MPs and means were separated using the Tukey test at 0.05 confidence level. Of the 116 RTE-MPs samples collected, 35 (30.17%) samples were found to be contaminated with some tested pathogens. Prevalence results showed that Escherichia coli, salmonella and Staphylococcus aureus were present in the samples. Mean total bacterial count was 23.82×106 cfu/g. The frequency of individual pathogens isolated was; Staphylococcus aureus 18 (15.51%), Escherichia coli 12 (10.34%) and Salmonella 5 (4.31%). Also, among the RTE-MPs tested, the total bacterial counts were found to differ significantly ($P < 0.05$), with 1.81, 2.41 and 2.9×104 cfu/g for tsire, kilishi, and balangu, respectively. The study concluded that the presence of pathogenic bacteria in balangu could pose grave health risks to consumers, and hence, recommended good manufacturing practices in the production of balangu to improve the products' safety.

M. I. Ribah is with the Department of Animal Science, Kebbi State University of Science and Technology, Aliero, Nigeria (corresponding author, phone: +234 7036333707; e-mail: ibrahim.ribah73@gmail.com).

M. Jibir and Y. A. Bashar are Professors with the Department of Animal Science, Usmanu Danfodiyo University, Sokoto (e-mail: mjibir@gmail.com, byahaya40@yahoo.ca).

S. S. Manga is with the Department of Microbiology, Kebbi State University of Science and Technology, Aliero, Nigeria. (e-mail: ssmanga2000@yahoo.com).

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I. Introduction

IN Nigeria, RTE-MPs including intermediate moisture meats like *balangu, tsire, guru* and dried meat products like *kilishi, dambun nama, banda*, were reported to be highly appreciated because of their characteristic taste, texture and storage stability [1]. The consumption of these products have been considered by [2] as safe due to the treatments that are usually involved during their production. However, [3] reported that during processing, handling, packaging and storage, these products are liable to contamination by pathogenic biological agents that could result in food poisoning.

The pathogenic microorganisms present in a food may be contributed by its own natural microflora or from the processing conditions like in the course of harvesting, manufacturing, storage, and transport. In some cases, the microflora has no discernible effect on the food quality and food safety, while in others they may affect the quality in several ways like causing food spoilage, food borne illness or food fermentation [4]. Several risk assessments conducted revealed that such pathogenic microorganisms include *Salmonella species, Campylobacter, Listeria monocytogenes, Escherichia coli, Staphylococcus aureus, Clostridium botulinum, Clostridium perfringens, Bacillus cereus, Brucella species, Vibrio Species, Yersinia enterocolitica, Streptococcus pyogenes*, *Shigella dysenteriae* and many other microorganisms associated with food poisoning [3].

These microorganisms were collectively included in the World Health Organization's (WHO) list of foodborne pathogens [5] and were reported to be the most important bacteria species in terms of public health risk and frequency of appearance in foodstuffs [6]. Consumer surveys revealed that a major source of concern, with respect to public health, is the unhygienic conditions under which meat products are often processed and retailed in Nigeria and other West African countries. For products such as *suya* and *kilishi*, the spices used in their processing are potential sources of microbial contamination. Microbial populations including coliforms exceeding acceptable limits for RTE-MPs and the presence of a wide spectrum of pathogenic bacteria have been reported in retail suya [7].

Several studies [8]-[15] have documented the presence of foodborne pathogens in different food products ranging from

raw retail meat to processed meat products. This suggests that consumers are at potential risk of *S. aureus* infection. Existence of foodborne pathogens in food products poses potential hazard for consumers' health, economic loss and loss in human productivity via food-borne disease infection. Therefore, the objective of this current study is to conduct hazard identification for pathogenic bacteria on some traditional RTE-MPs in North-Western Nigeria.

