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Microbiological Quality of Chicken Meats in the Traditional Shops at Zuwara, Libya

Adel A. Banana[1], Al-Gheethi AA[2], RMSR Mohamed[3], Efaq AN[4], Gadawi AMS[5]

[1]Environment Engineering Department, Subrata College, University of Zawia, Libya,
Email: adelbanana@yahoo.com,
[2]Faculty of Civil and Environmental Engineering, University Tun Hussein Onn Malaysia (UTHM), Johor, Malaysia
Email. alisaeed@uthm.edu.my
[2]Faculty of Civil and Environmental Engineering, University Tun Hussein Onn Malaysia (UTHM), Johor, Malaysia
Email. maya@uthm.edu.my

[4]School of Industrial Technology, Universiti Sains Malaysia (USM), Penang, Malaysia
Email: eanm1984@gmail.com
[5]Petroleum Research Centre Tripoli, Libya

Abstract

The daily activities of human in the recent years led to the wide distribution of chicken meats. However, these foods are one the main sources of food borne pathogens due to high contents of proteins and carbohydrate which represent an enriched media for growth and multiplication of pathogens. Therefore, the present study aimed to assessment the microbiological quality of chicken meats in the traditional shops of chicken at Zuwarah, Libya during the period between January and March 2015. The investigated pathogens included aerobic bacterial counts, total coliforms (TC), *Staphylococcus aureus* and *Salmonella* spp. as well as yeast and moulds. The results revealed high contaminations among the different samples examined in the study. The aerobic bacterial counts ranged from 10^2 to 10^6 CFU/gm. TC were presented in 97.47% with concentrations ranged from 10^1 to 10^6 CFU/gm. About 45.56% of the samples recorded heavily contaminated with the yeast and moulds. *S. aureus* were detected by 62%, while *Salmonella* spp. was detected in 78.4 %. These findings indicated that the poor microbiological quality of chicken in the traditional shops of meat production.

Key word: assessment, pathogens, *Salmonella* spp. shops, chicken

I. INTRODUCTION

The daily activities of human in the recent years led to the wide distribution of chicken markets. However, these foods are one the main sources of food borne pathogens due to high contents of proteins and carbohydrate which represent an enriched media for growth and multiplication of pathogens. Several pathogenic bacteria such as *Staphylococcus aureus*, *E. coli*, *Salmonella* spp. have been isolated from different foods. The most important are those transmitted by the faecal-oral route, which includes bacteria, viruses, and parasites [1,2]. Bacteria, unlike either viruses or parasites, can actually increase in their numbers in the environment and foods because bacteria do not require a host cell for replication [3]. Presence of these pathogens in the foods indicated to the absence of hygiene practice in the preparation and production of the foods.

Salmonella spp. are the most prevalent bacterial pathogens of widespread public health care concern that are able to create an important amount of foods contamination [4,5]. *Salmonella* spp. are the most relevant they can cause diseases to all organisms from insects to mammals [6]. Enteric fever is a collective term given to the invasive infections caused by *S. typhi*, the cause of typhoid fever, and by the strains of *S. paratyphi* that cause paratyphoid fever. *S. typhi* is a pathogen that only has humans as its natural host [7].

S. aureus has proposed as an indicator of hygiene for microbiological standards [8]. It is a bacterium that commonly colonises human skin and mucosa (e.g. inside the nose) without causing any problems. However, it can also cause disease, particularly if there is an opportunity for the bacteria to enter the human body such as in the case of burns [9].

The indicator bacteria are organisms inhabit the gastrointestinal tract but they have the ability to grow in the different environments [10]. Indicator organisms are used as indicators for faecal contamination and for the presence of pathogenic bacteria since their growth characteristics

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(temperature and pH) are similar to those of numerous pathogens for which detection and quantification are difficult or sometimes impossible [11].

The present study aimed to assessment the microbiological quality of chicken meats in the traditional shops at Zuwarah, Libya during the period between January and March 2015. The investigated pathogens included aerobic bacterial counts, total coliforms (TC), *Staphylococcus aureus* and *Salmonella* spp. as well as yeast and moulds.

II. MATERIALS AND METHODS

A. Collection of samples

Seventy nine of chicken meat samples were collected from twenty six traditional shops of chicken at Zuwarah, Libya during the period between January and March 2015. The samples were aseptically collected in sterile paper bags and transferred to the laboratory within ice box and stored in the refrigerator (the maximum storage time, overnight) for microbiological analysis.

