Detection of organ bacterial load in quails

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Abstract

A total of thirty normally quail birds were bought from local market in Mosul city in the period from September-October 2011. Quail birds were slaughtered and samples taken aseptically from internal organs of each bird for bacteriological investigation. The result showed isolation of 203 bacterial isolates from different organs of quail birds. The isolates ranged from *Corynebacterium spp.* 29.6 % (60 isolates) as a high percent, then *E. coli* 18.2% (37 isolates), *Staphylococcus aureus* 16.3 %(33 isolates), *Bacillus spp.* 14.8% (30 isolates), *Enterococcus faecalis* 9.9% (20 isolates), *Klebsiella pneumoniae* 6.4% (13 isolates), *Proteus spp.* 1.9% (4 isolates), *Pasteurella multocida* 1.9% (4 isolates) and *Coagulase -vestaphyloco-ccus* 1% (2 isolates). This study showed *Corynebacterium spp.* and *E. coli* were dominant bacteria in the internal organs of quail birds. Many studies reported that quail birdswere resistant to many bacterial diseases, so that these birds may act asmechanical 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. Available online at http://www.vetmedmosul.org/ijvs

الكشف عن الحمل الجرثومي في أعضاء طائر السمان محمد علي حمد، عمار محمود العالم، سمية ياسين عبد الله الدباغ و هيفاء حسين علي

فرع الاحياء المجهرية، كلية الطب البيطري، جامعة الموصل، الموصل، العراق

الخلاصة

جمعت ثلاثون عينة من طيور السمان السليمة من الاسواق المحلية في مدينة الموصل للفترة الممتدة بين شهري أيلولوتشرين الاول ٢٠١١، نبحت الطيور واخذت عينات من الاعضاء الداخلية تحت ظروف التعقيم لغرض تحديد الحمل الجرثومي. أظهرت النتائج عزل ٢٠٣ عزلة جرثومية من الاعضاء المختلفة للطيور. كانت جراثيم الوتديات بأعلى نسبة عزل اذ بلغت ٢٠٣ % ٢٠٠ عزلة)، تلتها جراثيم الايشريشيا القولونية ٢٠١ % (٣٠ عزلة) والعصيات ١٩٠٨ (٣٠ عزلة) لايشريشيا القولونية ٢٠١ % (٣٠ عزلة) والعصيات ١٩٠٨ (٣٠ عزلة) والباستوريللا والمكورات المعوية البرازية ٩٩٩ (٢٠ عزلة) والكلبسيلا الرئوية ٢٠٤ (٣٠ عزلة) والمتقلبات ١٩٠٩ (٤ عزلات) و الباستوريللا ملتوسيدا ٩١% (٤ عزلات) والمكورات العنقودية سالبة المخثر ١% (٢ عزلة). بينت نتائج الدراسة أن جراثيم الوتديات و الايشريشيا القولونية كانت السائدة في الاعضاء الداخلية لطيور السمان. أشارت الكثير من الدراسات الى مقاومة طيور السمان لمختلف الأمراض الجرثومية، لذا فإن هذه الطيور قد تلعب دور الناقل الميكانيكي لمعظم الانواع الجرثومية للحيوان والانسان مع خطورة نقلها للجراثيم المقاومة لمختلف المضادات الحيوية.

Introduction

Japanese quails are members of the pheasant family (phasianidae) (1,2). 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 (1,3,4). 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 (1,3,5,6). 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(7,8). Japanese quails is extensively distributed in several countries around the world and in some European countries (like France, Italy, Spain and Greece) considerable quantities of quail meat are used for human consumptiondue to their easily adapt to commercial management conditions, with good performance in term of meat and egg produc-tion (3,7,8). In Saudi Arabia and Egypt, quail farms start gaining popularity because their less feed requirements and space(6,8). In our country particularly in Mosul city many quail farms were established and today a considerable numbers of live quail birds are sell 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 birdswere bought from local birds markets in Mosul city and transported directly to laboratory of Microbiology in college of veterinary medicine, 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 (9).

