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## Common Pathogenic Bacteria Isolated from Broiler Chicken Farms in Khartoum State

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## **Abstract**

One Hundred swab samples were collected from modern broiler chicken farms in Khartoum State to investigate possible sources of bacterial contamination before slaughtering. These samples were taken from litter, chicken transport boxes and rinse water coops, cloaca, feathers and breast supports. The study revealed statistical significant difference (P< 0.05) between these points after conduction of total viable count (TVC). The isolated and identified bacteria in different points were *Escherichia coli* (41.66%), *Staphylococcus aureus* (33.33%), *Staphylococcus albus* (16.66%) and *Salmonella* species (8.33%). The level of microbial contamination in broiler chicken farms may reflect the hygienic status of poultry meat production.

Keywords: - Microbial contamination, meat hygiene, Poultry farms, Broilers

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#### Introduction

Microbial contaminants are responsible for causing a number of acute and chronic diseases in both poultry and humans (Maung, 2004). Contaminated poultry products are among the most important sources of food-borne outbreaks in humans. Microbial contaminants were reported more often from poultry and poultry products than from any other animal species (Maung, 2004). Infection status of the host population can be an important factor in the contamination status of the final food products. In 1988, Aho and Hirn found that broilers which were free from microorganisms at the farm were also found to be free from micro-organisms after slaughtering. Some factors play important role in broilers' infection status: age-dependent susceptibility to pathogens is important determinant colonization status of the host. Young chickens (<2 wk) are extremely susceptible to infection by Salmonella species while in contrast, colonization by Campylobacter species appears to be most common in broiler chickens (>2 wk) of age (Neill et al., 1984). Prior to processing, chickens are typically caught by hand, loaded into cages or crates, and transported on over-the-road trailers to the processing plant where they are held until slaughter (Lacy and Czarick, 1998; Northcutt and Berrang, 2006). During loading, transportation, and holding, cages become contaminated with feces, ingesta, dirt, feathers, litter, and other debris that may be carried into the processing plant on the birds' feet, feathers, and skin (Northcutt and Berrang, 2006). Transport of broilers to the processing plant was shown to increase the prevalence of birds positive for microorganisms because of fecal contamination of skin and feathers by neighboring birds during shipping (Stern et al., 1995; McCrea et al., 2006). Processing has been shown to increase contamination by Salmonella and Campylobacter in studies comparing onfarm prevalence to final product prevalence (Wempe et al., 1982; Mead et al., 1994). Others have established that an increase in microbial contamination of broiler chicken skin occurs during crating, transport, and processing (Stern et al., 1995; Carraminana et al., 1997 McCrea et al., 2006). Prolonged crating was identified by Rigby and Pettit (1980) as a contributor to the contamination of processed broiler carcasses. Current understanding of the sources of poultry colonization by human enteric pathogens is largely derived from work undertaken on Salmonellae. With this organism, recognition of the importance of both vertical and horizontal transmission routes of infection has been pivotal in the development of appropriate control and prevention strategies (Maung, 2004). In Campylobacters spp., most studies have focused on horizontal transmission, but most recently, vertical transmission has been more thoroughly investigated (Maung, 2004). The objective of this study was to detect contaminating micro-organisms before slaughtering process in broiler poultry farm.

# Materials and Methods Collection of samples:

The study was conducted in two modern broiler chicken farms between June and September 2011 in Khartoum State.

Hundred swab samples were taken from litter (30 swabs), chicken transport coops (30 swabs), rinse water coops (10 swabs), breast supports (10 swabs), feather (10 swabs), after immersing in 100 ml peptone water for 30 seconds and cloaca (10 swabs).

### **Bacteriological analysis:**

The Total Viable Count (TVC) was applied by using serial dilution to each swab sample (Harrigan and MacCance, 1976). The culture of the samples was also used according to the methods of Barrow and Feltham (2003) for isolation and identification of microorganisms.

### **Statistical Analysis**

The data were analyzed with Statistical Package for the Social Sciences (SPSS), version 16.0 software (SSPS Inc, and Chicago, IL, USA). All bacterial counts were converted to  $\log_{10}$  cfu/ml (g) for analysis and ANOVA was performed. Statistical significance was set at a *P-value* of p $\leq$ 0.05

#### **Results**

The study revealed a statistically significant difference at P-value (p $\le 0.05$ ) between the investigated points, as shown in Table 1. The TVC revealed the highest contamination level was in cloacal swabs  $9.98\pm0.01~\log_{10}~cfu/g$ , while the lowest contamination level was in coops swabs  $(2.76\pm0.11~\log_{10}~cfu/g)$ .

Table 1: Comparison of the Mean Total Viable Count of Bacteria  $(\log_{10} \text{ cfu/g}) \pm \text{Sd}$  at Different Points of Investigation

Operational points	Mean $\pm$ Sd of TVCs of bacteria ( $log_{10}$ cfu/g)	Significance
Litter sample	7.09±0.12	*
Cloacal sample	9.98±0.01	*
Feather sample	9.85±0.15	*
Coops	2.76±0.11	*
Coops rinse	6.14±3.05	*
Breast supports	9.33±0.24	*

Significal at p  $\leq 0.05$ 

Isolation and identification of bacteria at different points under investigation revealed 4 species of bacteria (Table 2). The isolates in litter were *Staphylococcus aureus* and *Staphylococcus albus* (8.33%), but in cloaca were *Escherichia coli* (8.33%) and *Salmonella* species (8.33%). In the feathers

Escherichia coli (8.33%) and Staphylococcus aureus (8.33%), whereas in transport coops and rinse water coops these microorganisms represented 16.66% and in chicken breast supports were found to be 8.33% (Table 2).