B. Microbiological analysis of chicken samples

The bacterial counts were enumerated by culture-based method (the colony forming unit, CFU) using standard serial dilution spread plate method [12]. A fix weight (100 g) of the chicken samples were uniformly homogenized by using food grinder under septic condition. The grinder was washed with boiled water and then properly cleaned with 70% ethanol solution before the utilization. A fix weight (25 g) of the samples were taken aseptically into 225 mL of sterilized bacteriological peptone water (*w/v*) and labelled as 10^{-1}. The diluted samples were shaken vigorously to uniformly distribute bacterial cells. A fixed volume of (1 mL) the diluent (10^{-1}) was aseptically removed with a sterile pipette and transferred into the next tube (9 mL) to prepare diluent 10^{-2}. These steps were repeated to prepare the serial dilutions to 10^{-6}.

The bacterial cell counts were obtained by spreading 0.1 mL serially-diluted using flamed-sterilized stainless-steel spreader onto Nutrient Agar for Total aerobic bacterial counts (TBC), MacConkey agar for total coliform (TC), Rose Bengal Agar (RBA) for yeasts and moulds count. The media used were dried at 35˚C before inoculation for 24 h to absorb the inoculum water. The experiments were conducted in triplicate. NA and MacConkey agar plate plates were incubated at 37ºC for 24-48 h, while RBA plates were incubated at 28 ºC for 2-3 days.

The counts of viable cells were enumerated in the plates using the colony counter and found in the range of 30-300 colonies. The viable numbers of the spores were expressed as CFU g^{-1} according to the Equation below;

$$\text{CFU per gram} = \text{Number of colonies on agar medium} \times \frac{1}{\text{Dilution factor}}$$

All colonies grown on NA were counted as TBC, pink or red coloured colonies on MacConkey agar were counted as TC. Pink cooler colonies on RBA medium were enumerated as Yeast and moulds.

For isolation of *Salmonella* spp. 25 g of each sample were put into a glass bottles containing 225 mL buffered peptone water and incubated in a shaker incubator at 37 °C, 125 rpm for 18. One mL was transported into 10 mL of selenite cystine broth and incubated for 20-24 h at 37°C. Thereafter 0.1 mL was streaked on XLD agar and incubated at 37 °C for 24 h. The grown colonies with red and black colour centre was selected and confirmed based on biochemical test which included (Indole, Methyl Red, Voges-Proskauer, Citrate and urease and glucose (TSI) [13,14].

For detection of *S. aureus* 25 g of the sample was taken into 225 mL of peptone water (w/v) and incubated in a sheker incubator at 37ºC, 125 rpm for 18 h. Thereafter, 0.1 mL was streaked on Mannitol Salt Agar (MSA). The plates were incubated at 37°C at 24-48 h. Then the yellow or white colonies grown were examined by biochemical tests such as gram staining, catalase and coagulase test [15].

III. RESULTS AND DISCUSSION

The increasing in the consumption of chicken meats is associated with their high nutritional value, lower cost, convenience and variety aspects for the consumer [15]. However, the presence of pathogens infectious represent a real hazards due to the potential to cause several disease of human. Chicken meat is a rich media for the growth and multiplication of these food borne pathogens. The prevalence of pathogenic bacteria in the chicken meat examined in this study is summarized in Table 1.

Table 1 Detection of pathogenic bacteria as well as yeast and mould in chicken samples

Bacterial group	**No. positive samples (%)**	**No. negative samples (%)**
TBC	79 (100%)	0
TC	77 (97.47%)	2 (2.53%)
S. aureus	49 (62.02%)	30 (37.97%)
***Salmonella* spp.**	62 (78.48%)	17 (21.5%)
Yeast and moulds	36 (45.56%)	43 (54.4%)

Total aerobic bacterial counts (TBC), total coliform (TC)

It can be noted that *S. aureus* was detected in 62% of the examined samples, while *Salmonella* spp. were detected in 78.4 % of the samples. *S. aureus* cause more than of 241,148 infection cases annually. Therefore, this bacterium is among top five pathogens causing domestically acquired foodborne illness in the U.S. [16]. The contamination of meat with *S. aureus* is due to the poor food safety practices during handling the meat or directly from infected food-producing animals [17-19].

The chicken meat have always topped the incidence of salmonellosis in several developing countries, the *Salmonella* spp. contamination occur during the production, processing, distribution, retail marketing, handling and preparation [20,21].

