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Phenotypic and Genotypic Characterization of Paratyphoid Salmonellae isolated from Poultry in Delta Area- Egypt

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Abstract

The present work aimed to isolate and characterize Salmonellae from chickens, ducks, quails and turkeys in five Egyptian Governorates. Polymerase chain reaction (PCR) was used for the detection of common virulence genes. A total of 265 flock samples (150 chickens, 60 ducks, 30 quails and 25 turkeys) were collected from Dakahlia, Kafrelsheik, Damietta, Sharkia and Gharbia Governorates. Birds were subjected to either clinical and/or post-mortem examination, in adittion to isolation and identification of salmonellae from internal organs including liver, lung, spleen, caecum and unabsorbed yolk sac. Biochmeical and serological identification of the isolates was done. Twenty eight birds (10.6%) were found positive for Salmonella isolation. The number and percentage of positive chickens, ducks, quails and turkeys were 16 (10.7%), 7 (11.7%), 3 (10%) and 2 (8%), respectively. *Salmonella* Typhimurium, *S.* Enteritidis, *S.* Kentucky, *S.* Paratyphi A, *S.* Molade, *S.* Heidelberg, *S.* Infantis and *S.* Apeyeme were isolated from chickens. While *S.* Enteritidis, *S.* Typhimurium, *S.* Paratyphi A, *S.* Kentucky, *S.* Inganda and *S.* Bargny were isolated from ducks. While, *S.* Virchow, *S.* Tamale and *S.* Typhimurium were isolated from Quails and *S.* Wingrove, finally, *S.* Kentucky were isolated from turkeys. Molecular characterization of common virulence genes Salmonella outer proteins (*sop*B), Plasmid encoded virulence gene (*spv*C), salmonella enterotoxin (*stn*) and bacterial colonization factor (*bcf*C) showed the presence of *stn* and *bcf*C genes in all isolates, while, *sop*B and *Spv* genes were present in 64.3% and 10.7%, respectively. It is concluded that salmonellae with common virulence genes were widely spread among domestic birds in Delta areas, Egypt, resulting in economic and public health problems which require the application of strictly biosecurity measures in poultry rearing.

Keywords: *Salmonella* spp., Poultry, Delta, Virulence Genes

Introduction

Paratyphoid (PT) infection is an infectious disease of all domestic and wild birds. More than 2400 serotypes of salmonellae were recognized, and they can infect humans and different animals [1]. Paratyphoid infection is bacterial disease causing high economic losses among avian species. Paratyphoid salmonellae are Gram–negative; non-spore forming, non capsulating and motile by means of peritrichous flagellae [2]. The clinical findings of paratyphoid infection in all species of young birds are similar and include a progressive state of somnolence manifested by a tendency to keep head downward, close eyes with droopy wings, ruffled feathers, marked anorexia, increased water consumption, profuse watery diarrhea with pasting of the vent and a tendency of birds to huddle together near to the source of heat [3-5]. The dead birds in acute state show septicemia, while, those dying later show necrotic foci in the liver and/or heart, enlargement of gall bladder and unabsorbed yolk sac [6]. However, in severe outbreaks of PT infection in newly hatched birds, rapidly developing septicemia can cause a high rate of mortality with few or no apparent lesions. When the course of the disease is longer, severe enteritis is often accompanied by focal necrotic lesions in the mucosa of the small intestine. Cheesy cecal cores are often observed, spleens and livers are commonly swollen and congested with hemorrhagic streaks or necrotic foci, while, kidneys may sometimes be enlarged and

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congested [7]. Fibrinopurulent perihepatitis and pericarditis have been reported on numerous occasions, In addition, unabsorbed, coagulated yolk sac and other lesions occasionally are observed including hypopyon, panophthalmitis, purulent arthritis, serous typhilitis, air sacculitis and omphalitis [7].

The gold standard method for Salmonella detection is bacteriological culture, while, serotyping can also be used [8]. *S.* Enteritidis and *S.* Typhimurium are the most common serotypes isolated from poultry [9]. Differences in virulence among Salmonella serovars and in the course of Salmonella infections in various host species have been attributed to the variable acquisition and evolvement of virulence genes [10]. *Salmonella* species contain upwards of sixty virulence genes and have three antigenic (H, O, and Vi) determinants [11].