II. Materials and Methods

A. Study Area

The study was conducted in Kebbi (A) and Sokoto States (B), North-West region of Nigeria. The study area is located between Latitudes 11°30' and 12°16'N, and Longitudes 4°00' and 6°25'E. Sokoto and Kebbi States lies in the Savanna regions of Nigeria with its characteristic grasslands and isolated hills. The study area has an annual average temperature of 28.3°C and the maximum daytime temperature could reach a little above 40°C [16].

The area is known for its abundance of livestock especially the popular Sokoto *Gudali*, *Uda* and *Yankasa* sheep, Sokoto red goat, and many poultry species like domestic fowls, guinea fouls and turkeys, and many other breeds of livestock [17]. According to [18], among all the livestock that makes up the farm animals in Nigeria, ruminants, comprising sheep, goats and cattle, constitute the farm animals largely reared by farm families in the country's agricultural system

The states have a variety of animal products that are obtained from the vast kinds of animals available in the region of which meat products predominates [11]. This could be evident from the many RTE meat joints sighted along major roads in both urban and rural areas of the region [19].

B. Sampling of RTE-MPs and Sample Size

The Trunk 'A1 and A26' Federal Highway, cutting across the study area served as the reference Transect along which sampling locations were mapped. RTE-MPs processors and consumers were sampled from strategic locations comprising all the metropolitan, Local Government Headquarters and areas of special interest in meat trading along the transect. The number of processors in each sampling location was obtained from leaders of the RTE-MP processors' Cooperatives and Unions in the respective locations. Fig. 1 shows the GPS map of the sampling transect.

A total of 116 samples (balangu-38, kilishi-39 and tsire-39) were obtained from all the sampling locations in the study area as indicated in Table I. Three samples (which might be a mixture of many or one type of RTE-MP) were randomly selected from the location (AB1) having the least number of processors and then proportionately increased the number of samples according to the number of processors in each sampling location. The samples were transferred in clean polythene bags and transported, as described by [21], to the laboratory for further analysis.

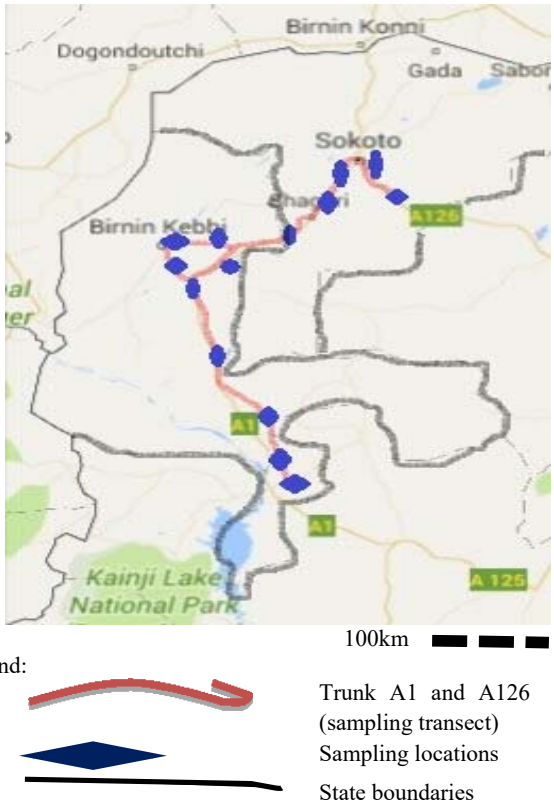

Fig. 1 Map showing the study area, sampling transect and sampling locations [20]

C. Microbiological Procedures

Microbiological analyses were conducted according to the procedures described by [22]. The microbiological analyses involved isolation in general (non-selective) and selective media for isolation and identification of isolates, followed by series of biochemical tests for confirmation of isolates.

