Prevalence of Virulent Genes in Salmonella Isolated from Some Raw Meat Products

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Abstract
Two hundred random samples of beef burger, sausage, minced meat and hot dog were collected from the markets in Port-Said city under aseptic condition for isolation of Salmonella spp. The results revealed the isolation of 7 Salmonella isolates with a percentage of 3.5%. The isolated Salmonellae were S. Anatum, S. Enteritidis, S. Hato and S. Lamberhurst with a percentage of 28.6%, 14.3%, 28.6% and 28.6% respectively. The antibacterial resistance of the isolates was detected for 12 antibacterial agents by disk diffusion method. Isolated Salmonellae were resistant to Amoxicillin/clavulanic a., Doxycycline and Erythromycin. One hundred percent of the isolated serovars were sensitive to Ciprofloxacin, Chloramphenicol and Gentamycin. PCR assays using specific primers for the detection of different virulence genes of Salmonella spp. proved the presence of invA, csgD, stn, ompA and ompF genes in all 7 Salmonella serovars. The public health hazard of Salmonella, as well as recommended measures to improve quality status of processed meat were discussed.

Key words: Salmonella spp., processed meat, antibacterial resistance genes, PCR, Public health.

Introduction
Salmonella considered one of the most preponderant bacterial causes of foodborne gastroenteritis all over the world after Campylobacter. Salmonella may spread through wildlife and domestic animals' fecal contamination, poor fertilization methods, contaminated water, and other activities (Meldruim and Wilson, 2005). Salmonella serotypes can grow and survive in many foods (Kimura AC, et al., 2005). Salmonella in foods is governed by a different type of ecological and environmental factors, as pH, water activity, chemical composition, the presence of synthetic or natural
antimicrobial agents, and also storage temperature. In addition, there are other factors such as the physical manipulation and heat treatment (Carraminana JJ, et.al., 2004). In developed countries in which active coordinated foodborne disease surveillance, serotypes such as Enteritidis and Typhimurium are frequently reported. Nowadays, global meat markets, poultry, pets, fruits, vegetables, and farm animals, considered an important sources of Salmonella contamination which were complex, and sometimes its control is difficult. One of the main sources of Salmonella infections were found in meat products. As a result of this study, surveillance of Salmonella contamination in meat products is further most important for the control and prevention of severe diseases (Ye et al., 2011).

Bacterial antibiotic resistance has been recognized as a major medical problem facing humankind and for preventing this problem, studying of their antibiotic susceptibilities, antibiotic resistance genes and their transmission is required (Adel and Sabiha, 2010). Food have been studied as important source of antibiotic resistant microorganisms, which may persist in processed food and subsequently transmitted to environment (Zhang, et al., 2009) and so, affecting bacterial virulence among bacterial population (Knezevic and Petrovic, 2008). An update technique based on molecular biology, such as PCR method, which is rapid, specific and sensitive method were used for the detection of food borne pathogens (Chiu et al., 1996).

Material and methods
Two hundred random samples of beef burger, sausage, minced meat and hot dog samples were collected from different markets in Port- Said city, Egypt under aseptic condition. All collected samples were transported in ice box to be bacteriologically examined for Salmonella isolation and identification.

Isolation and Identification of Salmonella spp.: Isolation and identification of Salmonella was done according to iso 6579 (2002).

Serological identification of Salmonella. Serological identification of Somatic (O) and flagellar (H) was carried out using Salmonella antisera (Denka Seiken Co., Japan), (Cruichkshank et al., 1975). (Kauffman, 1974).

Antibiotic susceptibility testing:
Determination of *Salmonella* susceptibility to different antimicrobial agents made using disc diffusion technique according to *(Finegold and Martin, 1982)*.

**Molecular examination of Pseudomonas:**

**DNA extraction:** was performed using the QIAamp DNA Mini kit (Qiagen, Germany, GmbH) with the modifications recommended by the manufacturer. Oligonucleotide Primers used were synthesized in reference lab. for veterinary quality control on poultry production *(Egypt)* and were listed in table (1).

**PCR amplification: DNA samples.** Primers were utilized in a 25- µl reaction containing 12.5 µl of Emerald Amp Max PCR Master Mix (Takara, Japan), 1 µl of each primer of 20 pmol concentrations, 4.5 µl of water, and 6 µl of DNA template. Extraction of DNA, preparation of PCR then cycling conditions of the primers during PCR.