The fimbrial gene (*bcf*C) is located on a fimbrial structure and has a role in cell invasion [12]. Moreover, *Salmonella* outer proteins (*Sop*) has a role in the invasion of the bacteria through deformation of membranes and rearrangement of the host cells' cytoskeleton [13,14]. *Spv* is related to survival and growth of the bacterium in host cells [15]. The salmonella enterotoxin (*stn*) gene encodes Stn protein, causing gastroenteritis with symptoms that include nausea, vomiting, abdominal pain, fever, and diarrhea [16]. The present study aimed to isolate salmonellae from birds in Delta area of Egypt and to determine the occurrence of PT in different poultry species. Moreover, detection of common virulence genes among isolated salmonellae was carried outusing PCR.

Material and Methods

Sample collection

A total of 265 flock samples of diseased and freshly dead chickens, ducks, quails and turkeys were collected from Dakahlia, Damietta, Gharbia, Kafrelsheik and Sharkia Governorates. Birds were subjected to either clinical and/or post-mortem examination for the isolation and identification of paratyphoid salmonellae from internal organs including liver, lung, spleen, caecum and unabsorbed yolk sac. The internal organs of 150 chickens, 60 ducks, 30 quails, 25 turkeys were collected under aseptic condition as possible to prevent cross contamination in ice box and were then transferred to the laboratory.

Isolation of Salmonella species

It was done according to ISO 6579 [17]. The tested sample was initially inoculated into a non-inhibitory liquid medium to favor the repair and growth of stressed or sublethally-injured salmonellae arising from exposure to heat, freezing, desiccation, high osmotic pressure or wide temperature fluctuations.

Samples were weighed and suspended in Buffered Peptone water as 1:10 dilution and then incubated at 37ºC ±1ºC for 18 ±2 h. From the pre-enrichment culture, 0.1 mL of the broth was transferred to a tube containing 10 mL of the Rappaport Vassiliadis broth and then incubated at 41.5ºC ± 1ºC for 24 ± 2 h. From the enrichment culture, 10 µL were inoculated onto the surface of Xylose Lysine Deoxycholate (XLD), Hektoen Enteric (HE) and MacConkey's plates, separately, then incubated at 37ºC ±1ºC for 24 ± 2 h. The plates were then checked for the growth of typical *Salmonella* colonies.

Biochemical identification

Hydrolysis of urea, H_2S production, TSI and Simmon's Citrate agar were done according to ISO 6579 [17]. Isolated strains were inoculated on to Christensen's urea agar slant and incubated at 37ºC ± 1ºC, then examined after four hours. If there was no change it was left for 24 h at 37ºC ±1ºC. A Simmon's citrate agar slopes were inoculated as a single streak on the surface with the tested isolates and incubated at 37°C for 48 h.

Serological typing of paratyphoid salmonellae

The isolates that were identified biochemically as *Salmonella* were subjected to serological identification according to Kauffman-White Scheme [18] for determination of somatic (O) and flagellar (H) antigens [19].

Molecular identification of virulence genes

All the isolates were examined by PCR for the presence of four virulence associated genes [20]. The genes under investigation were Salmonella outer protein B (*sop*B), Salmonella plasmid virulence (*spvC),* Salmonella enterotoxin encoding gene (*stn*) and bacterial colonization factor encoding gene (*bcf*C). The primers sequences' and PCR product sizes are showen in (Table 1) [12,21].

Table 1: Sequences of the used oligonucleotide primers for identification of virulence genes among Salmonellae in poultry

Genes	Specificity/ location	Sequence of nucleotides (5'-3')	Amplified product (bp)
Stn	Enterotoxin/ chromosomal	F- TTGTGTCGCTATCACTGGCAACC R-ATTCGTAACCCGCTCTCGTCC	617
***sop*B**	Effector protein/ SPI-5	F-TCAGAAGTCGTCTAACCACTC R-TACCGTCCTCATGCACACTC	517
***bcf*C**	Fimbrial usher protein/ chromosome	F-ACCAGAGACATTGCCTTCC R-TTCTGCTCGCCGCTATTCG	467
***spv*C**	Plasmid encoded virulence gene/ plasmid	F-ACCAGAGACATTGCCTTCC R-TTCTGATCGCCGCTATTCG	467

Results

The clinical signs of the examined birds were retarded growth, depression, lameness, ruffled feathers, chicks huddling together, respiratory troubles, whitish watery diarrhea and accumulation of faecal matter around the vent (Figure 1: A, B). The postmortem examination of both freshly dead and sacrificed birds revealed gross lesion in the form of septicemia, bronze discolouration enlarged liver with necrotic foci, splenomegaly with necrotic foci, pericarditis, enlarged heart, peritonitis, congested kidneys, inflammation of intestine and caecum and unabsorbed yolk sac in young birds (Figure 1: C,D,E,F,G,H).