25 g of each RTE-MP sample was picked, minced and homogenized. Then 1 g of the homogenized sample was weighed out and homogenized in 9 ml of buffered peptone water (LabM, UK) and hand shaken for two minutes to give a dilution of 1:10. A six-fold serial dilution was then prepared by pipetting 1 ml of the homogenate into the first test tube containing 9 ml of buffered peptone water to make the first dilution. From the first dilution, 1 ml was taken and pipetted into the second test tube containing 9 ml of diluent. The process was repeated until the sixth dilution was made and 1 ml from the last dilution was removed and discarded.

The pour plating method was used for colony counting. Petri dishes were prepared and labelled according to samples and dilutions selected. For aerobic plate count determination, about 10-12 ml of the molten Nutrient agar (Biomark, India) (cooled to 42-45°C) was poured into each Petri dish within 15 minutes from the time of preparation of the original dilution. 1 ml each from dilutions 10^2, 10^4 and 10^6 for every sample was respectively poured on a pre-labeled Petri plates. The media and dilutions were mixed gently swirling clockwise and anticlockwise, to and fro taking care that the mixture did not touch the lid and was allowed to set. The plates were

incubated inverted for 48 hrs at 35°C. Distinct colonies on plates were counted using a digital colony counting chamber (Quebec colony counter, Reichert, USA) and recorded per dilution counted. The actual number of colonies on dishes containing 30-300 colonies was counted and recorded. For dishes having more than 300 colonies, the dish was divided into four using a marker behind the dish, and a quarter of the dish was counted and multiplied by four to estimate the number of colonies on the dish. Dishes with congested growth were not considered.

TABLE I
LAYOUT FOR SAMPLING OF RTE-MPS

States	Sampling Locations	Number of RTE-MP Processors	Number of RTE-MP Samples
A B	AB1	8	3
	AB2	29	11
	AB3	22	8
	AB4	12	5
	AB5	25	9
	AB6	9	3
	AB7	47	18
	AB8	14	5
	AB9	10	4
	AB10	22	8
	AB11	18	7
	AB12	9	3
	AB13	67	25
	AB14	19	7
Total	**14**	**310**	**116**

AB= Study Area
AB1-AB14 = Sampling Locations

D. Identification and Confirmation of Salmonella spp.

Twenty five grams of the test sample was weighed into an empty wide sterile container with screw cap for pre-enrichment. Trypticase soy broth of 225 ml was added to the sample and thoroughly shaken to homogenize the suspension. The mixture was capped and allowed to stand for 60 min at room temperature. The mixture was incubated for 24±2 hrs at 35°C.

For selective enrichment, the incubated sample mixture was shaken 1ml was transferred to 10 ml of Selenite Cystine Broth and an additional 1ml to Tetrathionate Broth. The mixtures were incubated for 24±2hrs at 35°C. For selective media plating, the incubated selenite cystine broth was mixed using a vortex mixer and streaked with a 3 mm loopful on selective media plates of *Salmonella Shigella* agar (SSA). The incubated Tetrathionate Broth was also streaked on SSA. The SSA plates were incubated at 35°C for 24±2hrs and 48±2hrs. After incubation, plates were observed for typical *Salmonella* colonies with color changing from yellow to red or pink.

The typical colonies were picked with a needle. From the SSA plate and inoculated into a triple sugar iron agar (TSI) slant, streaked the slant and stabbed the butt and incubated for 24±2hrs at 35°C with loosely capped tubes to prevent excessive H_2S production. The reactions were observed.

To confirm *salmonella*, presumptive positive culture on the TSI slants were picked with a needle and inoculated into the following broths: urea broth, tryptone broth, potassium cyanide (KCN) broth, malonate broth and Methyl Red/Voges-Proskauer (MR/VP) broth. The reactions were observed. Results were expressed as presence or absence per 25 g of sample denoted by "1" or "0", respectively.

