Simultaneous Detection of Salmonella, Listeria Monocytogenes and Shigella in Poultry Samples by Triplex PCR

Zhao HK1,2,*, Wang WJ2, Zhao P1, Zhang HB3, Kong N4, Zhou MD5 and Zhang H1,2,6,7

1Shandong Engineering Research Center for Meat Food Quality and Safety, Qingdao Agricultural University, China
2College of Animal Science and Veterinary Medicine, Shandong Agricultural University, China
3Department of Respiratory Medicine, Affiliated Hospital of Zunyi Medical College, China
4Antimicrob, Z-BioMed, Inc., USA
*Corresponding author: Zhao HK, Shandong Engineering Research Center for Meat-Food-Quality Safety, College of Food Science and Engineering, Qingdao Agricultural University, Qingdao 266109, China

Zhang H, Z-BioMed, Inc., 15725 Crabbs Branch Way, Rockville, MD 20855, USA

Received: July 22, 2014; Accepted: July 28, 2014; Published: July 29, 2014

Abstract

Raw poultry is one of the important sources of major foodborne bacterial pathogens such as Salmonella, Listeria monocytogenes and Shigella. In this study, we developed and evaluated a triplex PCR method for simultaneous detection of these foodborne bacterial pathogens, Salmonella, Listeria monocytogenes and Shigella, with high specificity and sensitivity. A total of 502 samples were collected from chicken abattoirs, processing plants and retail vendors in Tai’an, Shandong Province of China, and used for the validation of a triplex PCR method. Results showed that Salmonella, L. monocytogenes and Shigella were detected in 26.9%, 6.2% and 5.2% of samples respectively. Our results demonstrate that the triplex PCR method can be used routinely to detect Salmonella, L. monocytogenes and Shigella during the poultry processing procedures in order to reduce the risk of foodborne disease outbreaks.

Keywords: Triplex PCR; Foodborne bacterial pathogens; L. monocytogenes; Salmonella; Shigella

Abbreviations

BHI; Brain Heart Infusion Medium; BPW; Buffered Peptone Water.

Introduction

Outbreaks and more than 250 known foodborne diseases could be caused by food contaminated with bacteria, viruses, parasites, and toxins, which continue to be a public health problem in the world [1-7]. In the United States, a total of 19,056 infections, 4,200 hospitalizations, and 80 deaths were reported in 2013 [8]. Raw poultry is considered to be one of the important sources of major foodborne bacterial pathogens such as Salmonella, Listeria monocytogenes and Shigella, with Salmonella and Listeria monocytogenes among the top five pathogens contributing to domestically acquired foodborne illnesses resulting in death in the United States [9]. The prevalence of bacterial pathogens in chickens has been well documented in many countries [10-13], however, the prevalence of bacterial pathogens in poultry products in Tai’an, Shandong Province of China has not been reported. The lack of microbiological monitoring systems in the poultry processing procedures in Shandong Province of China highlights the potential danger of cross-contamination of common bacterial pathogens from poultry products to humans.

The conventional methods for the detection of Salmonella, Listeria monocytogenes and Shigella are time-consuming and costly. Therefore, it is necessary to develop quick, simple, sensitive and cost-effective methods for simultaneous detection of these pathogens. Multiplex polymerase chain reaction (PCR) has been increasingly used for rapid detection of foodborne pathogens [14-20]. The objectives of the current study were to develop a triplex PCR method for simultaneous detection of Listeria monocytogenes, Salmonella and Shigella, also to evaluate the method in various samples collected from chicken abattoirs, processing plants and retail vendors in Tai’an, Shandong Province of China.

Materials and Methods

Bacterial strains

The L. monocytogenes, Salmonella enteric serotype Enteritidis and Shigella dysenteriae strains were obtained from the College of Animal Science and Veterinary Medicine, Shandong Agricultural University and used as representative target pathogens.

Sample collection and treatment

A total of 502 samples including chicken feces and feathers (60 each), chicken wash (92), chicken carcasses (50) from processing plants, fresh raw chickens (120), and frozen chickens (120) were collected in Tai’an, Shandong Province of China. Feces samples were collected immediately after arrival of the birds, placed into sterile polyethylene bags and processed. Briefly, 1 g of feces was diluted in 10 ml of 0.9% sterile saline solution and decanted for 5 min, and 1 ml of each sample was transferred to 5 ml of brain heart infusion (BHI) medium and incubated at 43°C for 12 h. Feather samples (25g) were added to 60 ml of PBS, and 1 ml was transferred to BHI medium

...
and incubated at 43°C for 12 h. Chicken washes were collected by placing the carcass into sterile polyethylene bags containing 300 ml of 0.1% peptone water. The solution was then transferred to a sterilized glass flask (300 ml) and incubated at 43°C for 18–24 h. Afterwards 1 ml of the solution was transferred to a tube containing 5 ml of BHI medium.