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 (10,11).

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 (11). Alsosome 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 (12,13).

Results

Results of the study revealed isolation of numerous bacterial types from different organs of quail birds that included 203 isolates from different organs, which involved *Corynebacterium spp.* in a high percent 29.6 % (60 isolates), then *E. coli* 18.2% (37 isolates), *staphylococcus aureus* 16.3% (33 isolates), *Bacillus spp.* 14.8% (30 isolates),

Enterococcus faecalis 9.9% (20 isolates), Klebsiella pneumoniae 6.4% (13 isolates), Proteus spp. 1.9% (4 isolates), Pasteurella multocida 1.9% (4 isolates) and Coagulase-vestaphylococcus 1% (2 isolates). These bacterial types classified according to the bird organs as following:

Liver specimens

Twenty one liver specimens were positive for bacterial isolation (70%). Six bacterial types (37 isolates) were isolated from specimens of livers (Table 1). *Corynebacterium spp.* appeared in a high percent between the total isolates from liver, and also isolated purely more than other bacterial types (Table 2).

Table (1): Isolated bacterial types from livers' specimens.

Bacterial type	Numbers of isolates	Percentage %
Corynebacterium spp.	13	35.14
E. coli	9	24.32
Bacillus spp.	8	21.62
Staphylococcus aureus	4	10.81
Klebsiella pneumoniae	1	2.70
Enterococcus faecalis	2	5.41
Total	37	100%

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

Numbers of liver specimens	Bacterial types	Percentage %
6	Corynebacterium spp.	28.57
3	E. coli	14.29
4	Coryne. + Bacillus	19.05
3	Coryne. + Staph. aureus+ E. coli	14.29
1	Bacillus spp. + E. coli + Enterococcus	4.76
1	Bacillus + E. coli + Staph. aureus	4.76
1	Bacillus + E. coli	4.76
1	Klebsiella + Enterococcus	4.76
1	Bacillus spp.	4.76
21	Total	100%

Lung specimens

All lung specimens were positive for bacterial isolation. Eight bacterial types (62 isolates) were isolated from specimens of lungs (Table 3). *Corynebacterium spp.* appeared predominant bacterial type from lungs as a pure or

mixed culture, follow-ed by *Staphylococcus aureus* (Table 4).

Table (3): Isolated bacterial types from lung specimens.

Bacterial type	Numbers of isolates	Percentage %
Corynebacterium spp.	20	32.25
Staphylococcus aureus	13	20.98
E. coli	9	14.52
Klebsiella pneumoniae	6	9.67
Bacillus spp.	6	9.67
Pasteurella multocida	4	6.45
Enterococcus faecalis	2	3.23
Coagulase –ve Staph.	2	3.23
Total	62	100%

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

Numbers of lung specimens	Bacterial types	Percentage %
7	Coryne. + Staph. aureus	23.33
5	Corynebacterium spp.	16.67
4	Staphylococcus aureus	13.33
4	E. coli+ Klebsiella pneumonia + Bacillus	13.33
2	spp. Coryne. + Enterococcus+ E. coli	6.67
2	Coryne. + E. coli+ Coagulase- Staphylococcus	6.67
2	Pasteurellamultocida + Coryne.	6.67
2	Pasteurella multocida + Klebsiella pneumonia + Bacillus spp.	6.67
1	Coryne. + Staph. aureus+ Proteus	3.33
1	Coryne. + E. coli + Staph. aureus	3.33
30	Total	100

Gizzards specimens

In gizzard specimens six bacterial types (47 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	Numbers of isolates	Percentage %
Bacillus spp.	13	27.65
Staphylococcus aureus	12	25.53
Corynebacterium spp.	9	19.15
Enterococcus faecalis	7	14.90
E. coli	4	8.51
Klebsiella pneumoniae	2	4.26
Total	47	100%

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

Numbers of gizzards specimens	Bacterial types	Percentage %
5	Corynebacterium spp.	16.67
5	Bacillus spp. + Enterococcus faecalis	16.67
4	Bacillus spp.	13.33
4	Staphylococcus aureus	13.33
4	Staph. aureus+Bacillusspp.	13.33
2	E. coli	6.67
2	Klebsiella pneumonia + Enterococcus faecalis	6.67
2	Coryne. + Staph. aureus	6.67
1	Coryne. + E. coli+ Staph. aureus	3.33
1	Coryne. + E. coli + Staph. aureus	3.33
30	Total	100

Intestinal specimens

Between seven bacterial types (included 57 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).