Figure 1: Signs and PM lesions of examined birds. A: Three days-old chick was sleepy with droopy wings. B: Diseased birds with pasty vent and whitish diarrhea. C: Twelve days-old Saso chicken died showing necrotic foci in the congested liver. D: 16 days-old chick showing several nodules on the heart and congested liver. E: 30 days-old chick showing Cecal cores,enteritis and septicemia. F: Ten days-old turkey with septicemia and cecal cores. G: Twenty days-old duckling died showing bronzy liver. H: Twenty five days-old quail died showing septicemia and nodules in the lungs and the heart.

Out of 265 flock samples (150 chickens, 60 ducks, 30 quails and 25 turkeys), twenty eight birds (10.6%) were positive for Salmonella isolation. The number and percentage of positive chickens, ducks, quails and turkeys were 16 (10.7%), 7 (11.7%), 3 (10%) and 2 (8%), respectively (Table 2). Salmonella isolates were serotyped using poly and monovalent "O" and"H" antisera and the results revealed that 16 strains isolated from chickens from different Governorates comporised of 4 (25%) *S*. Typhyimurium, 3 (18.8%) *S*. Enteritidis, 3 (18.8%) *S*. Kentucky, 2 (12.5%) *S*. Paratyphi A, 1 (6.25%) *S*. Molade, 1 (6.25%) *S*. Heidelberg, 1 (6.25%) *S*. Infantis and 1 (6.25%) *S*. Apeyene. Results of serotyping of 7 different salmonella strains from ducks showed 6 different serogroups identified as *S*. Entertidis (28.6%), *S*. Typhimurium (14.3%), *S*. Pararyphi A (14.3%), *S*. Kentucky (14.3%), *S*. Inganda (14.3%) and *S*. Bargny (14.3%). Serotyping of 3 different salmonellae from quails showed that 3 different serogroups were identified as *S*. Virchow (33.3%), *S*. Tamale (33.3%) and *S*. Typhimurium (33.3%). While, serotyping of 2 different salmonellae from turkeys showed 2 different serogroups identified as *S*. wingrove (50%) and *S*. Kentucky (50%).

Molecular characterization using PCR revealed *bcf*C and *stn* genes in 100% of Salmonella isolates while, *sop*B gene was detected in 18 (64.3%) isolates and *spv*C gene was detected in 3 isolates (10.7%) (Table 3 and Figure 2).

Table 2: The isolation rates of *Salmonella* serotypes from poultry flocks

Types of flocks	No of examined samples	Prevalence of *Salmonella* isolation				Isolated serotypes	
		Positive samples		Negative samples		serotype	Number (%)
		No	%	No	%		
Chickens	150	16	10.7	134	89.3	S. Typhimurium S. Enteritidis S. Kentucky S. Paratyphi A S. Molade S. Heidelberg S. Infantis S. Apeyeme	4(25%) 3(18.8%) 3(18.8%) 2(12.5%) 1(6.25%) 1(6.25%) 1(6.25%) 1(6.25%)
Ducks	60	7	11.7	53	88.3	S. Enteritidis S. Typhimurium S. Paratyphi A S. Kentucky S. Inganda S. Bargny	2(28.6%) 1(14.3%) 1(14.3%) 1(14.3%) 1(14.3%) 1(14.3%)
Quails	30	3	10	27	90	S. Virchow S. Tamale S. Typhimurium	1(33.3%) 1(33.3%) 1(33.3%)
Turkeys	25	2	8	23	92	S. Wingrove S. Kentucky	1(50%) 1(50%)
Total*	265	28	10.6	237	89.4	Total n. of isolates	28

* The percentage was calculated according to the total number of examined samples.

