MOLECULAR CHARACTERIZATION OF ANTIBACTERIAL RESISTANCE GENES OF SALMONELLA IN DUCKS

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ABSTRACT

Due to financial losses associated with avian salmonellosis, high costs of prohibiting its spread and prevention and its multiple drug resistance, Salmonella infection, particularly in ducks, attracted interest of many researchers as duck is a main reservoir of salmonella transmitted to human. Therefore, this study aimed at identifying circulating salmonella of ducks in Assiut governorate and assessing their antimicrobial susceptibility profile. Five hundred and sixty samples (150 livers and 410 cloacal swabs) of infected, freshly dead and apparently healthy ducks, were obtained from different farms in Assiut governorate for bacteriological, serological and molecular examination. An overall 16.6% Salmonella detection rate was recorded, where 15 isolates were identified serologically and molecularly as S. typhimurium (93.3%) and S. infantis (6.7%). Basing on antibiogram guidelines, detected Salmonella isolates were completely resistant (100%) to cephradine and amoxicillin, but had variable resistance degrees to colistin sulfate (80%), streptomycin (60%), chloramphenicol (33.3%), ampicillin and neomycin (26.7% of each). MIC test presented that all isolates were absolutely sensitive to colistin and doxycycline, but completely resistant to sulfaquinoxaline. High resistance rates occurred to cephradine, amoxicillin, streptomycin and florfenicol. sul-I, strA-strB, bla TEM, aadA and floR antibacterial resistance genes were assigned in variable frequencies (100%, 73.3%, 73.3%, 66.7% and 46.7%, respectively). In conclusion, S. typhimurium and S. infantis serovars are circulating among duck farms in Assiut. These serotypes exhibited genetic multiple drug resistance, that require special strict biosecurity and searching alternative effective control strategies.

Keywords: Ducks, Salmonella, PCR, MIC, Resistance gene.
INTRODUCTION

Having unique characters over other poultry types, duck industry forms important part of poultry sector worldwide either rural or enterprises. For many years, *Salmonella* infection was concerned researchers, veterinarians, and public health authorities due to its associated losses in livestock and risks of food poisoning, rank number one among the potentially foodborne bacteria. In spite exerted efforts and advances in prevention and control measures *Salmonella* infection still induce great economic losses. Being the most important reservoir of *Salmonellae* transmissible to human, duck received great interest among researchers (Yang et al., 2019). *Salmonella* infected birds show non-specific signs include depression, poor growth, weakness and diarrhea. The majority of mortalities usually occur in the first weeks of life. Rapidly developed septicemia is the origin of high mortality with limited or no clinical signs (Gast, 2008). Many *Salmonella* serotypes were detected in ducks, most of public health significance but some, including *S. gallinarum*, *S. pullorum*, *S. typhimurium*, *S. enteritidis* and *S. anatum* caused considerable losses in birds younger than few-weeks old (Buxton, 1957). *Salmonella* contains sequences unique invasion (invA) gene to this genus and confirmed to be a suitable target designed for PCR with a potential diagnostic application (Jamshidi et al., 2009). Like other pathogens of clinical and economic significance, *Salmonellae* face the problem of drug resistance, principally multidrug resistance that must be periodically assessed and monitored. Antimicrobial resistance is a phenomenon of huge concern for *Salmonella* and other foodborne pathogens. The extensive and misuse of antimicrobials in veterinary medicine is regularly incriminated in transfer of antibiotic resistance to human pathogens and spreading of multiple antibiotic resistant. Moreover, World Health Organization emphasized increasing number of non-typhoid *Salmonellae* resistant to antibiotics (McEwen, 2012). Polymerase chain reaction (PCR) is a molecular technique took up an increasingly significant space in the field of laboratory diagnostics, allowing the detection of various pathogens and their genetic properties like antibacterial resistance genes (Santos et al., 2001). So this study aimed at molecular identification of *Salmonella* isolates by conventional PCR, determining antibacterial susceptibility pattern and molecular characterization of antibacterial resistance genes among prevalent *Salmonella* serotypes.

MATERIALS AND METHODS

Sampling

Altogether, 560 samples (150 livers and 410 cloacal swabs) of infected, freshly dead and apparently healthy ducks, were obtained from different farms in Assiut and transported to laboratory of Faculty of Veterinary Medicine- Assiut University, Egypt.