E. Identification and Confirmation of Escherichia coli

For pre-enrichment, 25g of the test sample was weighed into an empty wide sterile container with screw cap. Sterile Trypticase soy broth of 225 ml was added to the sample and thoroughly shaken to homogenize the suspension. The mixture was capped and allowed to stand for 60 min at room temperature and incubated for 24±2hrs at 35°C. Three tubes of Lauryl Sulphate Tryptose (LST) broth were inoculated with 1ml of the homogenate and incubated for 24-48hrs at 35±0.5°C. Tubes showing gas production after 24 hrs were recorded and negative tubes were re-incubated for 24 hrs. Then, all tubes showing gas production were recorded. Gas production indicated presumptive coliforms.

To confirm coliforms, one loopful from each gas positive tube of LST was transferred to a separate tube of Brilliant-Green Lactose Bile (BGLB) broth and incubated for 48±2hrs at 35±0.5°C. The formation of gas confirms the presence of coliform bacteria. Hence, to test for *Escherichia coli,* one plate of Eosin Methylene Blue (EMB) agar was streaked from positive BGLB tube in a way to obtain discrete colonies and incubated for 24±2hrs at 35±0.5°C. The plate was examined for typical nucleated green metallic sheen. Two colonies were picked from each EMB plate and transferred to PCA slants and incubated at 35±0.5°C for 24 hrs. To confirm *E. coli*, colonies were transferred from PCA slants for biochemical tests. Results were expressed as presence or absence per 25 g of sample denoted by "1" or "0", respectively.

F. Identification and Confirmation of Staphylococcus aureus

The pre-enrichment was carried out by 25 g of the RTE-MP into a sterile jar and 225 ml of buffered peptone water was added. The jar was capped and shaken thoroughly for two minutes. Next, 1 ml of the Homogenate was pipetted in 9ml of peptone water and mixed well using a vortex mixer. Then, 1 ml of the homogenate was transferred into triplicate plates of Mannitol salt agar (MSA). The plates were incubated in an upright position in an incubator at 35-37°C for about 1 hr or until inoculum is absorbed by the medium, then the plates were inverted and incubated for 45-48 hrs. Catalase and coagulase tests were used to confirm *S. aureus.*

G. Biochemical Tests

Identification of isolates was conducted based on established conventional cultural, morphological and biochemical characterizations. The biochemical tests conducted were Gram staining, Mannitol salt ager, EMBA, SSA, Urease reaction test, sugar fermentation using TSI, Indole, citrate, MR VP test catalase and coagulate tests using methods described by [23].

H.Data Analysis

Determination of Total Bacterial Count and Prevalence of Pathogens in RTE-MPs

The colony forming unit per gram of the samples was calculated and results expressed as colony forming unit per gram of meat sample (cfu/g) using the following expression by [21]:

$$CFU= \Sigma C / [(N1 + 0.1\ N2)D] \quad (1)$$

where: CFU = colony forming units, ΣC = sum of all the colonies counted on all dishes retained, N1 = number of dishes retained in first dilution, N2 = number of dishes retained in the second dilution, 0.1 = constant, D = dilution factor corresponding to the first dilution.

The overall total bacterial count and prevalence of pathogens were determined after isolation, identification and confirmation of the isolates from all the 116 samples of RTE-MPs. The presence of tested pathogens in a sample was indicated with a value of "1" and "0" represented absence of tested pathogens. Total bacterial count was expressed in mean cfu/g, while general and pathogen specific prevalence results were expressed in frequencies and percentages. The prevalence of the pathogens according to the RTE-MPs was subjected to analysis of variance and differences were separated using the Tukey test at 5% level of significance.

III. Results and Discussion

A. Bacterial Load and Presence of Some Pathogens in Some RTE Meat Products

Culture test methods revealed the presence of *Escherichia coli*, *Salmonella* and *Staphylococcus aureus* in the observed RTE-MPs samples as shown in Table II. The mean total bacterial count (TBC) obtained from all the samples according to locations ranged between 21.22×10^6 cfu/g. Out of the 116 RTE-MPs samples collected, 35 samples were found to be contaminated with pathogens. The frequency of the individual pathogens isolated out of the contaminated samples include *Staphylococcus aureus* 18 (51.42%) in 10^4 dilution, *Escherichia coli* 12 (34.29%) in 10^2 dilution and *Salmonella* 5 (14.29%) in 10^2 dilution.

