



Incidence of some pathogens in beef burger sold in Cairo

Moustafa A.El-Shenawy*, Zeinab I. Sadek, Samy Mohamed Abdelhamid, Mohamed T. Fouad Department of Dairy Science, Division of Food Industries and Nutrition, National Research Centre, 12311 Dokki, Giza, Egypt



Abstract

Thirty burger samples were randomly collected from food shops super marks in Great-Cairo governorate. Samples were microbiologically investigated for the presence of some pathogenic microorganisms including Staphylococcus aureus, Escherichia coli 0157:H7, Salmonella typhimurium, Yersinia enterocolitica and Bacillus cereus. Staphylococcus aureus and Bacillus cereus were detected in 60% of the examined samples with an average counts of $14x10^2$ and 5.1x10² cfu/g. however, Escherichia coli 0157:H7, Salmonella typhimurium and Yersinia enterocolitica were detected in 50, 50 and 40% of the examined samples, with an average counts of $12x10^2$, $4.8x10^2$ and $5.1x10^2$ cfu/g respectively. Eighty -five isolates of pathogenic bacteria including 20 isolates each of Bacillus cereus and Staphylococcus aureus as well as 15 isolates each of Escherichia coli 0157:H7, Salmonella typhimurium and Yersinia enterocolitica were purified and identified following the biochemical identification tests (Bergey's Manual). Only 56 out of the testes 85 isolates were confirmed as pathogenic species using Hi identification kits and latex test kits. The obtained results indicated that these foods may pose a source of infection to the consumer. Measures to control the quality of the raw material, environmental and hygienic conditions during preparation and serving should be taken.

Keywords; Super-markets; Egyptian sausage; microbiological analysis; pathogens.

Introduction

Meat and meat products are among the most important protein sources in the daily diet of people living in developed countries. Beef burger is almost the most popular meat product consumed by millions of people from all over the world. The common processes (such as mincing, cooking, and salt addition) applied in the production of burgers enhance the formation of reactive oxygen species; therefore, the resultant product is highly vulnerable to oxidation [1, 2].

The increasing number and severity of food poisoning outbreaks worldwide has considerably increased public awareness about food [3], especially meat and meat products which are one of the most important sources of human infections with a variety of foodborne pathogens [4,5]. However, meat and meat products continues to be an important food group in the diet for many consumers [6-8], Staphylococcusaureus is considered to be one of the most important foodborne diseases worldwide due to its ability to produce wide arrays of toxins[9,10]. Meat products like luncheon, burger and minced meat are considered important sources of pathogenic Salmonella spp. which caused sever gastroenteritis in human, especially products manufactured from raw and minced meat and not subjected for heat treatment [11]. Yersinia enterocolitica in meat and meat products is a special concern since those organisms are capable of growth at refrigerator temperatures [12]. Yersinia enterocolitica is by far the most frequent cause of yersiniosis worldwide. Yersinia

*Corresponding author e-mail: elshenawy_moustafa51@yahoo.com (Moustafa A.El-Shenawy). Receive Date: 12 October 2021, Revise Date: 24 October 2021, Accept Date: 31 October 2021 DOI: <u>10.21608/ejchem.2021.100669.4677</u>

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enterocolitica occurs in several biotypes and serotypes, which differs in pathogenicity to humans, geographical distribution and animal reservoirs [13,14].

B. cereus occurred in 98% of test minced meat, 60% of sausage, 48% of rice grains, 44% of Koshari or ice-cream and 36% of pasteurized milk samples. [15]. Shehu and Adesiyun [16] reported 39.5% of milk to for Ε. Enterotoxigenic be positive coli. Escherichiacoli has been involved in food-borne illness and recovered from various food types, processed or raw [17]. Microbial food safety is an increase in public health concern worldwide. It is estimated that approximately 76 million foodborne illness occurring in the united states every year [18,19]. Contaminated, raw or undercooked poultry and red meats are particularly important in foodborne diseases. Microorganisms in fast and traditional fast foods are responsible for many human diseases. Salmonella is common cause of foodborne illness, particularly in chicken and undercooked eggs [20, 21], whereas Listeria spp. is common from chilled and frozen foods. Other foodborne microorganisms include Camphylobacterspp, Staphylococcus spp., E. coli and Yersinia spp., whose incidence was reported by Kaneko et al. [22] and Pelczaret al. [23, 24]. Consequently, this work has been done to evaluate the general bacteriological condition of the burger product sold in the Egyptian market. With a focus on the feasibility of the presence of some pathogenic microbes including Staphylococcus aureus counts, coli 0157:H7, Salmonella Escherichia typhimurium, Yersinia enterocolitica and Bacillus cereus in order to give a general idea of the health and safety condition of this food product.

