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ISOLATION AND DETECTION OF BACTERIAL SPECIES FROM VISCERAL ORGANS OF QUAILS

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Abstract: A total of thirty normal quail birds were bought from local market. Quail birds were slaughtered and samples taken aseptically from internal organs of each bird for bacteriological investigation. The result showed isolation of 154 bacterial isolates from different organs of quail birds. Among the 30 quail birds 22 birds were showed positive for microbial identification (73.33%). The isolates ranged from *E. coli* 20.77% (32 isolates), as a high percent, then *Corynebacterium spp. 19.48 %* (30 isolates), *Staphylococcus aureus* 16.23 %(25 isolates), *Bacillus spp.* 16.23% (25 isolates), *Enterococcus faecalis 11.68%* (18 isolates), *Klebsiella pneumoniae* 9.09% (14 isolates), *Proteus spp.* 2.59% (4 isolates), *Pasteurella multocida* 2.59% (4 isolates) and *Coagulase–ve staphyloco-ccus* 0.6% (1 isolate). This study showed *E. coli* and *Corynebacterium spp.* were dominant bacteria in the internal organs of quail birds. Many studies reported that quail birds were resistant to many bacterial diseases, so that these birds may act as mechanical transporting for different bacterial species to humans and animals with the risky of transporting of resistance bacterial species for many antibiotics.

Keywords*:* Wild birds; Bacterial isolates; Internal organs.

Introduction

Japanese quails are members of the pheasant family phasianidae (Naveen, 1997). Japan is the native place of this species of quail which was domesticated as long ago as the 12th century, at the beginning of this century these birds have been bred in large numbers for dual-purpose of meat and eggs production (Abd El-Gawad et al., 2008). Quail meat in some countries considered as a good food for all ages due to its high meat yield, little shrinkage during cooking, fast cooking and serving and also due to their delicacy and low level of cholesterol. In addition, quail meat is tender and fortified with nutrients (Mounteny, 1981). Because it is a perfect source of vitamin B6, niacin, thiamin, pantothenic acid and riboflavin, so quail meat favorite more than other species of poultry meat (Paulillo, 2009). Considerable quantities of quail meat are used for human consumption due to their easily adapt to commercial management conditions, with good performance in term of meat and egg production (Edris,

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1997). Today a considerable numbers of live quail birds are sold in local birds markets for human consumption, so the present study aimed to detect the bacterial types that may be found in the organs of these birds.

Materials and methods

Specimens

A total of thirty normally quail birds were bought from local birds markets and transported directly to laboratory, then slaughtered and samples taken aseptically from internal organs of each bird that included liver, lung, gizzard and intestine. The samples were put in sterile nutrient broths and incubated at 37°C for 24 hours (Quinn et al., 2003).

Culturing

Each broth was inoculated on three media included nutrient agar, sheep blood agar and MacConkeyagar and incubated aerobically at 37°C for 24-48 hours (Koneman et al., 1998).

Identification of Bacterial isolates

Purification was done and colonial characteristics and blood hemolysis were studied. After that smears from specific colonies were prepared and stained by Gram's stain to study the shape, arrangement and staining reaction (Quinn et al., 2004). Also some selective media were used like mannitol salt agar for staphylococci growth, Edward's medium for streptococci, Hoyle's medium for Corynebacterium and MacConkey agar for enterobacteriaceae. Biochemical tests were applied for each specific bacterial isolates and included catalase, oxidase, indole production, methyl red, VP, citrate utilization, gelatin hydrolysis, urease, triple sugar iron, nitrate reduction (Barrow, 2003).

Results

Results of the study revealed isolation of 154 bacterial isolates from different organs of quail birds. Among the 30 quail birds 22 birds were showed positive for microbial identification (73.33%). The isolates ranged from *E. coli* 20.77% (32 isolates), as a high percent, then *Corynebacterium spp. 19.48 %* (30 isolates), *Staphylococcus aureus* 16.23 %(25 isolates), *Bacillus spp.* 16.23% (25 isolates), *Enterococcus faecalis 11.68%* (18 isolates), *Klebsiella pneumoniae* 9.09% (14 isolates), *Proteus spp.* 2.59% (4 isolates), *Pasteurella multocida* 2.59% (4 isolates) and *Coagulase –ve staphyloco-ccus* 0.6% (1 isolate). These bacterial types were classified according to the bird organs as follows;

Liver specimens

Seventeen liver specimens were positive for bacterial isolation (56.66%). Six bacterial types (34 isolates) were isolated from specimens of livers (Table 1). *E.coli* appeared in a high

percent (26.47%) between the total isolates from liver, and also as a mixed isolate along with other bacterial types (Table 2).