The current study revealed total bacterial counts of between log 3.5 10^6 cfu/g to log 63.0×10^6 cfu/g according to the sampling locations with an overall mean of log 21.22×10^6 cfu/g. This could suggest the high level of unhygienic processing and handling of the RTE meat product as reported by [24]. The total bacterial count of up to log 21.22×10^6 cfu/g in the current study was much higher than the $2.05\text{-}2.89\times10^6$ cfu/g reported by [25], log 8.08 cfu/g [13], $0.3\text{-}0.85\text{x}10^5$ [12] and 7.17 x 10^6 cfu/g [11]. The variation in the TBC could not be unconnected with the number of samples, the size of the area covered and the nature of the covered area. Most of the previous studies covered only state capitals (urban) where the handling of the products could be better monitored than the rural areas due to the greater awareness of safety issues by who are expected to be more educated. The current study, on the other hand, covered 12 locations (rural areas) besides the two state capitals.

The overall presence of the isolated pathogens (*Staphylococcus aureus, Escherichia coli* and *Salmonella*) from RTE-MPs in the current study was from 35 out of 116 samples. Hence, the presence of these organisms depicts the poor sanitary practices employed in the slaughtering, processing and packaging of the RTE meats [26], [27]. The pathogens were classified among the indicator bacteria for RTE foods by [24]. According to [24], the presence of indicator bacteria in ready-to-eat food can be indicative of poor practice that may be as a result of one or a mixture of the following factors: poor quality of raw materials or food components, undercooking, cross-contamination, poor cleaning, poor temperature and time control, and that indicator bacteria may be associated with an increased likelihood of the presence of other pathogens. Consequently, the total and individual presence of the isolated pathogen could be connected to all of these factors which have consistently been observed to be characteristic of the study area.

TABLE II
Bacterial Load and Presence of *Staphylococcus Aureus, Escherichia Coli* and *Salmonella* in RTE-MPS

LCT	SS	TBC	Frequency of Isolates			TOT.
			S. aureus	*E. coli*	*S.* spp	
AB1	3	12.67	0	1	1	2
AB2	11	11.27	1	1	0	2
AB3	8	16.50	2	1	0	3
AB4	5	22.60	2	1	0	3
AB5	9	15.00	2	1	1	4
AB6	3	29.67	1	0	0	1
AB7	18	15.76	8	7	3	20
AB8	5	29.00	1	0	0	1
AB9	4	3.25	0	0	0	0
AB10	8	27.63	0	0	0	0
AB11	7	63.67	0	0	0	0
AB12	3	50.14	0	0	0	0
AB13	25	19.96	0	0	0	0
AB14	7	16.29	1	0	0	1
TOT. Pres. (%)	**116**	**21.22**	**18 (51.42)**	**12 (34.29)**	**5 (14.29)**	**35 (100)**

LCT= LocationSS= sample size TBC= total bacterial count TOT=total Pres.=presence *S. aureus*= ***Staphylococcus aureus*** ($\times10^4$ cfu/g), E.coli= ***E. coli*** ($\times10^2$ cfu/g), *S.* spp = ***Salmonella*** ($\times10^2$ cfu/g)