**Analysis of the PCR Products: Conventional PCR products.** The products of PCR were separated by electrophoresis on 1.5% agarose gel stain with Athidium Promide (Applichem, Germany, GmbH) in 1x TBE buffer at room temperature using gradients of 5V/cm. For gel analysis, 15 µl of the products was loaded in each gel slot. A 100 bp and 100 bp plus DNA Ladders (Qiagen, Germany, GmbH) were used to determine the fragment sizes. The gel was photographed by a gel documentation system (Alpha Innotech, Biometra) and the data was analyzed through computer software.

**Table (1):** Oligonucleotide primers sequences. (Source: Metabion, Germany).

<table>
<thead>
<tr>
<th>Primer</th>
<th>Sequence</th>
<th>Amplified product</th>
<th>References</th>
</tr>
</thead>
<tbody>
<tr>
<td><em>Stn</em></td>
<td>TTG TGT CGT TAT CAC TGG CAA CC</td>
<td>617 bp</td>
<td>Murugkar <em>et al.</em>, 2003</td>
</tr>
<tr>
<td><em>invA</em></td>
<td>GTGAAATTATCGCCACGTTCGGGCAA TCATCGCACCCTCAAAGGAACC</td>
<td>284 bp</td>
<td>Oliveira <em>et al.</em>, 2003</td>
</tr>
<tr>
<td><em>ompA</em></td>
<td>AGT CGA GCT CAT GAA AAAGAC AGC TAT CGC</td>
<td>1052 bp</td>
<td>Kataria <em>et al.</em>, 2013</td>
</tr>
<tr>
<td></td>
<td>AGT CAA GCT TTT AAG CCT GCG GCT GAG TTA</td>
<td></td>
<td></td>
</tr>
<tr>
<td><em>ompF</em></td>
<td>CCTGGCAGCGGTGATCC</td>
<td>519 bp</td>
<td>Tatavarthy and Cannons, 2010</td>
</tr>
<tr>
<td></td>
<td>TGGTTAATCTAGCCATC</td>
<td></td>
<td></td>
</tr>
<tr>
<td><em>csgD</em></td>
<td>TTACCGCCTGAGATTATCGT</td>
<td>651 bp</td>
<td>Bhowmick <em>et al.</em>, 2011</td>
</tr>
<tr>
<td></td>
<td>ATGTTTAATGAAGTCCATAG</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
Results of Polymerase Chain Reaction technique for \textit{invA} gene from DNA of the isolated \textit{Salmonella} species.

Seven \textit{Salmonella} isolates from a total of 7 isolates were examined by PCR for \textit{stn} gene. Seven isolates (7/7) (100\%) were positive for \textit{stn} genes giving amplification of 284 bp fragments. Also, the positive control showed 284 bp fragments whereas no amplification could be observed with the negative control.

Results of Polymerase Chain Reaction technique for \textit{csgD} gene from DNA of the isolated \textit{Salmonella} species.

Seven \textit{Salmonella} isolates from a total of 7 isolates were examined by PCR for \textit{csgD} gene. Seven isolates (7/7) (100\%) were positive for this gene giving amplification of 651 bp fragments. Also the positive control showed 651 bp fragments whereas no amplification could be observed with the negative control.

Results of Polymerase Chain Reaction technique for \textit{stn} gene from DNA of the isolated \textit{Salmonella} species.

Seven \textit{Salmonella} isolates from a total of 7 isolates were examined by PCR for \textit{stn} gene. Seven isolates (7/7) (100\%) were positive for this gene giving amplification of 617 bp fragments. Also, the positive control showed 617 bp fragments whereas no amplification could be observed with the negative control.

Results of Polymerase Chain Reaction technique for \textit{ompA} gene from DNA of the isolated \textit{Salmonella} species.

Seven \textit{Salmonella} isolates from a total of 7 isolates were examined by PCR for \textit{ompA} gene. Seven isolates (7/7) (100\%) were positive for this gene giving amplification of 1052 bp fragments. Also, the positive control showed 1052 bp fragments whereas no amplification could be observed with the extracted DNA of the negative control.

Results of Polymerase Chain Reaction technique for \textit{ompF} gene from DNA of the isolated \textit{Salmonella} species.