The concentrations of TBC and TC were quit high. It has reported that the presence of pathogenic bacteria in chicken meats represent one of the most important challenges and represent a health problems [22]. TC is bacterial group belongs to the family *Enterobacteriaceae* and includes the aerobic and facultative anaerobic, gram-negative, nonspore forming, rod-shaped bacteria that ferment lactose with gas production within 48 h at 35°C. It used as an indicator in several areas, primarily in drinking waters and foods [23].

Table 2 Concentration of pathogenic bacteria as well as yeast and moulds in the chicken samples collected from the traditional shops of meat production at Zuwarah, Libya during the period between January and March 2015

Shop No.	**Sample No.**	**TBC**	**TC**	***S. aureus***	***Salmonella* spp.**	**Yeast and mould**
1	**1**	3.0×10^4	2.0×10^4	*(+ ve)*	*(+ ve)*	+++
	2	1.1×10^2	< detection limits	*(+ ve)*	*(+ ve)*	+++
	3	4.6×10^4	5.8×10^4	*(+ ve)*	*(+ ve)*	+++
2	**4**	2.4×10^3	1.5×10^4	*(+ ve)*	*(-ve)*	+
	5	6.0×10^3	8.0×10^3	*(+ ve)*	*(+ ve)*	+++
	6	3.0×10^3	6.0×10^4	*(+ ve)*	*(+ ve)*	+++
3	**7**	1.0×10^3	6.5×10^4	*(+ ve)*	*(+ ve)*	+
	8	1.5×10^4	4.0×10^5	*(+ ve)*	*(+ ve)*	+++
	9	3.0×10^4	4.0×10^3	*(+ ve)*	*(+ ve)*	+++
4	**10**	$1x10^2$	2.1×10^3	*(-ve)*	*(+ ve)*	+++
	11	3.5×10^4	4.7×10^6	*(-ve)*	*(+ ve)*	+
	12	1.1×10^2	1.1×10^3	*(+ ve)*	*(+ ve)*	++
5	**13**	4.6×10^4	2.8×10^4	*(-ve)*	*(+ ve)*	+
	14	2.4×10^3	1.5×10^3	*(-ve)*	*(+ ve)*	+
	15	3.4×10^3	< detection limits	*(-ve)*	*(+ ve)*	+
6	**16**	3.0×10^3	1.0×10^3	*(-ve)*	*(+ ve)*	+
	17	2.7×10^3	2.1×10^3	*(+ ve)*	*(+ ve)*	+
	18	3.0×10^4	2.3×10^3	*(+ ve)*	*(+ ve)*	+++
7	**19**	3.8×10^4	2.6×10^3	*(+ ve)*	*(+ ve)*	+++
	20	2.0×10^4	4×10^4	*(+ ve)*	*(+ ve)*	+++
	21	3.6×10^2	5.0×10^4	*(+ ve)*	*(+ ve)*	+++
8	**22**	7.3×10^4	2×10^4	*(+ ve)*	*(+ ve)*	+++
	23	5.1×10^4	5×10^4	*(+ ve)*	*(-ve)*	+
	24	4.7×10^3	2.4×10^4	*(+ ve)*	*(+ ve)*	+++
9	**25**	4.0×10^3	3.5×10^4	*(+ ve)*	*(+ ve)*	+++
	26	1.0×10^3	3×10^5	*(+ ve)*	*(+ ve)*	+
	27	3.5×10^4	8.4×10^5	*(+ ve)*	*(+ ve)*	+++
10	**28**	5.0×10^4	5×10^4	*(+ ve)*	*(+ ve)*	+++
	29	3.5×10^2	7×10^4	*(-ve)*	*(+ ve)*	+++
	30	2.0×10^4	5.1×10^4	*(-ve)*	*(+ ve)*	+
11	**31**	3.6×10^3	1.6×10^3	*(+ ve)*	*(+ ve)*	+
	32	5×10^4	4×10^4	*(-ve)*	*(+ ve)*	+