Bacteriological and biochemical examination:

According to ISO 6579 (2002), samples were bacteriologically examined for *Salmonella* isolation. Briefly, swab from each sample was inoculated separately - under complete aseptic conditions- into 1:10 Buffered Peptone Water (pre-enrichment) and incubated aerobically at 37°C for 18 hours. Then, 0.1ml from the incubated broth was transferred to 10ml Rappaport Vassilidis Soy (RVS) broth
and incubated at 41.5°C for 24 hours. A loopful from the incubated RVS was streaked onto Xylose Lysine Deoxycholate (XLD) and incubated at 37°C for 24 hours. The suspected Salmonella colonies were gram stained for cellular morphology and identified biochemically by using (urease, TSI, lysine decarboxylation, indole and citrate utilization tests).

**Molecular identification of Salmonella isolates:**
Biochemically suspected Salmonella colonies were molecularly ascertained according to Dashti et al. (2009) and Oliveira et al. (2002). In brief, pure colonies were suspended in 5ml phosphate buffered saline (PBS) and centrifuged at 3000rpm (4°C) for 10minutes (repeated thrice till obtaining pellet). Pellets washed twice with PBS, re-suspended in 100 µl of degrade free water, heated for 10 min and chilled in ice for 30 min. and centrifuged at 3000xg for 5 min at 4°C. finally, supernatants were taken and used as template DNA it was amplified by Polymerase Chain Reaction assay using Salmonella specific invA gene primer set:

**Forward (F):** (5’-GTGAAATTATTCGC CACGTTCCGGGCAA-3’) and

**Reverse (R):** (5’-TCATCGCAACCGTCA AAGGAACC-3’) and Go Taq® Green Master mix (Promega) in Veriti thermocycler (Applied biosystems, Germany) following Oliveira et al. (2002) cycling conditions. Accurately, an initial hot start at 94°C for 5minutes, followed by 35 cycles, each consisting of 94°C for 30s, 55°C for 30s, and 72°C for 30s and the step of final extension at 72°C for 7minutes. The amplified products (5µl) were identified on 1.5% agarose gel stained with ethidium bromide and visualizing them with UV light in comparison to molecular size of 100-1,500bp DNA ladder (RTU, Cat.No.DM001.R500, 11bands).

**Molecular typing of Salmonella isolates:**
Multiplex and conventional PCR assays were carried out using primer sets specific for S. typhimurium with sequences:

**F1:** (5’-CAGCACCAGTTCCAACCTGA TAC-3’).

**R1:** (5’-GGCTTCCGGCCTATTGGA T A GC A -3’).

**F2:** (5’-ATAGCCATCTTTACCAGTTCC CCC-3’).

**R2:** (5’-GCTGCAACTGTACAGGATA TGCC-3’) (Lim et al., 2003) and **S. infantis** with sequence **F:** (5’-AACAAGCACAGCTATGCGG-3’) and **R:** (5’-CGACGTAAGGCACT 3’) (Kardos et al., 2007), producing amplicons with molecular weight of 663bp, 183bp and 413bp, respectively.

The reaction conditions for **S. typhimurium** (**Rfbj** and **FliC** genes) consisted of a primary denaturation at 95°C for 2 min, followed by thirty cycles of denaturation at 95°C for 1min, annealing at 57°C for 1min and extension at 72°C for 1min followed by final extension at 72°C for 10min. While, the PCR reaction conditions for **S. infantis** (**fljB** gene) consisted of an initial denaturation at 95°C for 6minutes, followed by 35 cycles of final denaturation at 95°C for 1min, annealing at 56°C for 15seconds and extension at 72°C for 1minutes followed by final extension at 72°C for 4minutes.

PCR products were screened as previously described for invA gene PCR.