Seven \textit{Salmonella} isolates from a total of 7 isolates were examined by PCR for \textit{ompF} gene. Seven isolates (7/7) (100\%) were positive for this gene giving amplification of 519 bp fragments. Also, the positive control showed 519 bp fragments whereas no amplification could be observed with the extracted DNA of the negative control.
Table 2. Incidence, Numbers and percentage of different serotypes from the isolated *Salmonella* samples. (n=7)

<table>
<thead>
<tr>
<th>Type of samples</th>
<th>Total sample processed</th>
<th>Total positive</th>
<th>serotypes</th>
<th>Positive cases</th>
<th>Percentage</th>
</tr>
</thead>
<tbody>
<tr>
<td>Beef burger</td>
<td>50</td>
<td>2</td>
<td><em>S. Anatum</em></td>
<td>1</td>
<td>14.3</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td><em>S. Enteritidis</em></td>
<td>1</td>
<td>14.3</td>
</tr>
<tr>
<td>sausage</td>
<td>50</td>
<td>2</td>
<td><em>S. Hato</em></td>
<td>1</td>
<td>14.3</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td><em>S. Lamberhurst</em></td>
<td>1</td>
<td>14.3</td>
</tr>
<tr>
<td>Minced meat</td>
<td>50</td>
<td>3</td>
<td><em>S. Anatum</em></td>
<td>1</td>
<td>14.3</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td><em>S. Hato</em></td>
<td>1</td>
<td>14.3</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td><em>S. Lamberhurst</em></td>
<td>1</td>
<td>14.3</td>
</tr>
<tr>
<td>Hot dog</td>
<td>50</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>total</td>
<td>200</td>
<td>7</td>
<td><em>S. Anatum</em></td>
<td>1</td>
<td>14.3</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td><em>S. Hato</em></td>
<td>2</td>
<td>28.6</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td><em>S. Lamberhurst</em></td>
<td>2</td>
<td>28.6</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td><em>S. Enteritidis</em></td>
<td>2</td>
<td>28.6</td>
</tr>
</tbody>
</table>

Table 3. Antigenic structure of the isolated *Salmonella* samples.

<table>
<thead>
<tr>
<th>No</th>
<th><em>Salmonella</em> serotypes</th>
<th>O antigen</th>
<th>H antigen</th>
<th>Phase I</th>
<th>Phase II</th>
</tr>
</thead>
<tbody>
<tr>
<td>1, 6</td>
<td><em>S. Anatum</em></td>
<td>3, {10}, {15}, {15,34}</td>
<td>e, h</td>
<td>1, 6</td>
<td></td>
</tr>
<tr>
<td>2</td>
<td><em>S. Enteritidis</em></td>
<td>9, 12</td>
<td>g, m</td>
<td></td>
<td>-</td>
</tr>
<tr>
<td>3, 4</td>
<td><em>S. Hato</em></td>
<td>1, 4, {5}, 12</td>
<td>g, m, s</td>
<td>{1, 2}</td>
<td></td>
</tr>
<tr>
<td>5, 7</td>
<td><em>S. Lamberhurst</em></td>
<td>3, 10</td>
<td>e, h</td>
<td>e, n, Z_{15}</td>
<td></td>
</tr>
</tbody>
</table>
Table 4. Antibiogram of the obtained Salmonella isolates.