Table (1): Isolated bacterial types from liver specimens

Bacterial type	Numbers of isolates	Percentage (%)
Corynebacterium spp.	7	20.58
E. coli	9	26.47
Bacillus spp.	8	23.52
Staphylococcus aureus	3	8.82
Klebsiella pneumoniae	1	2.94
Enterococcus faecalis	6	17.64
Total 100.00	34	

Table (2): Mixed and pure bacterial types isolated from liver specimens

Bacterial type	Number of liver specimens	Percentage (%)
Corynebacterium spp.	4	23.52
E. coli	3	17.64
Corynebacterium spp. + Bacillus spp.	2	11.76
Corynebacterium spp. + Staphylococcus aureus	1	5.88
+ E. coli	2	11.76
Bacillus spp. + E. coli + Enterococcus	2	11.76
Bacillus spp. + E. coli + Staphylococcus aureus	1	5.88
Bacillus spp. + E. coli	1	5.88
Klebsiella + Enterococcus	1	5.88
Bacillus spp.		
Total 100.00		17

Lung specimens

Among the lung specimens, only twenty specimens were positive for bacterial isolation. Eight bacterial types (44 isolates) were isolated from specimens of lungs (Table 3). *Corynebacterium spp.* appeared predominant bacterial type from lungs as a pure or mixed culture, followed by *Staphylococcus aureus* (Table 4).

Table (3): Isolated bacterial types from lung specimens

Bacterial type	Number of isolates	Percentage (%)
Corynebacterium spp.	10	22.72
Staphylococcus aureus	9	20.45

E. coli	7	15.90
Klebsiella pneumoniae	6	13.63
Bacillus spp.	6	13.63
Pasteurella multocida	4	9.09
Enterococcus faecalis	1	2.27
Coagulase –ve Staph.	1	2.27
Total	44	
100.00		

Table (4): Mixed and pure bacterial types isolated from lung specimens

Number of lung specimens	Bacterial type	Percentage (%)
3	*Coryne. + Staph. aureus*	13.63
3	*Corynebacterium spp.*	13.63
4	*Staphylococcus aureus*	18.18
4	*E. coli+ Klebsiella pneumonia + Bacillus spp.*	18.18
1	*Coryne. + Enterococcus+ E. coli*	4.54
1	*Coryne. + E. coli* + Coagulase –ve	4.54
2	Staphylococcus	9.09
2	*Pasteurellamultocida + Coryne.*	9.09
1	*Pasteurella multocida + Klebsiella pneumonia +*	4.54
1	*Bacillus spp.*	4.54
	Coryne. + Staph.aureus+ Proteus	
	Coryne. + E. coli + Staph. aureus	
22	Total	
100.00		

Gizzards specimens

In gizzard specimens six bacterial types (36 isolates) were isolated and the Gram positive bacteria were dominant, particularly *Bacillus spp.* and *Staphylococcus aureus* (table 5). More frequently mixed isolation from these specimens included *Bacillus spp.* with *Enterococcus faecalis* (table 6).

Table (5): Isolated bacterial types from gizzards specimens

Bacterial type	Number of isolates	Percentage (%)
Corynebacterium spp	5	13.88
Bacillus spp.	10	27.77
Staphylococcus aureus	10	27.77
Enterococcus faecalis	4	11.11
E. coli	4	11.11
Klebsiella pneumoniae	3	8.33
Total	36	
100.00		

Table (6): Mixed and pure bacterial types isolated from gizzards specimens

Number of gizzard specimens	Bacterial type	Percentage %
2	*Corynebacterium spp.*	9.09
3	*Bacillus spp. + Enterococcus faecalis*	13.63
4	*Bacillus spp.*	18.18
4	*Staphylococcus aureus*	18.18
3	*Staph. aureus + Bacillus spp.*	13.63
2	*E. coli + Klebsiella pneumonia*	9.09
1	*Klebsiella pneumonia + Enterococcus*	4.54
1	*faecalis*	4.54
2	*Coryne. + Staph. aureus*	9.09
	Coryne. + E. coli+ Staph. aureus	
22	Total	100.00

Intestinal specimens

Between seven bacterial types (40 isolates) isolated from intestines of quail birds, *E. coli* and *Corynebacterium spp.* represented in a high percent (table 7), also these two types isolated together more frequently as a mixed culture (table 8).