Discussion

The clinical signs of the examined birds were retarded growth, depression, lameness, ruffled feathers, chicks huddling together, respiratory troubles, whitish watery diarrhea and accumulation of faecal matter around the vent. The postmortem examination of both freshly dead and sacrificed birds revealed gross lesion in the form of septicemia, bronze discolouration enlarged liver with necrotic foci, splenomegaly with necrotic foci, pericarditis, enlarged heart, peritonitis, congested kidneys, inflammation of intestine and caecum and unabsorbed yolk sac in young birds. Similar signs obtained by Gast and Beard [3] Shivaprasad *et al*. [4] and Gast and Beard [5] and similar postmortem lesions obtained by Hoop and Posuschil [7] Shalaby

and Abdel-Hamid [22] and Abd El-Nasser *et al*. [23]. The occurrenec of Salmonella species was 10.6% from different poultry species. This is nearly similar to Taha [24] who isolated salmonellae from chicken with a percentage of 10% in Egypt, and Roy *et al*. [25] who isolated 11.99% *Salmonella* spp.) from poultry and poultry products. While, higher isolation rates were reported by Osman [26] who reported the islation of *Salmonella* spp. (30%) from poultry dropping from different broiler farms in Egypt. However, El-Zeedy *et al*. [27] reported lower isolation rate of *Salmonella* spp. from different poultry samples (4.1%) in Egypt. Such variation could be attributed to differences in environmental contamination, health control programs, management systems and/or the sensitivity of the procedure used in examination.

Table 3: Distribution of some virulence genes in the examined 28 *Salmonella* isolates among different poultry species

Code	Serovars	Source	*sop*B	*bcf*C	*spv*C	*stn*
1	*S*. Kentucky	chickens	+	+	_	+
2	*S*. Molade	chickens	+	+	_	+
3	*S*. Typhimurium	chickens	+	+	_	+
4	*S*. Kentucky	chickens	+	+	_	+
5	*S*. Heidelberg	chickens	+	+	_	+
6	*S*. Enteritidis	chickens	+	+	_	+
7	*S*. Paratyphi A	chickens	+	+	_	+
8	*S*. Typhimurium	chickens	+	+	_	+
9	*S*. Typhimurium	chickens	+	+	_	+
10	*S*. Infantis	chickens	+	+	_	+
11	*S*. Enteritidis	Chickens	+	+	_	+
12	*S*. Typhimurium	Chickens	+	+	_	+
13	*S*. Kentucky	Chickens	+	+	_	+
14	*S*. Paratyphi A	Chickens	+	+	_	+
15	*S*. Apeyeme	Chickens	+	+	_	+
16	*S*. Enteritidis	Chickens	+	+	_	+
17	*S*. Typhimurium	Ducks	+	+	_	+
18	*S*. Paratyphi A	Ducks	+	+	_	+
19	*S*. Enteritidis	Ducks	_	+	_	+
20	*S*. Kentucky	Ducks	_	+	_	+
21	*S*. Inganda	Ducks	_	+	_	+
22	*S*. Bargny	Ducks	_	+	+	+
23	*S*. Enteritidis	Ducks	_	+	_	+
24	*S*. Virchow	Quails	_	+	_	+
25	*S*. Tamale	Quails	_	+	+	+
26	*S*. Typhimurium	Quails	_	+	+	+
27	*S*. Wingrove	Turkeys	_	+	_	+
28	*S*. Kentucky	Turkeys	_	+	_	+
Total	28		18 (64.3%)	28 (100%)	3 (10.7%)*	28 (100%)

*** The percentage was calculated according to the total number of identified serovars.**

The number and percentages of positive chickens, ducks, quails and turkeys were 16 (10.7%), 7 (11.7%), 3 (10%) and 2 (8%), respectively. The highest percentage of Salmonella isolation was from ducks while the lowest percentage was from turkeys. The results of salmonella isolation from chickens (10.7%) in this study coordinated with El-Azzouny [28] who recorded a percentage of 10% in broilers and Rehan [29] who isolated *Salmonella* spp. from 12% of broiler chickens. Lower percentages were previously reported by Sadoma [30] and Mohamed *et al*. [31] who isolated *Salmonella* from chicken farms in Gharbia and Kafr-Elsheikh with an overall prevalence of 2% and 2.5%, respectively. However, higher percentage was recorded by Osman [26] who collected 150 random samples from different broiler farms and isolated 45 *Salmonella* strains with the

percentage of 30%. The variation in the percentage of Salmonella detection among poultry could be attributed to different factors including management, biosecurity, as well as, prophylactic antibiotics used in each circumstance [19].