Several studies have documented presence of *S. aureus* in many food products including raw retail meat and processed meat products indicating that consumers are at potential risk of *S. aureus* colonization and subsequent infection. The level of *S. aureus* in RTE-MPs in the current study revealed a 51.42% incidence representing the most prevalent among the isolated pathogens. Previous studies reported the presence of the pathogen with inconsistent frequencies ranging from lower to high numbers in RTE foods, 17.2% in retail RTE-MPs [28], 17.4% in RTE rice [29], 46% in fresh raw chicken, beef, goat and pork meat [27], 5.98% in RTE-MPs [30], 10.7% in *balangu* [31], 62% in suya [13], 13.9% [32], 16.7% in RTE meats [33], 29.9% in roasted meat [34]. The consistent

presence of *S. aureus* across locations may not be unconnected with the fact that it survives in the environment, on handlers' body and packaging materials [35], and can hence, cross-contaminate post-lethality exposed products. Furthermore, *S. aureus* was reported to be uniquely resistant to adverse conditions like osmotic stress, low water activity and high salt concentration [36]. All these attributes could give the pathogen additional advantage of survival and cross-contamination of RTE foods; hence, its higher presence.

Escherichia coli had been reported to be an important pollution indicator and its pathogenic strains are of a serious public health concern. *Escherichia coli* is known to be an indicator of faecal contamination, and its presence in food indicates the possible presence of other enteric pathogens. Some of the *E. coli* strains itself are highly pathogenic in human and animals [37]. The presence of *E. coli* in RTE foods has been established by many research works. The high presence of *E. coli* could be as a result of inadequate processing or through cross contamination by handlers, environment or utensils. The results relatively conform to some previous reported research results on RTE meats such as the report of [31] (7.1% in *balangu* meat) and [38] (11.1%). Higher incidences (25%) had also been reported by [39], [40] (40% in sandwiches) and [13] reported 64% in suya.

The presence of *Salmonella* (14.29%) in the present study was higher than was found in other related findings in different RTE foods such as the 3.0% in chicken, turkey, pork, and beef [41], 2.2% in raw and RTE turkey meat products [42], 2.0% in fresh raw chicken, beef, goat and pork meat [27], 3.5% in balangu [31] and [14] reported 2.3% in beef and related meat products. A higher presence of *Salmonella* (20%) was also reported by [38], 47% in suya [13], 26% in RTE-MPs [43], 31.1% in RTE-MPs [39], 33% in poultry meat [44], 7.2 % in local foods [45], and [46] reported 18% in fish and meat products. The variability in the presence of *Salmonella* might be due to the assertions of [45] that the predominance and distribution percentage of *Salmonella* serotypes in foods varies in different regions of the world according to the methods of isolation, quality of sample and growth characteristics of the serovars, particularly those adapted to a host species, and also the factors highlighted by [8], [24].

Generally, it was observed that the high presence of the pathogens was mostly reported by researchers from developing countries, as in the case of [38], [13], and [46], indicating the possible influence of regulatory agencies and adoption of HACCP in the developed world which is critically lacking in most developing countries.

B. Bacterial Load and Presence of Escherichia coli, Staph. aureus, and Salmonella According to RTE-MPs.

Table III shows the bacterial load and presence of some pathogenic bacteria isolated from some RTE-MPs. There were significant differences (P<0.05) between the RTE-MPs on the total bacterial count (TBC). The bacterial counts ranged between 1.81×10^4 cfu/g and 2.9×10^4 cfu/g. Also, there was significant differences (P<0.05) between the RTE-MPs on the presence of *Escherichia* ($0.08–0.11\times10^2$ cfu/g), *coli, Staphylococcus aureus* ($0.10–0.19\times10^4$ cfu/g) and *Salmonella* ($0.00–0.08\times10^2$ cfu/g) population isolated.