Chicken carcasses taken from broiler processing plants were picked up randomly from the final wash tanks at the abattoirs. Each carcass was placed in a sterile plastic bag containing 500 ml of PBS and shaken for 2 min. The carcass was suspended to allow the diluents to drain back in the plastic bag, and then returned to the wash tank. Frozen as well as fresh carcasses were obtained from abattoirs and street vendors, but only fresh carcasses were obtained from street vendors. Live chickens were sacrificed and plucked upon purchase. The primer pairs were selected based on their specificities reported in the literature. To find the best combination of primers for the triplex PCR, the computer simulation of different combinations of all the primer pairs considered was performed with the aid of software Web Primer available online (http://www.yeastgenome.org/cgi-bin/web-primer). The selected target genes were invA gene [21] for Salmonella, inlB gene [22] for L. monocytogenes, IpaH gene [4,23] for Shigella, and 16S rRNA gene [24] for the internal control. The name and sequence of selected primer sets for the triplex PCR are listed in Table 1.

**DNA extraction**

One milliliter of cell suspension was centrifuged at 8,000×g for 2 min. The cell pellet was washed twice with 400 µl of STE Buffer (100 mM NaCl, 10 mM Tris/HCl, 1 mM EDTA, pH 8.0) and centrifuged at 8,000×g for 2 min. The pellet was resuspended in 200 µl of TE buffer (10 mM Tris/HCl, 1 mM EDTA, pH 8.0) and 100 µl of Tris-saturated phenol (pH 8.0) were added followed by a vortex-mixing step of 60 s. The cell suspension was subsequently centrifuged at 13,000×g for 5 min at 4°C to separate the aqueous phase from the organic phase and 160 µl of the upper aqueous phase was transferred to a clean 1.5 ml tube containing 40 µl of TE buffer. The solution was mixed with 100 µl of chloroform and centrifuged for 5 min at 13,000×g at 4°C. The aqueous phase (160 µl) was transferred to a clean 1.5 ml tube containing 40 µl of TE buffer. The solution was mixed with 100 µl of chloroform and centrifuged for 5 min at 13,000×g at 4°C. The aqueous phase (160 µl) was transferred to a clean 1.5 ml tube containing 40 µl of TE buffer. The solution was mixed with 100 µl of chloroform and centrifuged for 5 min at 13,000×g at 4°C. The upper aqueous phase (150 µl), which contained purified DNA, was transferred to a clean 1.5 ml tube and used directly for the subsequent experiments or stored at -20°C.

**Primer design for triplex PCR**

The primer pairs were selected based on their specificities reported in the literature. The best combination of primers for the triplex PCR, the computer simulation of different combinations of all the primer pairs considered was performed with the aid of software Web Primer available online (http://www.yeastgenome.org/cgi-bin/web-primer). The selected target genes were invA gene [21] for Salmonella, inlB gene [22] for L. monocytogenes, IpaH gene [4,23] for Shigella, and 16S rRNA gene [24] for the internal control. The name and sequence of selected primer sets for the triplex PCR are listed in Table 1.

**PCR amplification and restriction enzyme digestion**

Triplex PCR amplification was performed in 50 µl reaction mixture containing 5 µl 10xPCR reaction buffer, 75 pmol MgCl₂, 10 pmol of dNTPs, 20 pmol inlB primers, 5 pmol invA primers, 5 pmol IpaH primers, 1 pmol 16S-rRNA primers, 5U Taq DNA polymerase (Takara), and 4 µl DNA template (20-200ng/µl). Amplification was carried out in a thermal cycler (Applied Biosystems 2720) using the following conditions: an initial denaturation at 94°C for 3 min followed by 28 cycles consisting denaturation at 94°C for 30s, primer annealing at 57°C for 1 min and extension at 72°C for 1 min 30s; and a final extension step at 72°C for 10min. DNA purified from reference strains was used as the positive control for triplex PCR reactions. PCR products were applied to 3% agarose gels in the TAE running buffer (40 mM Tris-acetate, 1 mM EDTA, pH7.5) containing 0.5 µg/ml of ethidium bromide for electrophoresis. The amplified DNA fragments were visualized and photographed under the UV light. PCR amplified products (6 µl) for invA, inlB, IpaH and 16S - rRNA genes were digested with 2 U of restriction enzyme KpnI (Gibco BRL), and digested DNA products were analyzed by electrophoresis on 3% agarose gels stained with ethidium bromide. Two DNA markers, 100 bp and 2K bp ladders, were used as size standards.

**Statistical analysis**

Statistical analysis was performed using the software Primer 5.0 System and Fisher’s exact test (Analyse-it Software, Ltd., Leeds, England).

