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Assessment of the Microbial Quality of Locally Produced Meat (Beef and Pork) in Bolgatanga Municipal of Ghana

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Abstract

Meat microorganisms are one of the main sources of foodborne illnesses, possessing serious challenges in developing countries including Ghana. This study determined the microbial quality of 100 meat (50 beef and 50 pork) samples collected from meat retail shops in the Bolgatanga Municipality. The surfaces of fresh (50) and smoked (50) meat samples were swabbed using a cotton swab and stored under 4℃ for transportation to the Laboratory. The meat samples were analyzed immediately on arrival at the Laboratory under aseptic conditions for total aerobic bacteria. The surrounding environments of the retail shops were also observed. Total aerobic count for smoked and fresh beef ranged from 4.75 – 6.58 log cfu/g and that of pork ranged from 4.33 – 6.94 log cfu/g. Smoked pork from Zobisi had the highest microbial load of 6.94 log cfu/g, followed by fresh beef (6.56 log cfu/g) from Jolly hut and fresh beef (6.52 log cfu/g) from Central mosque. Bacterial species identified on the fresh and smoked beef, pork and guinea fowl meat samples were Staphylococcus spp., Escherichia coli, Streptococcus spp., Pseudomonas spp., Proteus spp., Klebsiella spp. and Bacillus spp. Generally, beef samples were more contaminated than pork samples. Staphylococcus spp. and Escherichia coli were the most common identified bacteria. Physical observation revealed that meat sellers were involved in unhygienic practices such as using of knives without sterilising them, wearing of dirty aprons/clothes and busily conversing while selling meat. The identification of Staphylococcus spp., Escherichia coli and the other organisms in the fresh and smoked meat samples is an indication of the presence of pathogenic foodborne pathogens

Key words: Beef, Fresh, Microbial quality, Pork, Smoked

Introduction

Foodborne infections still remain one of the major problems of public health worldwide. Meat is an excellent source of protein in human diet and highly susceptible to microbial contaminations (Komba et al. 2012). The consumption of meat has been linked to a number of human foodborne infections although muscles of healthy animals are essentially sterile and do not contain microorganisms (Warriss, 2000, Alvarez et al. 2009; Adzitey and Nurul, 2011). Meat tissues get contaminated during the various stages of pre and post slaughter (Warriss, 2000; Alvarez et al. 2009; Adzitey, 2011; Adzitey and Nurul, 2011; Adzitey and Huda, 2012).

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A great diversity of microbes inhabit fresh meat, but different types may become dominant depending on pH, composition, textures, storage temperature, and means of transporting raw meat (Li et al. 2006; Adams and Moss, 2008).

Raw meat may harbour many important pathogenic microbes such as Salmonella spp., Campylobacter species, Yesinia enterocolitica, Escherichia coli, Staphylococcus aureus and, to some extent, Listeria monocytogenes, making the meat a potential risk for human health (Li et al. 2006; Adzitey et al. 2012a; Adzitey et al. 2012b; Adzitey et al. 2013; Adzitey et al. 2014; Bogere and Baluka, 2014; Huang et al. 2014). Major spoilage organisms in raw meat and poultry are Pseudomonas spp., Shewanella spp., Brochothrix spp. and members of Enterobacteriaceae (Doulgeraki et al. 2012).

The meat available at retail outlets comes through a long chain of slaughtering and handling, where each step may

pose a risk of microbial contamination. The sanitary conditions of abattoirs and its surrounding environment are major factors contributing to bacterial contamination of meat (Gill et al. 2000). Contaminations can be compounded during transportation, storage and handling of meat at the butcher shops (Adzitey, 2011; Adzitey et al. 2011). In developing countries like Ghana, the abattoir environment, its sanitary level, transportation and storage conditions not only contaminate but also enhance the growth of different types of spoilage (Adzitey et al. 2011; Adzitey et al. 2014). This study assessed the microbial load of beef and pork sold at retail outlets in different areas of the Bolgatanga Municipality.