Experimental

Three samples from 10 different food shops super markets in Great-Cairo governorate including (Bulak, Giza, Dokki, Ramsis, Bin El-Sarayat, El-Saeda, Ain-Shams, Attaba, Misr El-Gadida and Moasasa) were collected. The samples were handled in sterile plastic containers and transferred to the laboratory in ice-box within 2h of collection.

Samples preparation:

Twenty-five gm. of each sample was mixed, homogenized in sterile mixer and diluted with 225 ml buffered peptone water .Ten-fold dilutions of homogenates were prepared and subjected to all the microbiological analysis [25].

Microbiological Analysis:-

Ten-fold dilutions of the homogenates samples were inoculated onto plates of selective media. Enumeration of *Escherichia coli* O157: H7 was carried out by spreading 0.1 ml of each dilution onto plates of sorbitol MacConkey agar medium and colourless colonies counts were done after 24 hrs incubation at 35° C incubation [26]. For detection of *Salmonella typhimurium*, (25g) of each sample was mixed with 225ml of sterile buffer peptone water and incubated at 35 °C for 24 hrs. One to ten ml of this mixture was transferred to selenite cystein broth and incubated at 35 °C for 72 hrs. Plates of *Salmonella &Shigella* ager were streaked from the last process and incubated at 35 °C for 24 hrs. Growth of *Salmonella typhimurium* is appears as colorless colonies with black centers [27].

For Yersinia, Each sample (25 g) was homogenized and mixed with 225ml Yersinia selective enrichment in 500ml flasks. Flasks were incubated at 30 °C for 48 hrs, and then spread onto plates of Yersinia selective agar medium. After 18-24 hrs incubation at 35 °C, suspected colonies of Y. enterocolitica which appear form dark red colonies resembling bulls' eye were picked up and further tested for specific identification. Enumeration of S. aureus in samples was carried out by spreading 0.1 ml of each dilution onto the surface of Baird Parker media supplemented with egg yolk and potassium tellurite solution. Plates were incubated at 37 °C for 48 hrs, typical colonies, which appear gray-black, shiny and convex with a narrow white margin surrounded by a clearing zone, were counted [28, 29]. Suspected colonies were picked up and propagated for further specific morphological and biochemical tests.

Bacillus cereus was determined by the surface plating technique using the *Bacillus cereus* agar medium, supplemented with polymyxin B and egg yolk. Plates were incubated at 37 °C for 48 hrs, a typical colony, which appears peacock blue-coloured and surrounded by precipitation zone were counted and tested for further specific identification [26].

Purification and Identification of the isolated strains:-

Three to five suspected isolates of each organism, isolated from each positive sample, were subjected for identification using the microscopic examination well as their chemical and biochemical as confirmation tests according to Bergy's Manual [30]. Additional kits to help for accurate used identification including Hi Staphylococcus identification kit, Hi Staphylococcus Latex test kit, Hi E. coli identification kit, Hi E. coli 0157 Latex test kit. Hi Salmonella identification kit and Hi Salmonella Latex test kit. All results of identification tests done for these isolates were compared with a specific reference strains obtained from ATCC.

References strains

Strains of *Escherichia coli* 0157: H7 ATCC *6933*, *Bacillus cereus* ATCC 33018, *Staphylococcus aureus* ATCC 20231, *Yersinia enterocolitica* ATCC 27729 and *Salmonella typhimurium* ATCC 14028were obtained from the Department of Dairy Science, National Research Centre, Cairo, Egypt. The abovementioned strains were served as reference indicators for comparison among the tested strains.

Results and discussion

Meatand meat products are considered as a major vehicle of most reported food poisoning outbreaks. Therefore, it is important to use the microbiological criteria as it gives guidance on the acceptability of burger samples and their manufacturing, handling and distribution processes. The incidence of different pathogens in the burger samples in present study were presented in table 1.

The incidence of *Escherichia coli* 0157: H7 in the burger samples was high in the present study, in this work, this organism was detected in 20% of total samples, where *Escherichia coli* 0157: H7 contaminated with counts ranged from $7x10^2$ to $21x10^2$ cfu/g. (Table 1). Our results agreed with those obtained by Saleh et al. [31] and El-Dosoky et al. [32] they found that incidence (12%and 15%) in burger samples was reported by respectively, whereas very low incidence (5.12%) was reported by El Shrek and Ali (2012) [33] in cooked meat products.

