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, Kafr Elsheik, Damietta, Sharkia and Gharbia Governorates. Birds were subjected to either clinical and/or post-mortem examination, in addition to isolation and identification of salmonellae from internal organs including liver, lung, spleen, caecum and unabsorbed yolk sac. Biochemical 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. Apayeme 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 (sopB), Plasmid encoded virulence gene (spvC), salmonella enterotoxin (stn) and bacterial colonization factor (bcfC) showed the presence of stn and bcfC genes in all isolates, while, sopB 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 evolution 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 (bfcC) 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 out using 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 37°C ±1°C 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 41.5°C ± 1°C 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 37°C ±1°C for 24 ± 2 h. The plates were then checked for the growth of typical Salmonella colonies.

Biochemical identification

Hydrolysis of urea, H2S 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 37°C ± 1°C, then examined after four hours. If there was no change it was left for 24 h at 37°C ± 1°C. 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 (sopB), Salmonella plasmid virulence (spvC), Salmonella enterotoxin encoding gene (stn) and bacterial colonization factor encoding gene (bfcC). The primers sequences’ and PCR product sizes are shown in (Table 1) [12,21].
Table 1: Sequences of the used oligonucleotide primers for identification of virulence genes among Salmonellae in poultry

<table>
<thead>
<tr>
<th>Genes</th>
<th>Specificity/ location</th>
<th>Sequence of nucleotides (5’-3’)</th>
<th>Amplified product (bp)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Stn</td>
<td>Enterotoxin/ chromosomal</td>
<td>F- TTGTGTCGCTATCAGGGCAACC R-ATTCTAACCCTACTCTCCTC</td>
<td>617</td>
</tr>
<tr>
<td>sopB</td>
<td>Effector protein/ SPI-5</td>
<td>F-TCGACCTTCTAACCCTCCTC R-TACCTCCTCCTCTCATGCA</td>
<td>517</td>
</tr>
<tr>
<td>befC</td>
<td>Fimbrial usher protein/ chromosome</td>
<td>F-ACCAGAGACATTGCCCTCCTCC R-TTCTGTCCTGCCTGCTTTC</td>
<td>467</td>
</tr>
<tr>
<td>spvC</td>
<td>Plasmid encoded virulence gene/ plasmid</td>
<td>F-ACCAGAGACATTGCCCTCCTCC R-TTCTGATCCCTGCTATTTC</td>
<td>467</td>
</tr>
</tbody>
</table>

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 comprised of 4 (25%) S. Typhimurium, 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. Enteritidis (28.6%), S. Typhimurium (14.3%), S. Paratyphi 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 bcfC and stn genes in 100% of Salmonella isolates while, sopB gene was detected in 18 (64.3%) isolates and spvC gene was detected in 3 isolates (10.7%) (Table 3 and Figure 2).

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

<table>
<thead>
<tr>
<th>Types of flocks</th>
<th>No of examined samples</th>
<th>Prevalence of Salmonella isolation</th>
<th>Isolated serotypes</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Positive samples</td>
<td>Negative samples</td>
<td>serotype</td>
</tr>
<tr>
<td></td>
<td>No</td>
<td>%</td>
<td>No</td>
</tr>
<tr>
<td>Chickens</td>
<td>150</td>
<td>16</td>
<td>10.7</td>
</tr>
<tr>
<td>Ducks</td>
<td>60</td>
<td>7</td>
<td>11.7</td>
</tr>
<tr>
<td>Quails</td>
<td>30</td>
<td>3</td>
<td>10</td>
</tr>
<tr>
<td>Turkeys</td>
<td>25</td>
<td>2</td>
<td>8</td>
</tr>
<tr>
<td>Total*</td>
<td>265</td>
<td>28</td>
<td>10.6</td>
</tr>
</tbody>
</table>

* 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 occurrence 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 isolation 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