The results of salmonella isolation from ducks (11.7%) in this study coordinated with Abd El-Tawab *et al*. [32] who isolated Salmonella from ducks with the percentage of 9.6% and Hoszowski and Wasyl [33] who detected salmonella in ducks with percentage of 14.3%. Higher isolation rates were previously recorded by Osman *et al.* [26] who reported an isolation rate of *Salmonella* spp. from 18.5% of ducks. In addition, Ismail [34] reported the percentage of isolation from ducks was 27.02% .

The obtained results were nearly similar to those obtained by Abd El- Tawab *et al*. [32] who isolated *Salmonella* spp. from quails with the percentage of 10%, also, Palanisamy and Bamaiyi [35] reported *Salmonella* isolation from 11.11% of quails. However, the results were different than those reported in Iran, where, *Salmonella* isolation rate reached 40% as reported by Jalali *et al*. [36] and in Brazil reached 75% as reported by Neto *et al*. [37].

In the present study *Salmonella* spp. were isolated from turkeys with a percentage of 8%. This was nearly similar to 9.7% reported by Tel *et al*. [38] in fecal specimens and Alatfehy [39] who reported that Salmonella isolation rate was 6.25% in turkeys.

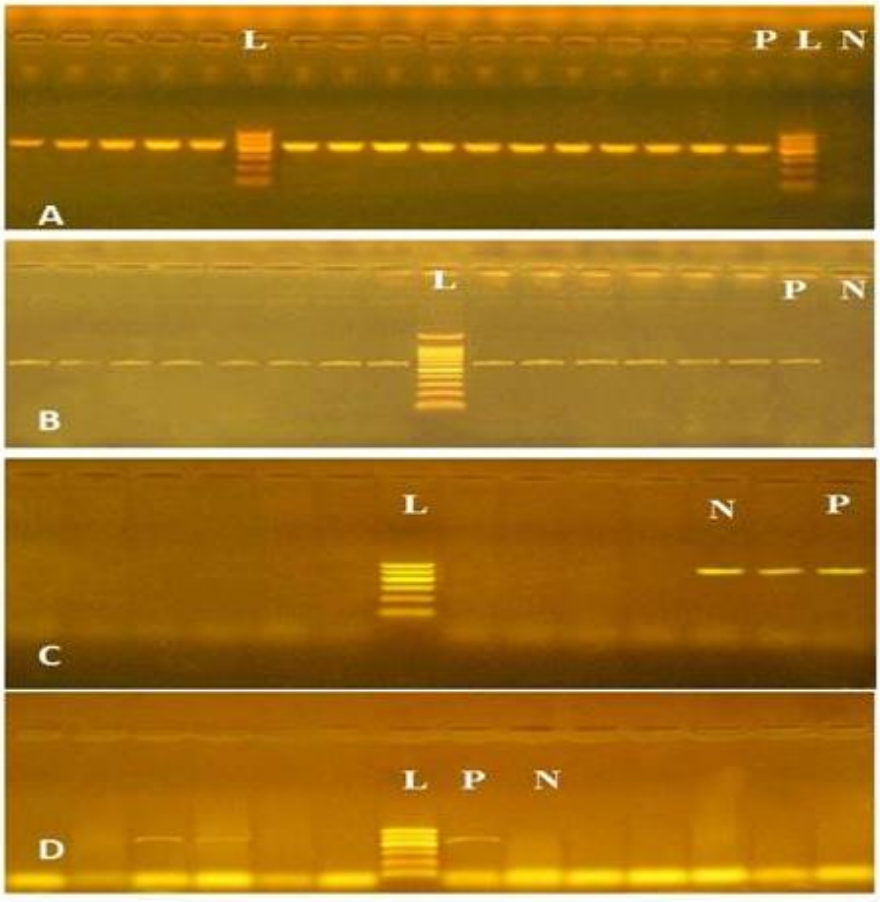

Figure 2: Agarose gel electrophoresis for amplified products of some virulence genes. A: PCR results for the *bcf*C gene showing positive amplification of 467 bp. B: PCR results for the *stn* gene showing positive amplification of 617 bp in all samples. C: PCR results for the *sop*B gene showing positive amplification of 517 bp.D: PCR results for the *spvC* gene showing positive amplification of 467 bp.