**Assessing Antibacterial Susceptibility Pattern of Salmonella isolates using Disc diffusion method:**
Antibacterial sensitivity of Salmonella isolates was assessed using 15antibacterial agents. The sensitivity and the resistance were determined by criteria of Clinical and Laboratory Standard Institute (CLSI, 2018).
Determining antibacterial Minimum Inhibitory Concentration (MIC) to Salmonella isolates: according to (Stanković et al., 2017). Susceptibility of Salmonella to streptomycin, gentamycin, neomycin, florfenicol, sulphaminoxalin, doxycycline, cephadrine and amoxicillin was checked in microtiter plate 96 wells using double fold micro-dilution method against all isolated Salmonella in a density of $10^5$ CFU (CLSI, 2018). Each antimicrobial had a concentration of 10µg/mL, and 2.56µl of each antimicrobial was added into two wells in the first row of the plate, followed by 50 µl tryptone soya broths with bacteria was added to all wells. Extra 50µl tryptone soya broth containing bacteria was put in to the 1st row of plate (antimicrobials wells) then two-fold serial dilution method was made and remove the last 50 µl. The broth containing bacterial inoculum was taken as a positive control while, broth without bacterial inoculum used as a negative control. after a 24-hours of incubation at 37ºC, the microtiter plates were examined for the lowest concentration showing no detectable growth (MIC).

Molecular identification of antibacterial resistance genes among Salmonella isolates using PCR:

Table 1: Primer’s sequences and amplicon size (bp) for identification of Florfenicol, β-lactams and Sulfonamides resistance genes among Salmonella isolates.

<table>
<thead>
<tr>
<th>Primers</th>
<th>Target</th>
<th>primer sequence</th>
<th>Amplicon size</th>
<th>References</th>
</tr>
</thead>
<tbody>
<tr>
<td>Florfencol</td>
<td>StCM-L</td>
<td>floR</td>
<td>CACGTTGAGCCTCTATATG</td>
<td>888bp</td>
</tr>
<tr>
<td></td>
<td>StCM-R</td>
<td></td>
<td>ATGCAGAAGTAGAAGCGAC</td>
<td></td>
</tr>
<tr>
<td>β-lactams</td>
<td>TEM-F</td>
<td>bl a TEM</td>
<td>ATCAGCAATAAACGAC</td>
<td>517bp</td>
</tr>
<tr>
<td></td>
<td>TEM-R</td>
<td>bl a TEM</td>
<td>CCCGAAGAACGTITTTTC</td>
<td></td>
</tr>
<tr>
<td>Sulfonamides</td>
<td>Sul 1-F</td>
<td>Sul 1</td>
<td>TCACCGAGGACCTTCTTC</td>
<td>316bp</td>
</tr>
<tr>
<td></td>
<td>Sul 1-R</td>
<td></td>
<td>AATATCGGGGATAGAGCG</td>
<td></td>
</tr>
</tbody>
</table>

Table 2: Showing PCR conditions applied for the detection of Florfenicol, β-lactams and Sulfonamides resistance genes among Salmonella isolates.

<table>
<thead>
<tr>
<th>Stage</th>
<th>Temperature/Time</th>
<th>floR gene</th>
<th>bla TEM gene</th>
<th>Sul-1gene</th>
</tr>
</thead>
<tbody>
<tr>
<td>Initial denaturation</td>
<td>95ºC/5min</td>
<td>94ºC/5min</td>
<td>94ºC/1min</td>
<td></td>
</tr>
<tr>
<td>Denaturation</td>
<td>95ºC/45s</td>
<td>94ºC/30s</td>
<td>94ºC/1min</td>
<td></td>
</tr>
<tr>
<td>Annealing</td>
<td>52ºC/45s</td>
<td>54ºC/30s</td>
<td>60ºC/1min</td>
<td></td>
</tr>
<tr>
<td>Extension</td>
<td>72ºC/1min</td>
<td>72ºC/1 min</td>
<td>72ºC/1min</td>
<td></td>
</tr>
<tr>
<td>Final extension</td>
<td>72ºC/10min</td>
<td>72ºC/10 min</td>
<td>72ºC/10min</td>
<td></td>
</tr>
</tbody>
</table>

Molecular identification of Streptomycin resistance gene by multiplex PCR:
Table 3: Presenting primers, its sequences and amplicon size (bp) for identification of streptomycin resistance gene among salmonella isolates.