**Results**

The target genes specific for three common bacterial pathogens were invA (287bp ampiclon for Salmonella, NC_003197.1), inlB (148bp ampiclon for L. monocytogenes, NC_003210.1) and ipaH (600bp ampiclon for Shigella, NC_008258.1). Each primer set was tested individually by using the DNA sample purified from the reference strain as a template in PCR to ensure its specificity. Results showed that each of the pathogen-specific primer sets generated a single band at the expected size (Fig. 1A). Sequencing results showed a 100% agreement with the reported nucleotide sequence of all the primer pairs considered.
confirmed that PCR products were 100% identical to those listed in the GenBank (data not shown). The 16S rRNA gene of foodborne bacterial pathogens was used as the internal control, which contained a conserved fragment flanking the variable regions 1 (V1) to 3 (V3) of the gene (475bp) and was designed previously for the oligonucleotide array [24]. The use of the internal control facilitates the interpretation of the amplification results, since a control gene product should always be amplified even when there is no target sequence present, and can thus indicate whether the PCR reaction works or not. This is particularly important for PCR-based diagnostic methods performed with complex samples such as meat products. PCR results showed that the internal control gene and target genes were amplified simultaneously (Figure 1).

Experimental results using specific primer sets and reference strains showed that three target genes were successfully amplified without nonspecific bands in the triplex PCR, demonstrating the specificity of this method (Figure 2). The sensitivity of the triplex PCR was then assessed by testing the mixture of DNAs extracted from the serial dilutions of the target pathogens (10^6, 10^5, 10^4, and 10^3 cells/ml) in the bacterial culture. The detection of three pathogens were achieved at the concentration of bacterial pathogens as low as 10^2 cells/ml (data not shown).

To validate the triplex PCR method, a total of 502 samples were collected from chicken abattoirs, processing plants and retail vendors in Tai’an, Shandong Province of China, and used for simultaneous detection of three foodborne pathogens. The results showed that Salmonella was detected in 26.9% (135/502) of various samples collected in Tai’an, China (Table 2). The highest rate of contamination by Salmonella spp. was detected in fecal samples (26/60, 43.3%) followed by the fresh raw chicken (46/120, 38.3%), frozen chicken (33/120, 27.5%), feather samples (10/60, 16.7%), chicken washes (14/92, 15.2%), and the processing plant in Tai’an (6/50, 12%).

The overall contamination rates of L. monocytogenes and Shigella spp. for various samples collected in Tai’an were 5.2% (26/502) and 6.2% (31/502) respectively. However, Shigella spp. and L. monocytogenes were not detected in samples collected from feces and feathers. Among samples collected from other four sources (chicken washes, processing plant, fresh raw chicken and frozen chicken), 2.17%~18% were contaminated by Shigella spp. and 4% ~ 10.8% were contaminated by L. monocytogenes (Table 2).

One or more of the bacterial pathogens were detected in 178 of 502 (35.5%) samples, with one pathogen detected in 164 (32.7%) samples, two pathogens detected in 11 (2.2%) samples, and three pathogens detected in 3 (0.6%) samples. In samples collected from frozen chickens, 55 out of 120 (45.8%) were contaminated by three common bacterial pathogens. No significant differences were observed among samples collected from fresh raw chickens (42.5%) and frozen chickens (45.8%). Twenty one samples from chicken washes (22.8%) and 15 samples from the processing plant (30%) were contaminated by three bacterial pathogens.

Discussion

In this study, a cost-effective triplex PCR method was developed for the simultaneous detection of three foodborne bacterial pathogens.

---

![Figure 1](image1.png)

**Figure 1:** PCR products obtained by using single primer set specific for one of the three target genes (A) and two primer sets specific one target gene and one internal control (16S rRNA). M, 2K DNA Marker; 1, inlB gene fragment (148bp) amplified from L. monocytogenes; 2, invA gene fragment (287bp) amplified from Shigella; 3, ipaH gene fragment (600bp) amplified from Salmonella spp.; (-), negative control. (B) M, 100bp ladder Marker; 1, ipaH gene fragment (600bp) and internal control (475bp) from Shigella; 2, invA gene fragment (287bp) and internal control from Salmonella spp.; 3, inlB gene fragment (148bp) and internal control from L. monocytogenes; (-), negative control.

![Figure 2](image2.png)

**Figure 2:** Amplification products obtained by multiplex PCR. M, 100 Ladder Marker and 2K Marker; 1, Multiplex PCR with L. monocytogenes; 2, Multiplex PCR with Salmonella spp.; 3, Multiplex PCR with Shigella spp.; 4, Multiplex PCR with L. monocytogenes and Salmonella; 5, Multiplex PCR with L. monocytogenes and Shigella; 6, Multiplex PCR with Salmonella spp and Shigella; 7, Multiplex PCR with L. monocytogenes, Salmonella and Shigella; (-), negative control.
Table 2: Incidences of Salmonella, Shigella spp and L.monocytogenes in samples collected from sources.

