Research article

Molecular detection of invA, ssaP in *Salmonella typhimurium* isolated from chicken in Al-Qadisiyah Province

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**Abstract**

*Salmonella* is considered the most important cause of foodborne diseases. Identification of *Salmonella typhimurium* evaluated using bacteriological assay followed by PCR technique. In this study, 40 intestinal content specimens of poultry were collected randomly from different farms of Al-Qadisiyah province. Out of 40 samples obtained, 14 isolates (35 %) were detected as *Salmonella typhimurium* according to conventional bacteriological characteristics, the Vitek 2 system for identification and molecular assays. Two sets of primers were designed for detecting *invA* and *ssaP* genes. These genes potent the virulence of *Salmonella typhimurium*. The primers were made in this study by using NCBI GenBank and design online. The primers were made by (Bioneer) company, Korea. Molecular assay of the isolates gives away specific PCR products of 677bp for the *invA* gene and 314bp for *ssaP* gene. The *invA* genes were amplified in 11 (78.5%) out of 14 isolates of *Salmonella typhimurium*, while *ssaP* genes were amplified in 10 (71.4%) out of 14 isolates of *Salmonella typhimurium*. The result of the study confirms the ability of these specific primers for detection of *salmonella typhimurium* in samples of chicken as well as the rapidly and sensitivity of the PCR method as a good tool for bacteriological identification.

**Keywords:** *Salmonella typhimurium*, Virulence factors, Poultry, PCR tech.

**Introduction**

*Salmonella* species is the most important pathogen in the world as source of food borne illness in chicken, it cause economic loos in poultry and poultry products industries (1). *Salmonella* caused about 80% of infections in human globally (2). Phylogenetec analysis of *Salmonella typhimurium* show the effects of different factors in the existence of *Salmonella* spp in animal, and cross-contamination among animals, feed and environment (3). Infections by *Salmonella* species in human caused by uncooked of meat poultry (4). However, *Salmonella* genus include two major species, *Salmonella enterica* subspecies *enterica* serovar *typhimurium* and *Salmonella bongori*. *Salmonella typhimurium* cause disease in human (5) (6). About 75-80% of human infection caused by beef, poultry meat and eggs which contaminated by *Salmonella* (3) (7). Almost, molecular detection of bacteria in is rapid, sensitive powerful tool in the bacteriological diagnostic compared to culture techniques. Therefore, determination of *Salmonella* in fecal material reduce time of disease diagnosis (8). Many of chromosomal virulence genes have been used to identify *salmonella* in fecal samples of poultry including *invA* and *ssaP*, these genes are target for PCR assay of *salmonella* serovar (9) also, and these genes are clustered in the islands of the pathogenicity of *salmonella* species (10). The *invA* gene is virulent and encoded a protein found in the inner layer of membrane of the bacteria, this gene contains sequences unique found in all
salmonella serovars, this gene is responsible for invasion of the bacteria in to epithelial cells of the host (11). ssaP contributes to attenuate of virulence also have been used to explain the importance of this gene at survival of the bacteria in the cells of host and at stages of infection (12). The goal of this research is to determination of salmonella typhimurium incidence in the chicken in Al-Qadisiyah Province by using conventional bacteriological methods including cultural and biochemical tests, also determination sequencing of invA and ssaP genes among the salmonella isolates by using specific PCR technique.

Materials and Methods

Ethical approval
The Animal Ethical Committee of Veterinary Medicine College, University of Al-Qadisiyah, Iraq, has approved the present study under permission No: 320

Sample collection:

Forty specimens of intestinal contents of chicken were collected randomly from different farms located in Al-Qadisiyah province.

Bacterial isolation:
Samples were transported to the laboratory of microbiology faculty of Veterinary Medicine\ University of Al-Qadisiyah for bacteriological assay. All specimens inoculated into Salmonella-Shigella agar at 37c for 24-48-hr, also all specimens were examined on XLD agar and of blood agar then incubated for 24 hours at 37°C. Then the isolates were activated by inoculated on-Salmonella CHROM agar and incubated at 37°C overnight. The biochemical reactions to identification of species of Salmonella such as catalase, oxidase, in dole production, urease and citrate utilization. Carried out according to (12). Also use of Vitek 2 system for rapid identification of five isolates.
**Bacterial DNA extraction and PCR Method**

PCR technique was performed to determination of virulence factors genes (InvA and ssaP gene) in *Salmonella typhimurium* based using specific primers were design in current study as following steps:

1. **DNA extraction:**
   
The bacterial isolates were subjected to bacterial nucleic acid extraction by using commercial DNA extraction kit (Presto Mini-DNA Bacteria Kit, Gene aid Biotech Ltd. USA). The extraction method was done according to the manufacture instructions.

2. **Nanodrop:**
   
The extracted DNA was estimated by nanodrop device at 260/280nm, and then kept at deep freezer until used in PCR method.

3. **Primers:**
   
The PCR primers that used in this study for detection virulence factors genes were designed in this study using NCBI Gene sequence database and primer 3 plus design. These primers were provided from Bioneer Company, Korea as following table (1).