The incidence of *Salmonella typhimurium* in burger samples was 50% total samples, where *Escherichia coli* 0157: H7 contaminated with counts ranged from $2x10^2$ to $11x10^2$ cfu/g. El-Dosoky et al. [32] reported(10%) incidence of *Salmonella typhimurium* in beef burger. An incidence of 20% and 14% and 5.71% were reported by Edris [34], Mousa et al. [35] and Ibrahim et al. [36] respectively, which are far less than the incidence observed in the present study in the burger samples.

Staphylococcusaureus could cause food poisoning and if it grows in large numbers can leave toxins in the product, which may survive heating. It lives on the skins of humans and animals and can easily be transferred to food products. Table (1) showed that Staphylococcusaureus was detected in 60% of total samples of examined burger. where Staphylococcusaureus contaminated counts ranged from $2x10^2$ to $20x10^2$ cfu/g. counts of $8.3x10^2$, 2.8×10^2 and 1.05×10^2 to 2.3×10^2 cfu/gm) were observed by Ali and Abd-El-Aziz [37], El-Mossalami et al. [38], and Min et al. [39] respectively, which were almost similar to the counts observed in the present study.

A rise in notified cases of food poisoning has occurred across the most of Europe and North America; in particular, in the incidence of microbial

Identification of the isolated pathogenic bacteria:

Table (2) summarizes the number of examined samples and the bacterial isolates detected, and their percentages. As shown in Table (2) all the selected 66 isolates of different pathogens bacteria were subjected to identification according to their morphological, physiological and biochemical characteristics as described in Bergy's manual of determinative Bacteriology [30].

Twenty typical isolate were picked up from Baird Parker media agar, 15 typical isolate were picked up from sorbitol MacConkey agar, 15 typical isolate were picked up from Yersinia selective agar medium, 15 typical isolate were picked up from Salmonella &Shigella ager and 20 typical isolate were picked up Bacillus cereus agar medium. After from Identification and confirmation, only 14 strains (out of 20) were found to belong to genus Staphylococcus aureus, representing 25% of the total strains (56), however the other 11(out of 15), 9(out of 15), 10(out of 15) and 12 (out of 20) isolates were belonged to Escherichia coli 0157:H7, Yersinia enterocolitica, Salmonella typhimurium and Bacillus cereus, representing 20, 16, 18 and 21% of the total strains respectively.

Final assessment of burger product according to Egyptian Standards (ES: 1688/2005)

According to the microbiological specifications of the Egyptian Standards (ES: 1668/2005), this product should be free of all examined pathogens. Consequently, most of burger samples representing 73% of total samples were not accepted to the ES due to one or more of criterion, however the remain 27% of the burger samples were accepted. The result demonstrates the fact that the unhygienic and poor sanitary conditions under which the meat and meat products are handled and processed are not acceptable from sanitary point of view. It has further evidence that the undesirable

food poisoning of animal origin [40]. Bacillus cereus was detected in 60% of examined burger. The presence of this bacterium in meat has been widely reported in different parts of the world [41]. For example Mosupye and Von Holy [42], reported (22%) incidence of B. cereus in a related study in South Africa, however Ismail [43] reported higher incidences (48%) in beef and Lamb ready to eat foods. Also table (1) indicated the incidence of Yersiniaenterocolitica isolated from burger samples as 40%. Our results overlap those obtained by Mousa et al. [35], who found that the incidence of Yersinia enterocolitica isolated from meat product samples including beef burger, luncheon, pasterma and sausage were 46, 40, 54 and 34%, respectively. Most common sources for this microorganism could be in factories during preparation of the examined product.

level of contamination which might have acquired from the environment and agents and to obtain wholesome, safe and sound meat products, the principles Good Manufacturing Practices (GMP) and Hazard Analysis and Critical Control Point (HACCP) must be adopted.