	33	2×10^4	3.9×10^3	*(-ve)*	*(+ ve)*	+
12	**34**	4.3×10^3	1.0×10^4	*(-ve)*	*(+ ve)*	+
	35	4.2×10^3	4.7×10^3	*(-ve)*	*(+ ve)*	++
	36	6×10^3	8.3×10^3	*(+ ve)*	*(+ ve)*	++
13	**37**	4.8×10^4	2.6×10^4	*(+ ve)*	*(+ ve)*	++
	38	4×10^4	5.3×10^3	*(+ ve)*	*(+ ve)*	+++
	39	3.0×10^4	5.0×10^3	*(-ve)*	*(-ve)*	+
14	**40**	5.0×10^3	4.0×10^3	*(+ ve)*	*(-ve)*	+
	41	6.6×10^4	8.8×10^4	*(-ve)*	*(+ ve)*	+++
	42	2.4×10^4	1.4×10^5	*(+ ve)*	*(+ ve)*	+
15	**43**	5.0×10^3	4.0×10^3	*(-ve)*	*(+ ve)*	+++
	44	4.0×10^3	3.0×10^3	*(+ ve)*	*(-ve)*	+
	45	5.4×10^3	6.5×10^4	*(-ve)*	*(-ve)*	+
16	**46**	5.0×10^4	4.0×10^5	*(-ve)*	*(+ ve)*	+++
	47	5.0×10^3	4.0×10^3	*(+ ve)*	*(-ve)*	+++
	48	5.0×10^3	5.1×10^4	*(+ ve)*	*(+ ve)*	+++
17	**49**	6.4×10^5	6.0×10^4	*(-ve)*	*(-ve)*	+
	50	8.0×10^3	3.5×10^3	*(+ ve)*	*(-ve)*	+
	51	4.9×10^4	5.1×10^4	*(+ ve)*	*(-ve)*	++
18	**52**	2×10^4	6.4×10^5	*(-ve)*	*(-ve)*	+
	53	7.1×10^3	3.0×10^5	*(+ ve)*	*(+ ve)*	+++
	54	5×10^4	8.3×10^3	*(-ve)*	*(-ve)*	+
19	**55**	7.9×10^3	4.5×10^4	*(+ ve)*	*(-ve)*	+
	56	3.5×10^4	9.4×10^5	*(-ve)*	*(-ve)*	+++
	57	7.0×10^3	7.4×10^3	*(+ ve)*	*(-ve)*	+++
20	**58**	2×10^4	2×10^4	*(+ ve)*	*(+ ve)*	
	59	1.4×10^5	7×10^4	*(+ ve)*	*(+ ve)*	+++
	60	3.5×10^3	5.8×10^5	*(+ ve)*	*(+ ve)*	+++
21	**61**	1×10^2	1.5×10^4	*(-ve)*	*(+ ve)*	+++
	62	2.2×10^3	8×10^3	*(+ ve)*	*(+ ve)*	+++
	63	2.4×10^5	6×10^4	*(+ ve)*	*(+ ve)*	+
22	**64**	5.7×10^3	1.5×10^4	*(+ ve)*	*(+ ve)*	+
	65	5.5×10^4	1×10^2	*(+ ve)*	*(+ ve)*	+++
	67	3.9×10^3	1.5×10^4	*(+ ve)*	*(+ ve)*	+++
23	**68**	2.9×10^5	3×10^4	*(+ ve)*	*(+ ve)*	+++
	69	4.3×10^4	7.0×10^3	*(-ve)*	*(+ ve)*	+
	70	1.8×10^2	1.2×10^4	*(+ ve)*	*(+ ve)*	+++
24	**71**	1.1×10^6	2.8×10^3	*(-ve)*	*(+ ve)*	+
	72	5.9×10^3	1.5×10^3	*(-ve)*	*(+ ve)*	+
	73	3.6×10^4	2×10^4	*(-ve)*	*(+ ve)*	+++
25	**74**	2.8×10^5	1×10^3	*(-ve)*	*(+ ve)*	+++
	75	6.3×10^2	10×10^3	*(+ ve)*	*(+ ve)*	+++
	76	1.8×10^6	2.8×10^6	*(-ve)*	*(+ ve)*	+
26	**77**	8.2×10^4	2.1×10^6	*(+ ve)*	*(+ ve)*	+
	78	4.2×10^4	8.2×10^4	*(+ ve)*	*(+ ve)*	+++
	79	3.3×10^5	2.9×10^4	(-ve)	(-ve)	+++

Total aerobic bacterial counts (TBC), total coliform (TC), Positive (+ve), negative (-ve), low contamination (+, less than 10^1 CFU/gm), Moderate contamination (++, between 10^1 to 10^3 CFU/gm), High contamination (+++, more than 10^5 CFU/gm)

IV. CONCLUSION

It can be concluded that the traditional shops of chicken meats represent a source of pathogenic bacteria. Therefore, more strength should be applied to prevent the transmission of these pathogens into human.

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