<table>
<thead>
<tr>
<th>Antibacterials</th>
<th>S. Anatum</th>
<th>S. Enteritidis</th>
<th>S. Hato</th>
<th>S. Hato</th>
<th>S. Lamberhut</th>
<th>S. Anatum</th>
<th>S. Lamberhut</th>
</tr>
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<tbody>
<tr>
<td></td>
<td>Code no. of samples</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>AMC</td>
<td>R</td>
<td>R</td>
<td>R</td>
<td>R</td>
<td>R</td>
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<tr>
<td>CTX</td>
<td>R</td>
<td>I</td>
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<td>S</td>
<td>R</td>
<td>S</td>
</tr>
<tr>
<td>C</td>
<td>S</td>
<td>S</td>
<td>S</td>
<td>S</td>
<td>S</td>
<td>S</td>
<td>S</td>
</tr>
<tr>
<td>CIP</td>
<td>S</td>
<td>S</td>
<td>S</td>
<td>S</td>
<td>S</td>
<td>S</td>
<td>S</td>
</tr>
<tr>
<td>CT</td>
<td>I</td>
<td>I</td>
<td>R</td>
<td>R</td>
<td>I</td>
<td>R</td>
<td>S</td>
</tr>
<tr>
<td>DO</td>
<td>R</td>
<td>R</td>
<td>R</td>
<td>R</td>
<td>R</td>
<td>R</td>
<td>R</td>
</tr>
<tr>
<td>E</td>
<td>R</td>
<td>R</td>
<td>R</td>
<td>R</td>
<td>R</td>
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<td>R</td>
</tr>
<tr>
<td>CN</td>
<td>S</td>
<td>S</td>
<td>S</td>
<td>S</td>
<td>S</td>
<td>S</td>
<td>S</td>
</tr>
<tr>
<td>NA</td>
<td>I</td>
<td>I</td>
<td>S</td>
<td>S</td>
<td>S</td>
<td>I</td>
<td>S</td>
</tr>
<tr>
<td>NOR</td>
<td>I</td>
<td>S</td>
<td>S</td>
<td>S</td>
<td>I</td>
<td>I</td>
<td>I</td>
</tr>
<tr>
<td>RF</td>
<td>I</td>
<td>S</td>
<td>R</td>
<td>R</td>
<td>I</td>
<td>I</td>
<td>I</td>
</tr>
<tr>
<td>SXT</td>
<td>I</td>
<td>S</td>
<td>I</td>
<td>I</td>
<td>I</td>
<td>I</td>
<td>I</td>
</tr>
</tbody>
</table>

S: sensitive, R: Resistance, I: Intermediate  
(AMC (amoxicillin / clavulnic acid), CN (gentamycin), CT (colistin-sulfate), CTX (cefotaxime), SXT (trimethoprim/sulphamethoxazole), DO (doxycycline), C (chloramphenicol), RA (rifampin), CIP (ciprofl oxacin e), NOR (norfloxacin e), NA (nalidixic acid) E (erythromycin)). So these antibiotics are the most use at the field.

Figure 1. Agarose gel electrophoresis for invA gene.  
Agarose gel electrophoresis showing specific PCR of Salmonella isolates using invA gene primer (284 bp).  
Neg = negative control & Pos = positive control & L= ladder (100-1000 bp) & all lanes showed positive results confirmed that all Salmonella isolates were positive for invA gene.
Figure 2. Agarose gel electrophoresis for csgD gene. 
agarose gel electrophoresis showing Salmonella specific PCR using primer for csgD gene (651 bp). 
Neg = negative control & Pos = positive control & L= ladder (100-1000 bp) & all lanes showed positive results confirmed that Salmonella isolates were positive for csgD gene.

Figure 3. Agarose gel electrophoresis for stn gene. 
agarose gel electrophoresis showing Salmonella specific PCR using primer for stn gene (617 bp). 
Neg = negative control & Pos = positive control & L= ladder (100 bp) & all lanes showed positive results confirmed that all Salmonella isolates were positive for stn gene.

Figure 4. Agarose gel electrophoresis for ompA gene. 
agarose gel electrophoresis showing Salmonella specific PCR using
primer for ompA gene (1052 bp).
Neg = negative control & Pos = positive control & L= ladder (100bp) & all lanes showed positive results confirmed that all Salmonella isolates were positive for ompA gene.

Figure 5. Agarose gel electrophoresis for ompF gene.
agarose gel electrophoresis showing Salmonella specific PCR using primer for ompF gene (519 bp).
Neg = negative control & Pos = positive control & L= ladder (100bp) & all lanes showed positive results confirmed that all Salmonella isolates were positive for ompF gene.

Discussion
Salmonella considered an important source for foodborne diseases, resulting in health problems worldwide. Differences in the prevalence of specific serotypes may be related to the movements of foods, animals and people. Nowadays, Typhimurium and Enteritidis considered the most frequent serotypes implicated in Salmonella outbreaks from foods all over the world (Zhou et al., 2019).