Table (7): Isolated bacterial types from intestines specimens

Bacterial type	Number of isolates	Percentage (%)
Corynebacterium spp.	8	20.00
E. coli	12	30.00
Enterococcus faecalis	7	17.50
Staphylococcus aureus	4	10.00
Klebsiella pneumoniae	4	10.00
Proteus spp.	4	10.00
Bacillus spp.	1	2.50
Total	40	
100.00		

Table (8): Mixed and pure bacterial types isolated from intestines specimens

Number of intestine specimens	Bacterial type	Percentage %
2	*Corynebacterium spp.*	10.00
3	*E. coli*	15.00
2	*Coryne. + E. coli*	10.00
4	*E. coli + Enterococcus faecalis*	20.00
1	*Coryne. + Enterococcus faecalis + Proteus*	5.00
1	*spp.*	5.00
2	*Coryne.+Staph. aureus + Bacillus spp.*	10.00
2	*Klebsiella pneumonia + Enterococcus*	10.00
3	*faecalis*	15.00

	Coryne. + Klebsiella pneumoniae *Proteus + E. coli + Staph.aureus*	
20	*Total*	100.00

Discussion

According to the results of this study many bacterial types were isolated from different organs of quail bird's involved *Corynebacterium spp.*, *E. coli*, *Staphylococcusaureus*, *Klebsiella pneumoniae*, *Enterococcus faecalis*, *Bacillus spp.*, *Proteus spp.*, *Pasteurella multocida and Coagulase -ve Staphylococcus.* These results were agreed to the results of previous studies about the isolation of same bacterial types from quail, but differed from them in rates of isolates (Roy et al., 2006). The differences between the results could be attributed to the variations in climate and environment of husbandry regions especially temperatures variation that effect on the bacterial growth (Dhasarathan, 2006).

Results of the liver samples revealed isolation of six bacterial types (Table 1) included *Corynebacterium spp*., *E. coli, Bacillus spp., Staphylococcus aureus, Klebsiella pneumonia* and *Enterococcus faecalis*. Many studies referred to the isolation of one or more of these bacterial species from livers particularly *E. coli, Enterococci* and *Staphylococci* (Lauková, 2009), while *Corynebacterium spp.* isolation was not referred previously; and this will confirm the environmental changes (Dhasarathan, 2006). The bacterial types isolated from liver specimens were similar to those isolated from intestine and this conclude that livers bacteria might passed from intestine to liver or may reach the liver by extension from adjacent air sacs or from less frequently, by extension up the biliary tree (Schmidt, 2003).

Eight bacterial types (44 isolates) were isolated from specimens of lungs (Table 3). *E.coli* appeared predominant bacterial type from lungs as a pure or mixed culture, followed by *Staphylococcus aureus, E. coli, Klebsiella pneumonia, Bacillus spp., Pasteurella multocida, Enterococcus faecalis, Coagulase –ve Staphylococci* (Table 4). Many researches were observed isolation of these bacterial species from lungs of diseased quails (Thenmozhi et al., 2010).

Gizzard specimens were appeared positive for bacterial isolation and this study showed isolation of six bacterial types (36 isolates) and also revealed that Gram positive bacteria were dominant, particularly *Bacillus spp.* and *Staphylococcus aureus* (Table 5) as mentioned by some studies (Burns, 2003). More frequently mixed isolation from these specimens included *Bacillus spp. with Enterococcus faecalis* (Table 6). The results of gizzard's specimens referred that these bacterial types may come from environment through

contaminated food and water, and then when passed to intestine definitely they spread to the other organs (Thomas, 2007).

Seven bacterial types (included 40 isolates) isolated from intestines of quail birds, *Corynebacterium spp.* and *E.coli* represented in a high percent (Table 7), also these two types isolated together more frequently as a mixed culture (Table 8). Other isolated bacteria from intestines were involved *Enterococcus faecalis, Staphylococcus aureus, Klebsiella pneumonia, Proteus spp.* and *Bacillus spp.* These results accepted with the previous studies in the same line which refered that the intestinal bacteria may be the main source for contamination of other internal organs (Hong-lin et al., 2010).

This study showed that *E.coli* and *Corynebacterium spp.* were dominant in the organs of quail birds, and some studies related these bacteria with many infections in humans (Collins, 1986). On the other hand the Japanese quail are reported to be resistant to many diseases and in addition many bacterial isolates obtained from Japanese quail and their environment showed high resistance to multiple drugs (Barnes, 1997), so that these birds may act as mechanical transporting for different bacterial species to humans and animals with the risky of transporting of resistance bacterial species.

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