Material and Methods

Location, data collection and duration. The study was carried out in the Bolgatanga Municipality, which is the capital town of the Upper East Region of Ghana. Ten (10) meat retail points where people prefer to buy beef and pork in the Bolgatanga Municipality were sampled. The retail points were Stanbic, Starlife, Central mosque, Jolly hut, and Mobile clinic shops for beef; and Soe, Atulbabisi, Pobaga, Zobisi, and Dagbew for pork. A total of 100 meat (25 fresh beef, 25 fresh pork, 25 smoked beef and 25 smoked pork) samples were examined. Ten (10) meat (5 fresh and 5 smoked) samples were collected from each retail shop. An area of 10 cm2 was swabbed and swaps transported under 4oC to the University for Development Studies (UDS) laboratory for microbial analysis. The experiment was carried out between the periods of April 2013 to June 2014.

Enumeration and identification of bacteria groups. This was done according to Adzitey et al. (2014). Swabs were placed in 10 ml sterile peptone water and thoroughly shaked to obtain the neat (10-1). One (1) ml of the neat was transferred into 9 ml sterile peptone water until a dilution of 10-6 was obtained. Serial dilutions (10-1 to 10-6) were spread plated onto blood and nutrient agar plates. Plates were incubated at 37 oC for 24 hours under aerobic condition and the colony forming units were counted to obtain the microbial load. Colony forming unit was calculated using the formula:

$N = \Sigma C / [(1 * n1) + (0.1 * n2)] * (d)$

where N = Number of colonies per cm2

ΣC = Sum of all colonies on all plates counted

n1 = Number of plates in first dilution counted

n2 = Number of plates in second dilution counted

d = Dilution from which the first counts were obtained (Maturin and Peeler, 2001).

Some colonies with different shape, colour and appearance were picked at random from plate count agar and identified using Gram staining. The morphology and colour of the colonies under the microscope was compared to that of Anonymous (2014) to aid in the identification of the various genera. Other tests like catalase test, oxidase test and growth on McConkey (lactose and sorbitol) agars and blood agar were used to confirm some of the isolates. General observations were also made during sampling to know the conditions under which they are slaughtered and smoked.

Statistical analysis. All data collected was analyzed using Analysis of Variance (ANOVA) of the Genstat Statistical Package, 6th Edition.

Results and discussion

The result obtained from sampling beef is presented in Table 1. From Table 1, the total aerobic count for beef ranged from 4.75 to 6.56 log cfu/g. There were no significant differences ($P > 0.05$) among the fresh and smoked beef samples collected from the five different beef sale points. In absolute terms, fresh beef samples from Jolly hut exhibited the highest total aerobic count of 6.56 log cfu/g and fresh beef from Star life exhibited the lowest total aerobic count of 4.75 log cfu/g. It can also be observed in Table 1 that about 80% (8/10) of the samples had total aerobic count of more than 5.00 log cfu/g.

Table 1. Total aerobic plate count of beef

Sale point/Type of Beef	Aerobic Plate Count (cfu/g)	log (cfu/g)
Stanbic Fresh	2.03×10^6	6.31
Stanbic Smoked	1.00×10^5	5.00
Star Life Fresh	5.68×10^4	4.75
Star Life Smoked	2.04×10^5	5.31
Central Mosque Fresh	3.32×10^6	6.52
Central Mosque Smoked	1.31×10^6	6.12
Jolly Hut Fresh	3.64×10^6	6.56
Jolly Hut Smoked	2.00×10^5	5.30
Mobile Clinic Fresh	1.52×10^5	5.18
Mobile Clinic Smoked	3.17×10^5	5.50
Sed	1418586	
P-value	0.074	

Sed = Standard error of difference

The result obtained for fresh and smoked pork is shown in Table 2. The total aerobic count for pork ranged from 4.33 to 6.94 log cfu/g, with smoked pork from Zobisi having the highest total aerobic count of 6.94 log cfu/g and fresh pork from Soe having the lowest total aerobic count of 4.33 log cfu/g. Significant differences ($P < 0.05$) existed among the fresh and smoked pork samples obtained from the five different pork sale points. Smoked pork samples from

Zobisi and Pobaga were significantly higher ($P < 0.05$) than the rests of the fresh and smoked pork samples examined. It is unusual for smoked meat samples to be higher in microbial load than fresh meat samples. It was expected that the heat the meats were expose to will reduce the microbial load. Nonetheless, the high microbial load could be due to cross contamination after smoking. It could also be that, the pork samples were not smoked properly.