In this study, the incidence of Salmonella in raw meat products (table2) was 3.5% (7 out of 200 raw meat products) and these results was nearly coincide with Bingol et al. (2013) who examined a total of 340 samples of meat and meat products (205 ground beef, 50 raw beef and 85 sausages) collected from producers and retailers in Istanbul. Salmonella spp. was detected in 1.18% of the tested meat and meat products. The isolated serovars were S. Anatum in ground beef and S. Reading and S. Meleagridis in sausage samples. Other studies stated the presence of Salmonella spp. in 1.4%, 2.0% and 2.08%, respectively (Scheelhaas et al., 1976; Kleinlein et al., 1989; Aabo et al., 1995).

The incidence of Salmonella spp. in raw meat products in this study was lower in comparison to those detected by Pietzsch and Kawerau. (1981), (45.2%),
Al-Rajab et al. (1986) (18.0%), El-Leithy and Rashad. (1989) (15.0%), Baskaya et al. (2004) (11.1%) and Woldemariam et al. (2005) (12.1%). The reason for high contamination rates may be due to the use of contaminated raw materials, lack of proper heating and inadequate packaging as indicated in EFTA report journal (2012).

In the present work, antibiogram was done by disk diffusion method to explore antibiogram result as shown in table 5.

Data in table 5 illustrated all 7 serotypes (100%) were found to be resistant to Amoxycillin, doxycyclin and Erythromycin, 4 (57.14%) to Colistin sulphate, 2 (28.57%) to Ceftriaxone and Rifampicin.

While, all isolated serotypes (100%) were found to be sensitive to chloramphenicol, ciprofloxacin and gentamicin, 4 (57.14%) to Nalidixic acid, 3(42.86) to Norfloxacin, 2 (28.57%) to Ceftriaxone, 1(14.29%) to Sulfamethoxazole-trimethoprim.

In present study susceptibility of Salmonella isolates to Ciprofloxacin, Chloramphenicol and Gentamicin was 100%. These results go hand in hand with Fazlina et al. (2012) who found that, susceptibility of their Salmonella isolates to gentamicin, ciprofloxacin and chloramphenicol was 95%, 90% and 80%, respectively, high resistance was observed against amoxicillin-clavulanic acid (100%) and erythromycin (80%). Also, these results agreed with the results obtained by Miko et al. (2005) who detected a lesser number of isolates that were resistant to gentamycin and high percentage of resistance to amoxicillin and Sulfamethoxazole-trimethoprim.

On the other hand, these results differ from those obtained by Yang et al. (2001) who found that, resistance of their Salmonella isolates to Sulfamethoxazole-trimethoprim, nalidixic acid, Amoxycillin, chloramphincol and Gentamycin was 58%,35%,32%,26% and 26% respectively. The same results obtained by Harakeh et al. (2005) who found that, 86 and 57% of Salmonella isolates from fast meat-based food in Lebanon were resistant to trimethoprim-sulfamethoxazole and gentamicin, respectively.

Regarding antimicrobial susceptibility testing of Salmonella serovars to 12 different antibacterial, Salmonella isolates showed different degree of sensitivity to antimicrobial agents, higher degree of sensitivity were
observed to ciprofloxacin, gentamicin and Chloramphenicol with percentages matched to those found in many developing countries, especially Bangladesh, Nigeria, and Pakistan (Habrun et al., 2012; Putturu et al., 2013; Umeh et al., 2014). Resistance of Salmonella to Amoxicillin/clavulanic acid was (100%). These results agree with another report in South India, (Suresh et al., 2006) and higher than results discovered in Eastern China (80%) (Lu et al., 2014). resistance to doxycycline was 100%. These results agree with the discussed results in Eastern China (Lu et al., 2014). This result differences may be attributed to illegal use of antimicrobials at therapeutic doses as food additives to stimulate growth and as chemotherapeutic agent to control the spread of epizootic diseases in farms.

In the present investigation, it was noted an incidence of multidrug resistance among all 7 Salmonella isolates which was higher than that obtained previously by Shen et al., (2008) (28.5%) and Ahmed et al., (2009) (14.4%). Schwarz et al. (2001) and Zouhairi et al. (2010) attributed the exacerbation of this MDR to the diminishing of new antibiotics and considered as a serious danger to public health. Many authors have detected multi drug resistance of isolates from meat (Yang et al., 2001; Capita, 2003; Romani et al., 2008; Hur et al., 2011; Yildirim et al., 2011).