Table (7): Isolated bacterial types from intestines specimens.

Bacterial type	Numbers of isolates	Percentage %
Corynebacterium spp.	18	31.58
E. coli	15	26.32
Enterococcus faecalis	9	15.79
Staphylococcus aureus	4	7.02
Klebsiella pneumoniae	4	7.02
Proteus spp.	4	7.02
Bacillus spp.	3	5.25
Total	57	100%

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

Numbers of intestines specimens	Bacterial types	Percentage %
5	Corynebacterium spp.	16.67
5	E. coli	16.67
5	Coryne. + E. coli	16.67
4	E. coli + Enterococcus faecalis	13.33
3	Coryne. + Enterococcus faecalis+ Proteus spp.	10
3	Coryne.+Staph. aureus +Bacillus spp.	10
2	Klebsiella pneumoniae+ Enterococcus faecalis	6.68
2	Coryne. + Klebsiella pneumoniae	6.68
1	Proteus + E. coli + Staph. aureus	3.33
30	Total	100

Discussion

According to the results of this study many bacterial types were isolated from different organs of quail birds involved *Corynebacterium spp.*, *E. coli*, *Staphylococcusaureus*, *Klebsiellapneumoniae*, *Enterococcus faecalis*, *Bacillus spp.*, *Prot-eus spp.*, *Pasteurellamultocida and Coagulase-veStaphylococcus*. 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 (8,14-16). The differences between theresults could be attributed to the variations in climate and environment of husbandry regions especially temperatures variation that effect on the bacterial growth (4,17).

Results of cultured 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* (16,18-20), while *Corynebacterium spp.* isolationwas not referred previously; and this will confirm the environmental changes (17). 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 (21).

Eight bacterial types (62 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, E. coli, Klebsiellapneumonia, Bacillus spp., Pasteurellamultocida, Enterococcus faecalis, Coagulase -veStaphylococci (Table 4). Many researches were observed isolation of these bacterial species from lungs of diseased quails (16,18,20,22,23). Gizzard specimens were appeared positive for bacterial isolation and this study showed isolation of six bacterial types (47 isolates) and also revealed that Gram positive bacteria were dominant, particularly Bacillus spp. and Staphylococcus aureus (Table 5) as mentioned by some studies (16,22). 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, then when passed to intestine definitely they spread to the other organs (2,24).

Seven bacterial types (included 57 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 intestineswere involved *Enterococcus faecalis, Staphyloc-occusaureus, Klebsiella pneumonia, Proteus spp.* and *Bacillus spp.* These results accepted with the previous studies in the same line (2,15,16,18,20,21), which refered that the intestinal bacteria may be the main source for contamination of other internal organs (21).

This study showed that *Corynebacterium spp.* were dominant in the organs of quail birds and this predominant may be explained by worldwide distribution of these bacteria during previous 2 decades and some studies related these bacteria with many infections in humans (17,25,26).

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 with 100% (like isolates of *E. coli*) resistance observed against ampicillin/cloxacillin, chloramphenicol, tetracycline, and cotrimoxazole and other antibiotics (16,27,28,29), 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.

Acknowledgements

The authors thank the College of Veterinary Medicine, University of Mosul for support.

Iraqi Journal of Veterinary Sciences, Vol. 26, Supplement II, 2012 (47-51) Proceedings of the 6th Scientific Conference, College of Veterinary Medicine, University of Mosul

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