Salmonella isolates were serotyped using poly and monovalent "O" and"H" antisera and the result of this study revealed that 16 strains were isolated from chickens from different Governorates. The results in this study revealed that *S.* Typhimurium predominated other serotypes. These results agreed with Hoszowski *et al*. [9] who reported that *S.* Enteritidis and *S.* Typhimurium were the most common serotypes isolated from poultry. Whereas, Dahal [40] recorded that *S.* Entertidis is the most frequently isolated serotype (84.62%) followed by *S.* Typhimurium (15.38%).

The results of serotyping of 7 different Salmonellae from ducks in the current study showed that *S.* Entertidis (28.6%)and *S.* Typhimurium (14.3%) predominated other serotypes. These results coincide with Hoszowski and Wasyl [33] who detected Salmonella in duck broilers with the percentage of 14.3% and the most frequent serovars were *S.* Entertidis, *S.* Infantis, *S.* Hadar and *S.* Typhimurium. However, El-Sawy [41] isolated *Salmonella* spp. from ducklings in Kalioubia Governorate and they were identified as: *S.* Typhimurium, *S.* Tshiongwe, *S.* Newport, *S.* Nchanga, *S.* Tuebingen and *S.* Bovis- mobificans.

Regarding serotyping of 3 different Salmonella isolates from quails, 3 different serogroups were identified as *S.* Virchow (33.3%), *S.* Tamale (33.3%) and *S.* Typhimurium (33.3%). Different *Salmonella* spp. were previously serotyped by Neto *et al*. [37] who reported *S.* Corvalis; *S.* Give; *S.* Lexington; *S.* Minnesota; *S.* Schwarzengrund; *S.* Rissen and *S.* Typhimurium from meat-type quails in Brazil.

In the present study, 2 different serogroups were identified as *S.* wingrove (50%) and *S.* Kentucky (50%) from turkeys. Hird *et al*. [42] reported that *S.* Kentucky, *S.* Anatum, *S.* Heidelberg, *S.* Reading, and *S.* Senftenberg were identified from turkeys at the California Veterinary Diagnostic Laboratory System. The variation of prevelance might be due to geographical variation, differences in management, type of samples, age of examined birds, season, poor hygienic conditions and inadequate nutrition.

Results of PCR for the detection of *bcf*C from 28 isolated strains showed that it was present in all the isolates (100%). Nearly similar results were obtained by Osman *et al.* [26] who reported *bcf*C gene in 100% of the Salmonella serovars isolated from humans and day-old ducklings. Also, Alatfehy [39] recorded that *bcf*C gene with the percentage of 95.7% was identified in Salmonella isolates from poultry. However, El-Sayed [43] reported the absence of *bcf*C gene in Salmonella strains isolated from ducklings.

The results of our study revealed that *sop*B gene was detected in 18 isolates with the percentage of 64.3%. Nearly similar results were obtained by Osman *et al*. [26] who detected *sop*B gene with the percentage of 54.3%. However, lower percentage (15.4%) was reported by El-Sayed [43].

In the present study, *spv*C gene was detected in 3 isolates only with the percentage of 10.7%. Similar results was obtained by El-Azzouny [28] who identified *spv* gene in 6% of Salmonella isolates. The results disagreed with Amini *et al*. [44] who detected *spv* gene in 30% of Salmonella strains isolated from poultry and Moussa *et al*. [45] who reported that *spv* gene was present in 31.5% in *S.* Entertidis and 30% in *S.* Typhimurium isolated from poultry. In addition, the result of our study revealed that the *stn* gene was present in all of the isolates (100%). In accordance, Murugkar *et al*. [21] and Shalaby [46] reported that *stn* gene was detected in all the isolated Salmonella strains. Moreover, Zou *et al*. [16] identified *stn* gene in all 425 isolates (100%) of poultry origin.

Conclusion

In conclusion, different *Salmonella* species of different serotypes carrying common virulence genes were recovered from domestic birds in the examined areas of Delta, Egypt. Therefore, strictly hygienic and biosecurity measures must be applied in poultry management to avoid spread of salmonellae.