<table>
<thead>
<tr>
<th>Primers</th>
<th>Target</th>
<th>Primer sequence</th>
<th>Amplicon size</th>
<th>References</th>
</tr>
</thead>
<tbody>
<tr>
<td>streptomycin</td>
<td>aadA-F</td>
<td>GTGGATGGCCGGCCTG AAGCC</td>
<td>525bp</td>
<td>Madsen et al., 2000</td>
</tr>
<tr>
<td></td>
<td>aadA-R</td>
<td>AATGCCAGTCGGCAGCG</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>strA-strB-F</td>
<td>ATGGTGAGCCCTAAA ACTCT</td>
<td>891bp</td>
<td>Tamang et al., 2007</td>
</tr>
<tr>
<td></td>
<td>strA-strB-R</td>
<td>CGTCTAGGATCGAGCAAAAG</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

PCR reaction conditions consisted of a primary denaturation at 94°C for 4 min, followed by 35 cycles of denaturation at 94°C for 45 s, annealing at 60°C for 45 s and primary extension at 72°C for 45 s, followed by a last extension at 72°C for 10 minutes.

RESULTS

The overall incidence of Salmonella infection in ducks was 16.6%. 36 suspected Salmonella isolates were undergoing serological identification according to Kauffman – White scheme gave 15 isolates were positive for Salmonella spp. with a percentage rate (41.6 %) and 21 gave negative for Salmonella spp. with a percentage rate (58.3%). 14 (93.3%) of isolates belonged to S. typhimurium and one (6.6) isolates belonged to S. infantis.

All fifteen Salmonella isolates were harbored invA gene and amplified at 284 bp fragments as shown in Fig. (1). Out of 15 invA gene positive Salmonella isolates, 1 (6.6%) isolate was positive for fljB gene indicating Salmonella infantis. Out of 15 invA gene positive Salmonella isolates, 14 (93.3%) isolates were positive for Rfbj and fljC genes indicating Salmonella typhimurium as shown in Fig. (2).

Antibacterial sensitivity test of Salmonella isolates using the disc diffusion technique:
All Salmonella isolates were completely sensitive (100%) to amikacin, ciprofloxacin, enrofloxacin and Sulfamethoxazole/trimethoprim and they had a variable sensitivity to tetracycline and oxytetracycline (86.7% of each), doxycycline and gentamicin (80% of each), chloramphenicol and ampicillin (60% of each) and colistin sulfate (20%). They had intermediate sensitivity to neomycin (73.3%), streptomycin (33.3%), Ampicillin (13.3%), and (6.7%) for doxycycline and chloramphenicol. All isolates were completely resistance (100%) to cephardine and amoxicillin, while they showed a variable degree of resistance to colistin sulfate (80%), streptomycin (60%), chloramphenicol (33.3%), ampicillin and neomycin (26.7% of each), gentamicin (20%) and (13.3%) for tetracycline, oxytetracycline and doxycycline as shown Fig. (3).

Antibacterial sensitivity test of Salmonella isolates using MIC technique:
All examined salmonella isolates were absolutely sensitive to colistin and doxycycline, while they were completely resistant sulphaquinoxalin and highest
rate of resistance was against cephradine, amoxicillin, streptomycin and florfenicol, but the lowest degree of resistance for gentamicin and neomycin.

Detection of resistance genes in *Salmonella* isolates:
All *Salmonella* isolates were positive (100%) for *Sul-I* gene (Sulfonamide resistance gene) which giving amplification at 316 bp fragments as shown in Fig. (4). Eleven *Salmonella* isolates (11/15) (73.3%) were positive for *bla TEM* gene (β-lactams resistance gene) from the 15 examined *Salmonella* isolates which giving amplification at 517 bp fragments as shown in Fig. (4). Seven *Salmonella* isolates (7/15) (46.7%) were positive for *floR* gene (florfenicol resistance gene) from the 15 examined *Salmonella* isolates which giving amplification at 888 bp fragments as shown in Fig. (5). Eleven *Salmonella* isolates (11/15) (73.3%) were positive for *strA-strB* (streptomycin resistance gene) while, Ten *Salmonella* isolates (10/15) (66.7%) were positive for *aadA* gene (streptomycin resistance gene), from the 15 examined *Salmonella* isolates which giving amplification at 891bp and 525bp fragments as shown in Fig.(6).