From the above-mentioned results, it is important to note that, Salmonella can easily acquire multiple resistances to most antimicrobials and transfer them to human especially through food chain. Recently, the generation and transmission mechanisms of the drug resistance genes became an important research topic to control the spread of multidrug-resistant bacteria. The high occurrence of resistant bacteria reported in a lot of publications may be because of the worldwide overuse of antibacterial among different fields, inducing high pressure for the proper selection of antibiotic resistance among different bacterial pathogens. Oliveira et al. (2003) revealed that, PCR is highly specific and sensitive and a fast procedure than traditional microbiological techniques for isolation and identification of Salmonella. PCR using primers of invA specific for Salmonella, considerably decreases false-negative results which usually occur in laboratories. Amplification of invA gene is
now considered as an international procedure for *Salmonella* identification.

The PCR targeting *OmpA* specific for *Salmonella* cosidered highly specific in detection of *Salmonella* serovar alone and its' sensitivity was up to 68.8 fg. *(Kataria et al., 2013)*. In the present study, PCR assay made for the detection of *invA* gene in seven isolated strains. It has been revealed that, it was present in all isolates (100%) that was detected by the presence of 284 bp PCR amplified fragment. The results in the present study were agreed with *(Nagappa et al. (2007); Dione et al. (2011); Shanmugasamy et al. (2011)).* No amplified DNA fragments were obtained from non-*Salmonella* spp. The *invA* gene contains sequences unique to *Salmonella* and proved to be a suitable PCR target, with an important diagnostic applications *(Rahn et al., 1992)*.

PCR was made for detection of *csgD* gene from isolated serotypes showed that, it was present in all of isolates (100%) which was proved by the presence of a 651 bp PCR product. The results obtained in this study was in corroboration with *(Eckmann et al., 1997).* In this study, PCR carried out for the detection of *stn* gene in *Salmonella* isolates showed that, the gene was present in all isolates (100%) and was detected by the presence of a 617 bp PCR product. These findings agreed with *(Prager et al., 1995; Rahman, 1999; Murugkar et al., 2005).*

Observations from this study proved that, *stn* gene is widely distributed among *Salmonella* serotypes.

In addition to that, PCR carried out for the detection of *ompA* gene for *Salmonella* isolates showed that, the gene was present in all isolates (100%) that was detected by the presence of 1052 bp PCR product. We found an agreement with our results in previous studies *(Nair et al., 2006; Dadmehr et al., 2011; Kataria et al., 2013; Fekry et al., 2018).*

Finally, the detection of *ompF* gene in the isolated *Salmonella* samples was carried out using PCR assay. The gene was present in all isolates (100%) that was detected by the presence of a 519 bp PCR product. These findings agreed with *(Coldham et al., 2010; Al-Habsi et al., 2018).*

**References**


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الملخص العربي

في هذه الدراسة تم تجميع 200 عينة عشوائيا من مصنفات اللحوم المبردة المباعة في أسواق مدينة بورسعيد للكشف عن مدى تواجد ميكروبات Salmonella. و أظهرت النتائج أن الميكروب تم عزله بنسبة 3.5% من العينات. و كانت أنواع العترات المعزولة من مصنفات اللحوم المبردة هي S.Anatum بنسبة 28.6% و S.Lumberhurst بنسبة 28.6% و S.Hato بنسبة 14.3% و S. Enteritides بنسبة 28.6%.

وقد أجرى اختبار الحساسية لعدد 7 عترة من ميكروبات ال Salmonella و وافرت النتائج إلى أنها حساسة بالجرمانامس سبيروفوكساسين الكولومينكول سلفات الكولستين والانروفلوكساسين بينما وجد الارثرومايسين والفلومكوين أقل تأثيراً على أنواع السالمونيلا. وكانت (invA,csgD,sm_ompA,ompF) النتائج إيجابية بنسبة 100% وذلك بظهور التتابع الجيني الصحيح لكل الجينات المذكورة. و في جنس السالمونيلا فقط وذلك بالتفريد الكهربي على جهاز الفصل الكهربي لحصص الديوكسي ريبونوكليز. مما يدل أن تقنية PCR سريعة للتحري عن تواجد جينات المقاومة لل مضادات الحيوية في ميكروبات ال Salmonella المخفية. وقد تم مناقشة النتائج وبيان أهمية الميكروب المعزول و خطورته على الصحة العامة للمستهلك وعمل التوصيات للتقليل من مخاطرها.

الإنجليزية