Conflict of interest

All the authors have no conflict of interest to declare.

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الملخص العربى

التوصيف المظهري والوراثي للسالمونيلا باراتيفويد المعزولة من الدواجن في منطقة الدلتا- مصر

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تهدف هذه الدراسة الي وتصنيف ميكروب سالمونيلا باراتيفويد من الدجاج ,البط ,السمان و الرومى من خمسه محافظات مصريه. كما تم إستخدام تفاعل البلمرة المتسلسل لتحديد جينات الضراوة الشائعة في السالمونيلا. ولهذا الغرض تم تجميع عينات من ٢٦٥ مزرعة دواجن و كانت العينات مقسمه الى ١٥٠ من مزارع الدجاج ,٦٠ من مزارع البط, ٣٠ من مزارع السمان و ٢٥ من مزارع الرومى من محافظات الدقهليه, كفر الشيخ, دمياط, الشرقيه و الغربيه. تم فحص الطيور اكلينيكيا وكذلك اجراء الصفة التشريحيو وعليه تم أخذ العينات من الكبد ,الرئه , الطحال, الاعورين و كيس المح لعزل السالمونيلا. كما تم اجراء الاختبارات البيوكيميائيه للعزل كما تم تصنيف المعزولات سيرولوجيا بالاختبارات الخاصه لتصنيف السالمونيلا. تم عزل ٢٨ عينه ايجابيه من ٢٦٥ عينه من الدواجن بنسبه (١٠.٦%) حيث تم عزل ١٦ عتره بنسبه (١٠.٧%) من الفراخ, تم عزل ٧ عترات من البط بنسبه (١١.٧%), تم عزل ٣ عترات من السمان بنسبه (١٠%) و تم عزل ٢ عتره من الرومى بنسبه (٨%). و بإجراء الاختبارات السيرولوجيه للمعزولات تبين انها ٤ سالمونيلا تيفيميوريم, ٣ سالمونيلا انترتيدس, ٣ سالمونيلا كنتاكى, ٢ سالمونيلا باراتايفاى ا ,١ سالمونيلا مولادى, ١ سالمونيلا هيدلبرج ,١ سالمونيلا انفانتيس ,١ سالمونيلا ايبيمى من الدواجن بنسبه (٢٥%) ,(١٨.٨%), (١٨.٨%), (١٢.٥%) ,(٦.٢٥%), (٦.٢٥%), (٦.٢٥%) ,(٦.٢٥%) ,(٦.٢٥%) بالترتيب. و ايضا تم عزل ٢ سالمونيلا انترتيدس , ١ عتره سالمونيلا من كل من سالمونيلا تيفيميوريم, سالمونيلا باراتايفاى ا, سالمونيلا كنتاكى, سالمونيلا انجاندا , سالمونيلا بارجنى من البط بنسبه (٢٨.٦%),(١٤.٣%),(١٤.٣%),(١٤.٣%),(١٤.٣%),(١٤.٣%),(١٤.٣%) بالترتيب. تم عزل ١ عتره من كل من سالمونيلا فيرشاو , سالمونيلا تامالى , سالمونيلا تيفيميوريم بنسبه (٣٣.٣%) لكل منهما فى السمان. و ايضا تم عزل ١ عتره من كل من سالمونيلا انجروف و سالمونيلا كنتاكى بنسبه (٥٠%) لكل منهما فى الرومى. على الجانب الأخر تم إجراء اختبار تفاعل البلمره المتسلسل لعدد ٢٨ عتره معزوله من الدواجن لكل جين من جينات الضراوه الأكثر شيوعا و هم (*sop*B, *bcf*C, *spv*C, *stn*) و قد تبين تواجد جين *bcf*C, *stn* بجميع المعزولات بنسبه (١٠٠%) يليهما *sop*B و كانت نسبه تواجده (٦٤.٣%) من المعزولات ثم *spv*C بنسبه (١٠.٧%) من المعزولات. يستخلص من الدراسة أن عترات مختلفة من ميكروب السالمونيلا التي تحتوي علي جينات الضراوة الأكثر شيوعا منتشرة بين الطيور فى المزارع بمحافظات الدلتا بمصر مما قد يسبب أعباء اقتصادية وصحية والتي تتطلب الي التطبيق الصارم لإجراءات الأمن الحيوي في مزارع الدواجن.