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Microbial Quality of Carcass in Khartoum State

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Abstract:
A total of 60 random swab samples were collected from cattle, camel and sheep carcasses at Omdurman slaughter houses to evaluate the contamination level with Enterobacteriaceae .The results obtained indicated that the mean values of bacterial counts in the examined swab samples of cattle, sheep and camel were 3.6, 3.13 and 2.72 Mean Log_{10} cfu/cm^2 and 3.4,2.9 and 2.34 Mean Log_{10} cfu/cm^2 for the total coliform count, respectively. There was a significant difference between Enterobacteriaceae and coliform counts.E.coli (20%), Citrobacter (10%), Enterobacter (35%), Klebsiella (25%) and Proteus species(30%) ,were the predominant bacterial species among the isolates. From all the three types of carcasses No salmonella species were detected in any sample.

Keywords: *Carcass, slaughter- house, coli forms*

1. Introduction

Fresh meat is highly perishable due to its biological components. Microbial contamination of the carcass during the slaughtering process results in spoilage of meat, reduced shelf-life of meat and public health hazards (Narasimha Rao, 1992)**,**(Nortje, Nel, Jordaan, badenhorst, Goedhart, & Holzapfel, 1990)**.**Almost most food borne diseases are related to use of meat containing pathogenic microorganisms. There is high possibility of external contamination of carcasses i from the early stages of slaughtering till the moment consumption. Good manufacturing practices during slaughter have a profound effect on the microbial load of meat. Contact with the hide, skin or feet, and the gastric content are considered as potential sources for meat contamination by microorganisms. Water sources, air, instrument used for slaughter operations such as (knives, saws, cleavers or hooks) play a role in meat contamination(Jawelz, E.J.; Meluick, L.and E.A.Adelbery., 1982).The Enterobacteriaceae family contains a large number of organisms, some of non faecal origin, that are useful as an indicator of the overall process hygiene in the abattoir. E. coli is the indicator bacteria of choice associated with faeces (Delhalle, de Sadeleer, Bollaerts, Farnir, & Saegerman, 1994) (Ghafir, China, Dierick, & De Zutter, 2008) and (McEvoy, Sheridan, & Blair, 2004)Enteric organisms, such as coliforms were frequently isolated from meat indicating that the rumen of the slaughtered animals is a common source of contamination (ICMSF I. C., 1980).Therefore, the objective of the current study was to determine the level of Enterobacteriaceae contamination of sheep, cattle and camel carcasses during slaughtering and to identify their pathogenic strains.

2. Materials and Methods

2.1. Collection of Samples

A total of 60 random swab samples were collected from slaughtered cattle, camel and sheep carcasses at Omdurman slaughter houses, using a sterile wire template with an approximate area of 100 cm^2 .The swabs were delivered immediately to the laboratory for testing. Samples were collected according to(ICMSF I. C., 1978)

2.2. Bacterial Counts

Enterobacteriaceae count was determined as by using Violet Red Bile Glucose Agar and the purple colonies were calculated as Enterobacteriacae. For the Determination of coliform count Violet Red Bile agar plates were used (ICMSF.International Commission on Microbiological Specification for Foods., 1996).MacConkey broth and Eosin Methylene Blue plates were used for detection of *E.coli*. The metallic green colonies were picked up and identified biochemically (ICMSF.International Commission on Microbiological Specification for Foods., 1996) . For salmonellae detection peptone water was used as pre enrichment medium, Rappaport Vassiliadis as an enrichment broth and Hekton agar was used for plating.

2.3. Statistical Analysis

Bacterial counts were transformed into log cfu/cm^2values.data were tested using SPSS version 16(SPSS inc.Chicago).Turkeys' test was used as a post hoc test. Mean differences were considered significant at $p< 0.05$.Data was represented in form of tables and graphs.