<table>
<thead>
<tr>
<th>Code</th>
<th>Serovars</th>
<th>Source</th>
<th>sopB</th>
<th>bcfC</th>
<th>spvC</th>
<th>stn</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>S. Kentucky</td>
<td>chickens</td>
<td>+</td>
<td>+</td>
<td>-</td>
<td>+</td>
</tr>
<tr>
<td>2</td>
<td>S. Molade</td>
<td>chickens</td>
<td>+</td>
<td>+</td>
<td>-</td>
<td>+</td>
</tr>
<tr>
<td>3</td>
<td>S. Typhimurium</td>
<td>chickens</td>
<td>+</td>
<td>+</td>
<td>-</td>
<td>+</td>
</tr>
<tr>
<td>4</td>
<td>S. Kentucky</td>
<td>chickens</td>
<td>+</td>
<td>+</td>
<td>-</td>
<td>+</td>
</tr>
<tr>
<td>5</td>
<td>S. Heidelberg</td>
<td>chickens</td>
<td>+</td>
<td>+</td>
<td>-</td>
<td>+</td>
</tr>
<tr>
<td>6</td>
<td>S. Enteritidis</td>
<td>chickens</td>
<td>+</td>
<td>+</td>
<td>-</td>
<td>+</td>
</tr>
<tr>
<td>7</td>
<td>S. Paratyphi A</td>
<td>chickens</td>
<td>+</td>
<td>+</td>
<td>-</td>
<td>+</td>
</tr>
<tr>
<td>8</td>
<td>S. Typhimurium</td>
<td>chickens</td>
<td>+</td>
<td>+</td>
<td>-</td>
<td>+</td>
</tr>
<tr>
<td>9</td>
<td>S. Typhimurium</td>
<td>chickens</td>
<td>+</td>
<td>+</td>
<td>-</td>
<td>+</td>
</tr>
<tr>
<td>10</td>
<td>S. Infantis</td>
<td>chickens</td>
<td>+</td>
<td>+</td>
<td>-</td>
<td>+</td>
</tr>
<tr>
<td>11</td>
<td>S. Enteritidis</td>
<td>Chickens</td>
<td>+</td>
<td>+</td>
<td>-</td>
<td>+</td>
</tr>
<tr>
<td>12</td>
<td>S. Typhimurium</td>
<td>Chickens</td>
<td>+</td>
<td>+</td>
<td>-</td>
<td>+</td>
</tr>
<tr>
<td>13</td>
<td>S. Kentucky</td>
<td>Chickens</td>
<td>+</td>
<td>+</td>
<td>-</td>
<td>+</td>
</tr>
<tr>
<td>14</td>
<td>S. Paratyphi A</td>
<td>Chickens</td>
<td>+</td>
<td>+</td>
<td>-</td>
<td>+</td>
</tr>
<tr>
<td>15</td>
<td>S. Apeyeme</td>
<td>Chickens</td>
<td>+</td>
<td>+</td>
<td>-</td>
<td>+</td>
</tr>
<tr>
<td>16</td>
<td>S. Enteritidis</td>
<td>Chickens</td>
<td>+</td>
<td>+</td>
<td>-</td>
<td>+</td>
</tr>
<tr>
<td>17</td>
<td>S. Typhimurium</td>
<td>Ducks</td>
<td>+</td>
<td>+</td>
<td>-</td>
<td>+</td>
</tr>
<tr>
<td>18</td>
<td>S. Paratyphi A</td>
<td>Ducks</td>
<td>+</td>
<td>+</td>
<td>-</td>
<td>+</td>
</tr>
<tr>
<td>19</td>
<td>S. Enteritidis</td>
<td>Ducks</td>
<td>+</td>
<td>+</td>
<td>-</td>
<td>+</td>
</tr>
<tr>
<td>20</td>
<td>S. Kentucky</td>
<td>Ducks</td>
<td>+</td>
<td>+</td>
<td>-</td>
<td>+</td>
</tr>
<tr>
<td>21</td>
<td>S. Inganda</td>
<td>Ducks</td>
<td>+</td>
<td>+</td>
<td>-</td>
<td>+</td>
</tr>
<tr>
<td>22</td>
<td>S. Bargny</td>
<td>Ducks</td>
<td>+</td>
<td>+</td>
<td>-</td>
<td>+</td>
</tr>
<tr>
<td>23</td>
<td>S. Enteritidis</td>
<td>Ducks</td>
<td>+</td>
<td>+</td>
<td>-</td>
<td>+</td>
</tr>
<tr>
<td>24</td>
<td>S. Virchow</td>
<td>Quails</td>
<td>+</td>
<td>+</td>
<td>-</td>
<td>+</td>
</tr>
<tr>
<td>25</td>
<td>S. Tamale</td>
<td>Quails</td>
<td>+</td>
<td>+</td>
<td>-</td>
<td>+</td>
</tr>
<tr>
<td>26</td>
<td>S. Typhimurium</td>
<td>Quails</td>
<td>+</td>
<td>+</td>
<td>-</td>
<td>+</td>
</tr>
<tr>
<td>27</td>
<td>S. Wingrove</td>
<td>Turkeys</td>
<td>+</td>
<td>+</td>
<td>-</td>
<td>+</td>
</tr>
<tr>
<td>28</td>
<td>S. Kentucky</td>
<td>Turkeys</td>
<td>+</td>
<td>+</td>
<td>-</td>
<td>+</td>
</tr>
</tbody>
</table>