Table 2. Total aerobic plate count of pork

Sale point/Type of Pork	Aerobic Plate Count (cfu/g)	log (cfu/g)
Zobisi Fresh	$1.39x10^{5b}$	5.14
Zobisi Smoked	$8.66x10^{6a}$	6.94
Pobaga Fresh	$1.00x10^{5b}$	5.00
Pobaga Smoked	$1.09x10^{6a}$	6.04
Soe Fresh	$2.13x10^{4b}$	4.33
Soe Smoked	$7.02x10^{4b}$	4.85
Atulbabisi Fresh	$2.33x10^{5b}$	5.37
Atulbabisi Smoked	$1.77x10^{5b}$	5.25
Dagbew Fresh	$6.32x10^{5b}$	5.80
Dagbew Smoked	$1.77x10^{5b}$	5.25
Sed	2290967	
P-value	0.015	

Sed = Standard error of difference; Means in the same column with different superscript are significantly different.

The differences in the load can be attributed to the way the meats were handled. Various poor handling and unhygienic practices were observed during data collection. For instance, it was observed that butchers handling meat paid little or no attention to their personal hygiene and served the meat with dirty hands and clothing. Meats were put on tables which are not well cleaned before and after the day's work and also in the open exposing the meat to houseflies. Poor sanitation was also observed in the immediate environment were meats are sold. Adzitey et al. (2014) observed similar unhygienic practices in the handling of meat in the Yendi Municipality of the Northern Region of Ghana. The afore-mentioned practices contributed to the high microbial load and the differences in the load observed.

Other factors also contribute to high microbial load in meat and meat products. Mukhopadhyay (2009) reported that, hot and humid climate areas contribute to increasing total aerobic counts on meat; and that could have contributed to the high total aerobic counts of the meat in this study since Bolgatanga is a hot and humid area. Under poor processing conditions pathogenic and non-pathogenic microorganisms are introduced during slaughtering of animals and processing of carcasses into meat (Warriss, 2000; Alvarez et al. 2009; Adzitey, 2011; Adzitey and Nurul, 2011). In addition the high nutritional value of meat makes it susceptible to high levels of microbial contaminations (Warriss, 2000; Komba et al. 2012). In this study 75% (15/20) of samples obtained had more than 5.0 log cfu/g which indicates high meat contamination. High levels of microbial presence on meat increase the chances of the meat getting spoiled within the shortest possible time. Although microbial load on the meat samples were high, they were below 7.0 log cfu/g. This is the required level for meat spoilage to occur (Warriss, 2000). The higher level of aerobic plate count in this study is in accordance with studies by other researchers (Bhandare et al. 2007; Hassan et al., 2010; Adzitey et al. 2014; Bogere and Baluka, 2014; Huang et al. 2014).

Tables 3 and 4 show the genera of bacteria identified in the smoked and fresh beef and pork, respectively. From Table 3 and 4, five different bacteria genera namely Staphylococcus spp., Streptococcus spp., Salmonella spp., Klebsiella spp. and Escherichia coli were identified in the beef samples. Staphylococcus spp. runs through most of the samples obtained and this can be due to the contamination from the skin of the animal or humans. Postgate (2000) reported that Staphylococcus spp. is part of the normal flora on the skin of humans and animals which can be transmitted from person to meats and meat products through unhygienic practices. The genera of bacteria identified in this study include those that can be pathogenic and has been associated with symptoms, conditions and/or infections in humans.