<table>
<thead>
<tr>
<th>Primer</th>
<th>Sequence</th>
<th>Amplicon</th>
<th>GenBank</th>
</tr>
</thead>
<tbody>
<tr>
<td>invA</td>
<td>TCCTTTGACGGTGCGATGAA</td>
<td>677bp</td>
<td>M90846.1</td>
</tr>
<tr>
<td>R</td>
<td>CTGTTATCGTCAGGCCCTC</td>
<td></td>
<td></td>
</tr>
<tr>
<td>F</td>
<td>TGAGGGAAGTTGGGTTGC</td>
<td></td>
<td></td>
</tr>
<tr>
<td>ssaP</td>
<td>ACCCATATGCAGCACTGA</td>
<td>314bp</td>
<td>NC-003197.2</td>
</tr>
<tr>
<td>R</td>
<td>ACCCATATGCAGCACTGA</td>
<td>314bp</td>
<td>NC-003197.2</td>
</tr>
</tbody>
</table>

4. **PCR master mix preparation:**
   
The mix was prepared using (Accu-Power PCR-PreMix-Kit) master mix reagent and done according to company instructions as a following table (2).

<table>
<thead>
<tr>
<th>Master mix</th>
<th>Volume</th>
</tr>
</thead>
<tbody>
<tr>
<td>DNA template (10 ng/ µl)</td>
<td>5 µl</td>
</tr>
<tr>
<td>Forward primer (10 pmol)</td>
<td>1 µl</td>
</tr>
<tr>
<td>Reverse primer (10 pmol)</td>
<td>1 µl</td>
</tr>
<tr>
<td>PCR water</td>
<td>12 µl</td>
</tr>
<tr>
<td>Total volume</td>
<td>20 µl</td>
</tr>
</tbody>
</table>

   The PCR mix that revealed in table above placed in AccuPower PCR-PreMix that contain all other PCR components, which needed to reaction such as (Taq DNA polymerase, dNTPs, 10 PCR buffer). Then, all the PCR tubes transferred into vortex centrifuge for 3 minutes. Then transferred into thermocycler (MyGene, Bioneer, Korea).

5. **PCR thermocycler conditions:**

<table>
<thead>
<tr>
<th>PCR</th>
<th>Temp</th>
<th>Time</th>
<th>repeat</th>
</tr>
</thead>
<tbody>
<tr>
<td>Initial Denaturation</td>
<td>95C</td>
<td>5min</td>
<td>1</td>
</tr>
<tr>
<td>Denaturation</td>
<td>95C</td>
<td>30 sec.</td>
<td>30 cycle</td>
</tr>
<tr>
<td>Annealing</td>
<td>60C</td>
<td>30 sec.</td>
<td></td>
</tr>
<tr>
<td>Extension</td>
<td>72C</td>
<td>1min</td>
<td></td>
</tr>
<tr>
<td>Final extension</td>
<td>72C</td>
<td>5 min</td>
<td>1</td>
</tr>
<tr>
<td>Hold</td>
<td>4C</td>
<td>Forever</td>
<td>-</td>
</tr>
</tbody>
</table>

6. **PCR product analysis:**

   The PCR products were examined by electrophoresis in a 1% agarose gel using 1X TBE buffer, stained with ethidium bromide, and investigation under UV transilluminator.

**Results**

Firstly, detection of *Salmonella typhimurium* in current study first by cultural features. By using conventional bacteriological methods: 14 out of the 40 chicken samples (35%) were culture positive for salmonella. In present study, two primer sets were designed to detect the virulence factors of *Salmonella* species by using PCR, targeting the invA gene and ssaP. This research confirms the ability of the specific
primer sets to detect the isolates as Salmonella. All isolates were subjected to specific gene invA positive by the predicted product a 677-bp DNA fragment. While to gene ssaP positive by the predicted products a 314-bp. The result shows that invA and ssaP genes were present in 78.5% (11/14), 71.4% (10/14) of the samples (figure 1 and figure 2).

![Image of Agarose gel electrophoresis showing analysis of product of the PCR for invA genes in Salmonella typhimurium isolates. M marker (2000-100bp), lane (1-14) isolates were positive in (677bp) product of PCR except the isolates (6, 9, 14) were negative.](image1)

![Image of Agarose gel electrophoresis showing analysis of product of the PCR for ssaP genes in Salmonella typhimurium isolates. M marker (2000-100bp), lane (1-14) isolates were positive in (314bp) product of PCR except the isolates (3, 4, 5, 7) were negative.](image2)

**Discussion**

Recently, there are attempts to establish assay which specific and sensitive to reduce the time of identification of Salmonella species and their virulence genes from different samples, so the present study supports to confirm the identification of the Salmonella by the specific primers that are selected.(13)(14). Detection by conventional culture assay show 35% positive for Salmonella typhimurium in other countries studies have recorded the prevalence s of Salmonella spp in poultry samples with percentages of contamination range from 3% to 6% (15). Other researches from a total of 1125 samples from poultry, 22.2% were identified as Salmonella typhimurium (16).while (17) obtained 8.3% of poultry carcasses were found to be contaminated with Salmonella. InvA gene is essential for invasion of tissue for Salmonella virulence (18). In this study presence of invA gene in Salmonella typhimurium from chicken samples was 78.5%, while in several studies in different areas about invA genes confirmed that this gene record 100% of the Salmonella (19). The sequences of primer
that are tested from the gene invA of *Salmonella typhimurium* have ability to detect rapidly *Salmonella* species rapidly in this study. Also (20) designated a study about invA gene was detected in all isolates of *Salmonella*, also this result agreed with those which obtained by (21) in south of Brazil. In this article, all bacteria from *Salmonella typhimurium* showed a 677bp amplicon; result from InvA gene pair of primer. While (17) reported 284-bp DNA fragment. In extant study presence of ssaP gene in *Salmonella, typhimurium* from chicken samples was 71.4%. The (12) detect ssaP gene in 100% of the samples from seafood associated *Salmonella* isolate in India. The differences as compared between current studies with previous researches may be due to cross contamination methods that used for detection sample collection as well as the origin of samples.

**References**