The total bacterial count obtained in the current study revealed that balangu had higher bacterial population (2.9×10^4 cfu/g). It was followed by Kilishi (2.41×10^4 cfu/g) and tsire which had the least counts (1.81×10^4 cfu/g). The variation in colony counts could be as a result of variations in processing methods where tsire, at post-lethality, is in most cases kept warm around the members of a fire which could assist in killing the bacterial population, unlike balangu and kilishi, which are usually displayed in open trays and table tops, making the products vulnerable to bacterial contamination. The lower counts in tsire and kilishi could also be due to the presence of spices added during processing which were reported to have significant anti-microbial and anti-oxidant effects [47], [48]. In most cases, balangu is processed without the addition of spices, which could be added while serving. Previous research works reported comparatively similar results for the products. Reference [49] recorded similar total plate counts in suya samples in the order of $\times10^5$ cfu/g and $\times10^6$ cfu/g. [11] isolated a range of $0.07–2.22\times10^5$ cfu/g from suya collected from different locations. In terms of public health significance, the results of the current study placed the studied RTE-MPs consumed in the study area within acceptable limits according to [50], [24] standards of up to log 9×10^6 in related RTE-MPs. However, the values obtained for individual bacteria indicated that the detection of *Salmonella* spp. in the RTE-MPs placed the products under unsatisfactory and potentially injurious to health and or unfit for human consumption according to [24].

TABLE III
BACTERIAL LOAD AND PRESENCE OF *ESCHERICHIA COLI, S. AUREUS,* AND *SALMONELLA* IN ACCORDING TO RTE-MPS

RTE-MPs	TBC	Presence of pathogens		
		Escherichia coli	*S. aureus*	*Salmonella*
Balangu	2.9^c	0.11^b	0.19^b	0.08^b
Kilishi	2.41^b	0.08^a	0.12^a	0.08^b
Tsire	1.81^a	0.08^b	0.10^a	0.00^a
SE	**0.076**	**0.006**	**0.006**	**0.005**

a, b, c = means with different superscript along the same column within a subset differ significantly (P<0.05)

The values for *staphylococcus aureus* and *Escherichia coli* were however satisfactory since they were found to be within the limits of $<20\times10^4$ cfu/g and $<20\times10^2$ cfu/g, respectively, recommended by [24] to be the satisfactory limits of the two isolated bacteria could be acceptable in RTE-MPs. In Nigeria, similar results were reported for various RTE-MPs such as [11] who recorded *E. coli* range of $0.12–0.24\times10^5$ cfu/g, *S. aueus* range of $0.53–1.67\times10^5$ in balangu. References [51], [52] reported $<1.0\times10^1$ of *E. coli* and 3.1×10^2 of *S. aureus* isolated from chicken RTE-MP. Higher isolates were recorded by [13] from suya with *E.coli* ranging between log 0.0 and 5.48×10^5 cfu/g, *S. aureus* ranging between log 0.0 and 6.25×10^5 cfu/g and *Salmonella* ranging between log 0.0 and 5.7×10^5 cfu/g. The current study revealed that balangu had higher TBC and individual bacterial counts than kilishi and

tsire. Incidentally, balangu was the most commonly consumed among the identified products in the study area.

IV. Conclusion

The bacterial hazards identified in the study included but were not limited to *Staphylococcus aureus, Escherichia coli* and *Salmonella* spp. to be prevalent in RTE-MPs in the study area, and hence, people are exposed to risks of infections. Also, of the three pathogens isolated, *Staphylococcus aureus* was found to be more prevalent across all locations. It was concluded that the bacteria identified are of public health significance and their presence in RTE-MPs poses health risks. Good manufacturing practices in the production and consumption of RTE-MPs were recommended to improve their safety and quality. The study recommended that the governments of the affected States should conduct full-scale risk assessment studies on RTE meat products in order to ascertain the levels of public exposure to foodborne pathogens, particularly of the hazards identified, and initiate a framework to protect public health by creating awareness to processors and consumers.

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Ribah, M. Ibrahim was born in Ribah, Kebbi State, Nigeria in 1976. He received his Ph.D in 2017 in Animal products technology at Usmanu Danfodiyo University, Sokoto, Nigeria.

He is currently a Faculty member at the Department of Animal Science in Kebbi State University of Science and Technology, Aliero, Nigeria, and has several publications on Animal products and.