![Fig. (1): Detection of *invA* gene in *Salmonella* isolates. Positive samples produce band (284 pb), Lane M: 1Kb DNA Ladder, Lane: 1 to 5 were positive samples produce band (284 bp)](image1)

![Fig. (2): Detection of *Rfbj* and *fltC* genes specific for *S. typhimurium* and *fljB* gene specific for *S. infantis* in samples. Positive samples produce bands (663 and 183bp) specific for *S. typhimurium* and (413 bp) specific for *S. infantis*. Lane M: 1 Kb DNA Ladder, Lane: (1 to 5) positive samples for *S. typhimurium* (produce bands 663 and 183bp) while, Lane: (8) positive samples for *S. infantis* produce band (413bp).](image2)
Fig. (3): antibacterial sensitivity and resistance percentages of isolated Salmonellae

Fig. (4): Detection of Sul-1 and bla TEM gene in Salmonella isolates. Positive samples produce band (316 and 517bp), respectively. Lane M: 1Kb DNA Ladder, Lane: 1, 2, 3, 4 and 5 were positive samples produce band (316bp) for Sul-1gene and Lane: 6,7,8,9 and 10 were positive samples produce band (517bp) for bla TEM gene.
Fig. (5): Detection of floR gene in Salmonella isolates. Positive samples produce band (888bp). Lane M: 1Kb DNA Ladder, Lane: 1, 2, 6, 9, 10, 12 and 13 were positive samples produce band (888bp) while, Lane: 3, 4, 5, 7, 8, 11 and 14 were negative samples.

Fig. (6): Detection of strA-strB and aadA genes in Salmonella isolates. Positive samples produce bands (891 and 525bp) respectively, Lane M: 1Kb DNA Ladder, Lane: 1, 2, 3, 4, 6, 7, 8, 9, 11 were positive samples produce band of 525bp for aadA gene while, Lane: 3, 4, 5, 7, 8, 9, 10, 11 were positive samples produce band (891bp) for strA-strB gene and lane: 3, 4, 7, 8, 9, 11 were positive samples produce 2 bands (891 and 525bp) for strA-strB and aadA genes, respectively.

Table 4: Distribution of resistance genes among Salmonella isolates with different serotypes.

<table>
<thead>
<tr>
<th>Serotype (No.tested)</th>
<th>No. of resistance genes positive isolates (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Sul-1</td>
</tr>
<tr>
<td>S.typhimurium(14)</td>
<td>14(100)</td>
</tr>
<tr>
<td>S.infantis (1)</td>
<td>1(100)</td>
</tr>
<tr>
<td>Total examined (15)</td>
<td>15(100)</td>
</tr>
</tbody>
</table>

Sul-1= resistant gene for sulfonamide.
Bla TEM = resistant genes for β-lactams
FloR= resistant gene for florfenicol.
aadA and strA-strB= resistant gene for streptomycin.
DISCUSSION

Pathogenic *Salmonella* isolates in ducklings and duck farms can be identified using Polymerase Chain Reaction (PCR) (Yang *et al.*, 2019). The invasion gene (*invA*) encodes a protein found in bacteria's inner membrane that is required for invasion of the host's intestinal mucosa (Singh *et al.*, 2013) and a common unique marker gene in all isolates of *Salmonella* species (Liu *et al.*, 2012). In this study, The PCR confirmed the conventional tests performed and all 15 examined isolates were positive for *invA* gene with 100% specificity, the size of amplified product was 284bp as shown in Fig. (1). similar findings have been described by (Elgohary *et al.*, 2017) who detected *invA* genes in all *Salmonella* serovars isolated from duck farms. Fourteen salmonella isolates (93.3%) were positive for Rfbj and fliC genes indicating *S. typhimurium* and one (6.7%) was positive for fljB gene indicating *S. infantis* as shown in Fig. (2). The predominant serotype in this study was *S. typhimurium* in duck farms. These results went in parallel with these reported by (Niu *et al.*, 2020) who found that *S. typhimurium* was the common serotype recovered from ducks in China, (Abel-Tawab *et al.*, 2020 and El shabrawy *et al.*, 2021) who reported that *S. typhimurium* was the predominant isolated from ducks in Egypt these results in contrast to (Enany *et al.*, 2018) who found that *S. ruzizi, S. give and S. enteritidis* isolated from local duckling with 0.5% for each. (Han *et al.*, 2020) who found that *S. Indiana* (26.3%) as one of the prevalent serovars in duck carcasses from China. The 2nd common serotype in this study was *S. infantis* (6.7%) and detected in high percentage (14.6%) in retail duck meat in China by (Chen *et al.*, 2020). This was due to the fact that the distribution of the most common *Salmonella* serotypes is largely determined by geographical factors that change over time (Huehn *et al.*, 2010), and may be related to sampling methods and isolation techniques (Vanantwerpen *et al.*, 2016), despite the fact that several serotypes are consistently detected at a high rate around the world (Gast, 2007).