Conclusion

The results of this study indicate that hygienic conditions of burger were very poor and may constitute a considerable hazard to human health. Using of high quality raw materials, efficient heat treatment, adequate cleaning and sanitization of utensils may assist reducing this cross contamination. **Acknowledgment**

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| | Table 1: Incidence | e of different path | ogens in burger | • samples from | different sour | ces |
|-----|--------------------|---------------------|--------------------|---------------------|--------------------|---------------------|
| No. | Source | E. c. | Sal. | Sta. | B.c. | Yers. |
| 1 | Bulak | 7 x10 ² | 6 x10 ² | 18x10 ² | 3 x10 ² | Nil |
| | | Nil | $7 \text{ x} 10^2$ | $14x10^{2}$ | 5x10 ² | $7 \text{ x} 10^2$ |
| | | Nil | Nil | Nil | Nil | Nil |
| 2 | Giza | 9 x10 ² | $5 x 10^2$ | Nil | Nil | Nil |
| | | Nil | Nil | Nil | Nil | Nil |
| | | Nil | Nil | 16x10 ² | 3x10 ² | 5×10^2 |
| 3 | Dokki | 18 x10 ² | Nil | $12 \text{ x} 10^2$ | 8 x10 ² | 9 x10 ² |
| | | Nil | $3 x 10^2$ | Nil | $7x10^{2}$ | Nil |
| | | Nil | Nil | Nil | Nil | Nil |
| 4 | Ramsis | 11 x10 ² | $2 x 10^2$ | 15x10 ² | $2 x 10^2$ | $11 \text{ x} 10^2$ |
| | | $12x10^2$ | 6x10 ² | $17x10^{2}$ | 6x10 ² | Nil |
| | | Nil | Nil | Nil | 3x10 ² | Nil |
| 5 | Bin El-Sarayat | 16 x10 ² | Nil | $2 x 10^2$ | Nil | Nil |
| | | Nil | Nil | Nil | Nil | Nil |
| | | Nil | 3 x10 ² | 9x10 ² | 7x10 ² | 3 x10 ² |
| 6 | El-Saeda | Nil | Nil | Nil | Nil | Nil |
| | | 12 x10 ² | $4 x 10^2$ | 17x10 ² | 5x10 ² | 8 x10 ² |
| | | Nil | Nil | $11x10^{2}$ | Nil | 3 x10 ² |
| 7 | Ain-Shams | 18x10 ² | 7 x10 ² | $23x10^{2}$ | 4x10 ² | Nil |
| | | Nil | Nil | Nil | Nil | Nil |
| | | Nil | Nil | Nil | Nil | Nil |
| 8 | Attaba | $10 \text{ x} 10^2$ | Nil | $14x10^{2}$ | 6 x10 ² | 10x10 ² |
| | | $16 \text{ x} 10^2$ | 6 x10 ² | 8x10 ² | 8x10 ² | 6 x10 ² |
| | | 9 x10 ² | $3 	ext{ x10}^2$ | 13x10 ² | $4x10^{2}$ | Nil |
| 9 | Misr El-Gadida | Nil | $5 x 10^2$ | $17x10^{2}$ | Nil | 3×10^2 |
| | | Nil | Nil | Nil | Nil | Nil |
| | | $13 \text{ x} 10^2$ | Nil | Nil | $4x10^2$ | Nil |
| 10 | Moasasa | $21x10^{2}$ | $4 x 10^2$ | $12 \text{ x} 10^2$ | $2x10^{2}$ | Nil |
| | | $11 \text{ x} 10^2$ | 6x10 ² | 19x10 ² | 7x10 ² | 8 x10 ² |
| | | $13 \text{ x} 10^2$ | $5 x 10^2$ | 16x10 ² | 5x10 ² | $4 x 10^2$ |

Table 1: Incidence of different pathogens in burger samples from different sources

Sta.=Staphylococcus aureus; E.C.= Escherichia coli 0157:H7; Yers.= Yersinia enterocolitica; Sal.= Salmonella typhimurium; B.c. = Bacillus cereus

| | No. | Sta. | E.c. | Yers. | Sal. | B.c. |
|------------------|-----|-----------|-----------|-----------|------------|-----------|
| Sausages samples | 30 | 18* (60%) | 15* (50%) | 12* (40%) | 15 * (50%) | 18* (60%) |
| Total isolates | 85 | 20 (23%) | 15(18%) | 15 (18%) | 15 (18%) | 20(23%) |
| Total strains | 56 | 14 (25%) | 11 (20%) | 9 (16%) | 10 (18%) | 12 (21%) |

Sta.=*Staphylococcus aureus;* E.c.= *Escherichia coli* 0157:H7; Yers.= *Yersinia enterocolitica*; Sal. = *Salmonella typhimurium*; B.c. = *Bacillus cereus*, () no. of isolates/ strains, *; positive samples