Table 3. The genera of bacteria identified from fresh and smoked Beef in Bolga Municipal

Source	Fresh Beef	Smoke Beef
Stanbic	*Staphylococcus spp.* *Streptococcus spp.* *Salmonella spp.* *Klebsiella spp.*	*Streptococcus spp* *Staphylococcus spp.* *Salmonella spp.* *Escherichia coli*
Star-Life	*Staphylococcus spp.* *Streptococcus spp.* *Escherichia coli*	*Staphylococcus spp.* *Streptococcus spp* *Salmonella spp.* *Escherichia coli*
Central-Mosque	*Staphylococcus spp.* *Salmonella spp.* *Streptococcus spp.*	*Staphylococcus spp.* *Salmonella spp.* *Streptococcus spp.*
Jolly-Hut	*Salmonella spp.* *Escherichia coli*	*Staphylococcus spp.* *Streptococcus spp.* *Salmonella spp.* *Escherichia coli*
Mobile-Clinic	*Salmonella spp.* *Streptococcus spp.* *Klebsiella spp.*	*Staphylococcus spp.* *Streptococcus spp.* *Salmonella spp.* *Escherichia coli*

Table 4. The genera of bacteria identified from fresh and smoked pork in Bolga Municipal

Source	Fresh Pork	Smoke Pork
Zobisi	*Staphylococcus spp.,* *Streptococcus spp* *Salmonella spp.* *Escherichia coli*	*Streptococcus spp.* *Klebsiella spp.* *Escherichia coli*
Pobaga	*Staphylococcus spp.* *Streptococcus spp.* *Salmonella spp.* *Escherichia coli*	*Klebsiella spp.* *Salmonella spp.* *Escherichia coli*
Soe	*Klebsiella spp.* *Escherichia coli*	*Salmonella spp.* *Staphylococcus spp.* *Escherichia coli*
Atulbabisi	*Staphylococcus spp.* *Streptococcus spp.* *Salmonella spp.* *Escherichia coli*	*Salmonella spp.* *Staphylococcus spp.* *Escherichia coli*
Dagbew	*Staphylococcus spp.* *Streptococcus spp.* *Salmonella spp.* *Escherichia coli*	*Salmonella spp.* *Staphylococcus spp.* *Escherichia coli*

For instance, Pathogenic Escherichia coli and Salmonella spp. can cause gastroenteritis, urinary tract infections, neonatal meningitis, hemolytic-uremic syndrome, peritonitis, mastitis, septicemia and pneumonia (Jay, 2000; Adams and Moss, 2008). Pathogenic Staphylococcus spp., cause infections such as arthritis, black pox, boil, bronchitis, carbuncle, cystitis, endocarditis, meningitis, osteomyelitis, pneumonia, and scalded skin (Kluytmans et al., 1997). Pathogenic Streptococcus spp. can cause septic sore throat, scarlet fever, septicemia infections, meningitis, endocarditis, erysipelas and necrotizing fasciitis (CDC, 2014). Pathogenic Klebsiella spp. organisms can lead to a wide range of disease states, notably pneumonia, urinary tract infections, septicemia, meningitis, diarrhea, and soft tissue infections (Podschun and Ullmann, 1998).

The presence of different bacteria genera in the meat samples confirms the poor slaughtering, handling and environmental conditions under which animals, carcasses, and meats are handled, processed or sold in the Bolgatanta Municipality of Ghana. Bhandare et al. (2007) reported that the unhygienic practices of meat processing in developing countries results in these meats being contaminated with microorganisms.

Conclusion

Beef and pork sold in the Bolgatanga Municipality are contaminated by bacteria. Averagely, 5.86 log cfu/g of fresh beef and 5.45 log cfu/g smoked beef were contaminated, while 5.13 log cfu/g of fresh pork and 5.67 log cfu/g of smoked pork were contaminated. Five different bacteria species (Staphylococcus spp., Streptococcus spp., Salmonella spp., Klebsiella spp. and Escherichia coli) were identified from the fresh and smoked beef and pork samples. Staphylococcus spp. was the most common specie. Consumers of meat in and around the Bolgatanga Municipality need to take caution since they are at risk of foodborne infection. Adequate cooking of the fresh and/or smoked meat is required in order to kill all pathogens.

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