According to the results concerning antimicrobial susceptibility test presented in Fig. (3). Fifteen salmonella isolates showed the highest percentage of resistance (100%) to cephradine and amoxicillin followed by colistin sulfate (80%), streptomycin (60%) and chloramphenicol (33.3%). These findings were higher than those reported by (Abouzeid *et al.*, 2020) who documented that amoxicillin/clavulanic resistance was 70% in Salmonella isolated from diarrheic ducklings. In contrary to these results (Abd El-Tawab *et al.*, 2018) who found that salmonella isolated from laying ducks were sensitive to amoxicillin and streptomycin. This was associated to excessive use of these antibacterial agents in duck farms as result of the increased rates of duck diseases due to the development of intensive animal husbandry and high stocking density (Guo *et al.*, 2020).

In this work, all *Salmonella* isolates were 100% sensitive to amikacin, ciprofloxacin, enrofloxacin and trimethoprim/ sulphamethoxazole, followed by tetracycline (86.7%), gentamicin (80%), ampicillin and chloramphenicol (60% for each). These results to some extent agree with (Abouzeid *et al.*, 2020) who reported that salmonella isolates were amikacin...
sensitive by 100%, followed by gentamicin and sulphamethoxazole/trimethoprim (50% for each). In contrary to these results (El-shabrawy et al., 2021) who found that salmonella isolates displayed high resistance rate to tetracycline (85%), amikacin and sulphamethoxazole/trimethoprim (62.8% for each) and ampicillin (51.4%).

In this study, antibacterial sensitivity test by using MIC showed that all examined salmonella isolates were absolutely sensitive to colistin and doxycycline, while the highest rate of resistance was against sulfadiazine, cephradine, amoxicillin and florfenicol, while variable degree of resistance for streptomycin, gentamicin and neomycin. these findings nearly in agreement with (Chen et al., 2020) who reported that the highest levels of resistance were observed for sulfadiazine, followed by florfenicol, streptomycin, and gentamicin. These findings differed with (Zhao et al., 2017) stated that most 56 isolates recovered from ducks were resistant to tetracycline, ampicillin and ciprofloxacin.

In this study, PCR was a perfect tool for perfect detection of Salmonella resistant genes and the results that the sul-I gene, a gene encoded for sulfonamide resistance was reported in the present study with a percentage of 100% among salmonella isolates as shown in Fig. (4). these results consistently, (Niu et al., 2020) who detected sul-I gene in 92 salmonella isolates isolated from duck farms in south China was 97.8%, these results were higher than results obtained by (Chen et al., 2020) who found that sul-I gene with percentage of 63% and (Abd El-Tawab et al., 2015) who reported that Sul-1with percentage of 87%.

The bla TEM gene, a gene encoded for β-lactamases resistance was reported in the present study with a percentage of 73.3% (11 out of 15 isolates) which giving amplification at 517bp fragments as shown in Fig. (4). These results were higher than results obtained by (Abdallah et al., 2015) who reported that bla TEM gene with percentage of 41.2% and (Zhao et al., 2017) who reported that bla TEM gene with percentage of 35.7% among 56 isolates recovered from ducks.

The floR gene, a gene encoded for florphenicol resistance was reported in the present study with a percentage of 46.7 % (7 out of 15 isolates) which giving amplification at 888 bp fragments as shown in Fig. (5). These results were higher than results obtained by (Zhao et al., 2017) who reported that floR gene with percentage of 23.2% among 56 isolates recovered from ducks. These results were lower than results obtained by (Abd El-Tawab et
al., 2015) who reported that floR gene with percentage of 77.8% and (Niu et al., 2020) who detected floR in 92 salmonella isolates obtained from duck farms in south China was 97.8%.