**Table 2: Bacteria Species Isolated in Different Points** 

<b>Operational points</b>	E. coli	Staph. aureus	Staph. albus	Salmonella	Total
Litter Samples	0 (0.00%)	1 (8.33%)	1 (8.33%)	0 (0.00%)	2 (16.66%)
Cloacal Samples	1 (8.33%)	0 (0.00%)	0 (0.00%)	1 (8.33%)	2 (16.66%)
Feather Samples	1 (8.33%)	1 (8.33%)	0 (0.00%)	0 (0.00%)	2 (16.66%)
Coops	2 (16.7%)	0 (0.00%)	0 (0.00%)	0 (0.00%)	2 (16.66%)
Coops Rinse	0 (0.00%)	2 (0.00%)	0 (0.00%)	0 (0.00%)	2 (16.66%)
<b>Breast Supports</b>	1 (8.33%)	0 (0.00%)	1 (8.33%)	0 (0.00%)	2 (16.66%)
Total	<b>5</b> (41.7%)	<b>4</b> (33.33%)	2 (16.7%)	1 (8.33%)	<b>12</b> (100.0%)

#### Discussion

In the present study, the mean TVC obtained from the litter  $(7.09\pm0.12 \log_{10}$ cfu/g) was lower than those recorded by Terzich et al. (2000); Lu et al. (2003) and Macklin et al. (2006). Dissimilarities existed in internal- external profile of different types of bacteria on broilers contaminated meat from the live bird originated from gastrointestinal tract, feathers and skin which have been most important sources (Vučemilo et al., 2007). Also in this study the mean TVCs of litter and cloaca were higher than that reported by Nasrin et al. (2007) and this could be due to differences of disinfection protocols practiced. In cloacal swabs the mean TVC was 9.98±0.01 log<sub>10</sub> cfu/g, while Berndtson et al. (1996) and Mead et al. (1994) recorded that colonization levels in the intestines especially ceca and cloaca ranged from  $10^5$  to  $10^9$  cfu/g. In this study the result of TVC from feathers was 9.85±0.15 log<sub>10</sub> cfu/g, which is higher than that reported by Morar et al., (2008). The reduction of bacterial counts in transport and rinse water coops (2.76±0.11 and 6.14±3.05 cfu/g) may be due to continuous washing. These findings are in agreement with the findings of Northcut and Berrany (2006). In breast supports the TVC was 9.33±0.24 cfu/g, this is the first time breast supports to be investigated as a potential source of microbial contamination in broilers.

In this study Staphylococcus aureus and Staphylococcus albus were isolated from the litter, similar to the findings recorded by Vizzier-Thaxton etal.(2003).organism Escherichia coli was isolated in this study from cloaca, feathers, transport coops and breast supports and this finding is supported by previous studies (Kathryn and Pandya, 1995: Blanco et al., 1998; Morar, et al., 2008). Broiler's feathers are contaminated from fecal material in during loading transport coops transportation to slaughterhouse (Berrang et al., 2003). Rigby and Pettit (1980) stated that feces carried in feet and feathers are important routes for introduction pathogenic bacteria into the processing plant. Clean feather reduce bacterial load during slaughtering process (Corry and Also Atabay. 2001). in this study Salmonella species was isolated from cloaca and Staphylococcus albus from breast supports (Maung, 2004).

In conclusion, the levels of microbial contamination in broiler chicken farms may reflect the hygienic status of poultry meat production. Bacterial contamination on

processed broiler carcasses may originate from environment, plant equipments and employees. Therefore, hygiene is an important factor to be considered in intensive poultry farms as it has considerable impacts on the health of both animals and humans working in the industry.

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# الباكتيريا الممرضة العامة التي تم عزلها من مزارع الدجاج اللاحم بولاية الخرطوم

محمد نجيب مصطفى ، ياسر آدم شعيب ، سهام الياس سليمان و محمد عبدالسلام عبدالله كلية الطب البيطري – جامعة السودان للعلوم والتكنولوجيا

### المستخلص

جمعت مائة عينة عن طريق المسح من مزارع دجاج لاحم حديثة في ولاية الخرطوم للتعرف على أماكن مصادر حدوث التلوث البكتيري قبل الذبح. أخذت هذه العينات من مهاد النشارة, و اقفاص الترحيل, من ماء غسيل الأقفاص, الذرق, الريش و دواعم الصدر. بالتحليل الإحصائي أوضحت الدراسة أن هناك فرق معنوي بين هذه النقاط (P<0.05) بعد العد الحي الكلي للبكتيريا . و البكتيريا التي تم عزلها و تم التعرف عليها هي الاشريكية القولونية 41.66%, العنقودية البيضاء 41.66% و أنواع السالمونيلا 81.8% . إن مستوى التلوث الجرثومي في مزارع الدجاج اللاحم قد يعكس الحالة الصحية في إنتاج لحم الطيور الداجنة.