Total 28

<table>
<thead>
<tr>
<th></th>
<th>18</th>
<th>28</th>
<th>3</th>
<th>28</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>(64.3%)</td>
<td>(100%)</td>
<td>(10.7%)*</td>
<td>(100%)</td>
</tr>
</tbody>
</table>

* 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 Bamaipi [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 bcfC 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 sopB 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. Enteritidis 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. Enteritidis (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. Enteritidis, S. Infantis, S. Hadar and S. Typhimurium. However, El-Sawy [41] isolated Salmonella spp. from ducklings in Kaloubia 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 prevalence 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 bcfC 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 bcfC gene in 100% of the Salmonella serovars isolated from humans and day-old ducklings. Also, Alatfehy [39] recorded that bcfC gene with the percentage of 95.7% was identified in Salmonella isolates from poultry. However, El-Sayed [43] reported the absence of bcfC gene in Salmonella strains isolated from ducklings.

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

In the present study, spvC gene was detected in 3 isolates only with the percentage of 10.7%. Similar results was obtained by El-Azzouney [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. Enteritidis 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.
References


الميلس العربي

التصنيف المظهرى والوراثى للسامونيليا باراتيفيدز المعوزة من الدواجن في منطقة الدلتا، مصر

يشمل السامونيليا باراتيفيدز المعوزة من الدواجن، وهو نوع من الفصيلة الفيروذية من طائفة السامونيليا، فضلاً عن أنواع أخرى من السامونيليا، وكلها تتماثل على أنها يمكن أن تسبب الامام أو الأمراض الأخرى. إنها تنتشر في جميع أنحاء العالم، بما في ذلك في مصر.

تهدف هذه الدراسة إلى وصف ومعرفة السامونيليا باراتيفيدز المعوزة من الدواجن في مصر. كما تم استخدام تحليل اللافتة المقتشر، لتحديد جينات الاستجابات المتنوعة للفيروس في السامونيليا. وللتحقيق في هذه الدراسة، تم جمع عينات من مزارع دواجن وكتابة العينات المقدمة إلى 150 من مزارع الدواجن، 70 من مزارع السامان، 10 من مزارع الطيور. تم تحليل الأفراد، وعمر الأفراد، وعدد الجرعة، والظروف الجوية المختلفة.

ال🚨 الفرامل النهائية للإنتاج الداجني: معهد بحوث صحّة الحيوان - الدقي - الجزيرة - مصر


الملخص العربي

تهدف هذه الدراسة إلى وصف ومعرفة السامونيليا باراتيفيدز المعوزة من الدواجن في مصر، وما هي تأثيرات الفيروسات على النمو والصحة الحيوانية. كما تم استخدام تحليل اللافتة المقتشر، لتحديد جينات الاستجابات المتنوعة للفيروس في السامونيليا. وللتحقيق في هذه الدراسة، تم جمع عينات من مزارع دواجن وكتابة العينات المقدمة إلى 150 من مزارع الدواجن، 70 من مزارع السامان، 10 من مزارع الطيور. تم تحليل الأفراد، وعمر الأفراد، وعدد الجرعة، والظروف الجوية المختلفة.

(outline of the Arabic summary)

- Uses of this dataset to understand the impact of salmonella on animal health and animal growth and development.
- Collection of data from various farms and farming conditions.
- Analysis of the data using statistical methods to identify causal relationships.
- Discussion of the results and their implications for animal health and productivity.