The StrA-strB and aadA genes, genes encoded for streptomycin resistance were reported with a percentage of (11 out of 15 isolates) 73.3 % and (10 out of 15 isolates) 66.7 %, respectively as shown in Fig. (6) these results were lower than results obtained by (Niu et al., 2020) who detected aadA1 in 92 salmonella isolates obtained from duck farms in south China was 100%, (Chen et al., 2020) who documented that StrA gene and aadA1 with percentage of 94.1% and 83.8%, respectively while these results were higher than (Abd El-Tawab et al., 2015) who reported that aadA2 gene with percentage of 53.1%. (Abdallah et al., 2015) who reported that aadA2 gene with percentage of 47%. The detection rates of resistant genes greatly differ among diverse studies due to the various circumstances and dosages of antibiotics used in the farms (Niu et al., 2020) and as result of the excessive number of related genes that mediate resistance to these antibacterial agents or alternatively, due to changes in the Salmonella resistance mechanism result from geographical or other factors (Chen et al., 2020).

REFERENCES


resistance, virulence genes and genetic diversity of Salmonella isolated from retail duck meat in southern China. Microorganisms, 8(3): 444.


التوصف الجزيئي للجينات المقاومة للمضادات البكتيرية للسالمونيلا في البط
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نتيجة للخسائر الاقتصادية الناجمة عن محاولة التغلب على الإصابة بالسالمونيلا في الدواجن والتكاليف الباهظة لمنع انتشارها ومقاومةها المتعددة للأدوية، فقد حظيت الإصابة بهذه البكتيريا بالاهتمام الكبير لكونها أهم مستودعات السالمونيلا التي تنتقل إلى الإنسان. وذلك هدف هذه الدراسة إلى تحري عن انتشار السالمونيلا في البط بمحافظة أسوان، حيث تم تجميع 60 عينة (20 كبدًا و40 مسحة مجمع) من بط سليم ظاهريا أومصاب أو نافق حديثًا، وخضعت العينات للاختبارات البكتيرولوجية والسيرولوجية (وفقاً لمخطط Kauffman-White) والبيولوجية الجزيئية، وتقييم هشاشة الدراسات البيئية المختلفة باستخدام اختبار الحساسية وتأتي أقل جرعة مثبطة من هذه الأدوية، والتحقق من الحساسيتها لمضادات البكتيرية المختلفة باستخدام اختبار MIC test و tecnhique واحصائية باستخدام برنامج Excel.

وكشفت النتائج عن 16.6% نسبة الإصابة الكلية بالسالمونيلا في البط، حيث تم تعرف 15 معزولة من السالمونيلا (سيرولوجيا وجينيا)، كسالونيلا تيفيموريم (97.3%)، والسالمونيلا أفاتينيس (2.7%). وتم إجراء اختبار الحساسية العملي لهذه المعزولات ضد مضادات البكتيرية المختلفة باستخدام MIC test و tecnhique ومسح الأساليب الشائعة، وحصيلة الأدوات البكتيرية وحيث السيرفوولكسين والسيبروفلوكساسين وكالفولوكساسين وسلفاميثوكسيدوز، ويراجع الانتهاز البكتيرائي وحصيلة الأساليب الشائعة، وحصيلة الأدوات البكتيرية. عند دراسة مدى تأثير أقل جرعة مثبطة من مضادات البكتيرية على معزولات السالمونيلا وجد أن جميع معزولات المختبرة كانت حساسة تماماً للكلوريسين والدويسكسيكليرين بينما كا نأعلى نسبة مقاومة ضد سلافاكوسكلين ويسفرادين وأموكسيلين. وفولفيكونول والستربتومايسين. وبعد ذلك تم تشخيص (PCR) للكشف عن الجينات المقاومة الموصوفة. وتم تحصيلها في معزولات السالمونيلا من سلائف الكلاسيكية، كانت جينات المقاومة التي تحصلت هي معزولات السالمونيلا سلم (Sulبلا TEM floR وSul) لمعزولات مقابلة للكلوريسين، وaadA والستربتومايسين، وaadA floR وSul في معزولات سلم (Sulبلا TEM floR وSul) لمعزولات مقابلة للكلوريسين، وaadA خصصت (100%) للجين المقاومة الحساس السلم (Sulبلا TEM floR وSul) للجين المقاومة الخاص بالستربتومايسين والفلورفينول (FloR وaadA)

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