3. Results

Carcasses	Positive samples		Mean Log_{10} cfu/cm^2
	No	%	
Cattle	16	80	3.6*
Sheep	8	40	3.13
Camel	5	25	2.72

*Table 1: Mean Log_{10} cfu/cm^2 of Total Enterobacteriaceae counts recovered from different animal carcasses (n=20). *Significant difference ($P \leq 0.05$)*

Carcasses	Positive samples		Mean Log_{10} cfu/cm^2
	No	%	
Cattle	18	90	3.4**
Sheep	15	75	2.90
Camel	12	60	2.34

*Table 2: Mean Log_{10} cfu/cm^2 of Total coliform counts recovered from different animal carcasses (n=20). ** High Significant difference ($P \leq 0.01$)*

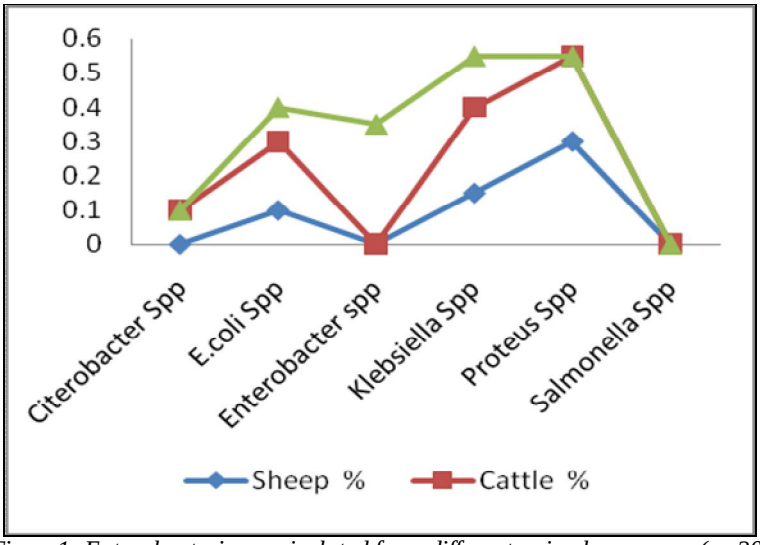

Figure1: Enterobacteriaceae isolated from different animal carcasses (n=20)

4. Discussion

The obtained results in table (1) and (2), indicate that the total Enterobacteriaceae count in the examined swab samples were varied from 2.72 to 3.4 Log_{10} cfu/cm^2 with an average of 3.4 Log_{10} cfu/cm^2 for cattle, 3.13 Log_{10} cfu/$cm^2$for sheep and 2.72 Log_{10} cfu/cm^2 for camel. Significant differences were detected among different species of carcasses at ($P \leq 0.05$).Nearly similar results were obtained by (Hamdy, 1989)**,** (Samaha, 1993)**.**Higher results were obtained by (Al-dughaym, 2001) **,** concerning the mean values of Enterobacteriaceae count on the surface of camel carcasses before and after skinning, and at the inspection point. While, lower results were obtained by (Pearce, 2005) and (Fliss & Simrad, 1991),(Vanderlinde, 1999)**,** (Yalcin & Nizamlioglu, 2001) during the different stages of slaughter operations. Regardless of animal species; counts were relatively higher for freshly produced meat.

Different species of microorganisms were isolated from the samples, as *E,coli & Klbsiella* were isolated from all animal species carcasses., *Proteus* from sheep and cattle,while *Citrobacter* was isolated from cattle carcasses only , all species carcasses were found free of Salmonella Figure (1).All examined swabs from the three species carcasses were free from Salmonellae. This finding agrees with some researchers, who could not detect Salmonellae spp., from any of the examined samples, although (WHO, 1988) records showed that**,** the incidence of Salmonella in raw meat and organs in some countries was up to10% and 3%, respectively**,** globally *Salmonella* is implicated in most food poisoning outbreaks occurring as a result of consumption of contaminated meat and meat products. Members of the Enterobacteriaceae are responsible for causing foodborne disease and some also cause food spoilage and therefore contribute to substantial economical losses and food wastage. The initial Enterobacteriaceae contamination level in the raw materials is predominantly governed by Good Agricultural Practices (GAP) during primary production and subsequently during slaughter of livestock at the abattoir (Chris Baylis, 2011).

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6. References

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