<table>
<thead>
<tr>
<th>Type of samples</th>
<th>Number</th>
<th>Overall No. (%)</th>
<th>Salmonella spp. No. (%)</th>
<th>Shigella spp. No. (%)</th>
<th>L.monocytogenes No. (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Feces</td>
<td>60</td>
<td>28 (43.3)</td>
<td>26 (33.3)</td>
<td>0 (0)</td>
<td>0 (0)</td>
</tr>
<tr>
<td>Feathers</td>
<td>60</td>
<td>10 (16.7)</td>
<td>10 (16.7)</td>
<td>0 (0)</td>
<td>0 (0)</td>
</tr>
<tr>
<td>Chicken washes</td>
<td>92</td>
<td>21 (22.8)</td>
<td>14 (15.2)</td>
<td>2 (2.17)</td>
<td>9 (9.8)</td>
</tr>
<tr>
<td>Processing plant</td>
<td>50</td>
<td>15 (30)</td>
<td>6 (12)</td>
<td>9 (18)</td>
<td>2 (4)</td>
</tr>
<tr>
<td>Fresh raw chicken</td>
<td>120</td>
<td>51 (42.5)</td>
<td>46 (38.3)</td>
<td>3 (2.5)</td>
<td>7 (5.8)</td>
</tr>
<tr>
<td>Frozen chicken</td>
<td>120</td>
<td>55 (45.8)</td>
<td>33 (27.5)</td>
<td>12 (10)</td>
<td>13 (10.8)</td>
</tr>
<tr>
<td>Total</td>
<td>502</td>
<td>178 (35.5)</td>
<td>135 (26.9)</td>
<td>26 (5.2)</td>
<td>31 (6.2)</td>
</tr>
</tbody>
</table>

(Salmonella, Listeria monocytogenes and Shigella). This PCR-based method is highly specific and sensitive, which can be used routinely in resource-limited locations to detect these pathogens simultaneously. The possibility of false positive results was minimized by using the internal amplification control, and could be identified when the internal control was not amplified. Based on our experience, the primer concentration for the 16S-RNA gene in the triplex PCR is a critical aspect, since low concentrations of 16S-RNA primers could lead to substantial variations in the 16S-RNA gene amplification while high concentrations could negatively affect the PCR sensitivity. Therefore, the initial 16S-RNA primer concentration in the PCR should be reproducibly tested, and kept as low as possible to avoid the inhibition of the specific target amplification. In order to determine the optimal primer concentration for the 16S-RNA gene, tenfold dilution series of the 16S-RNA primers were made and tested in the triplex PCR as described in the Materials and Methods section. Results indicated that 1pmol of 16S-RNA primers could be used in the triplex PCR without significantly affecting the amplification of the target genes (data not shown). The competitive effect of 16S-RNA primers on the specific amplification of invA, invB and ipaH genes was negligible.

Furthermore, this triplex PCR method was successfully used to investigate the risk of potential foodborne bacterial contaminations in 502 samples collected from many sources in Tai’an, Shandong Province of China. Our data showed that poultry samples appear to be prominent reservoirs of Salmonella and the prevalence of Salmonella in total samples (26.9%) was four or five times higher than that of other two pathogens. Fecal samples and feather samples showed high rates of contamination by Salmonella, but no contamination by L.monocytogenes and Shigella, suggesting that they were unlikely the source of L.monocytogenes and Shigella. The extent of Salmonella presence from the fresh raw chicken and frozen chicken were similar; however, significantly more samples were contaminated with Salmonella compared to other categories. The prevalence of Salmonella in the UK poultry was found to be 25–29% using the cultural methods [25]. Using the multiplex-PCR method, Salmonella typhimurium and Salmonella enteritidis strains were detected in 30.6% of environmental swabs of poultry houses in Ploufragan, France [26], and 2.9% of the fish samples in Iran [27]. Thus, the incidences of Salmonella in Tai’an, China were higher than those reported for the European poultry. The rates of contamination for the other two pathogens were much lower than that of Salmonella. The level of L. monocytogenes contamination in frozen samples was significantly higher than that in fresh samples (Table 2). This is consistent with observations that L. monocytogenes can grow over a wide range of environmental conditions such as refrigeration temperatures [13], which allows it to overcome the food preservation and safety barriers, and creates a potential risk to human health. The prevalence of L.monocytogenes in retail poultry in Leon, Spain, was 32% [12], while the organism was isolated from 62% of broilers tested at abattoirs, processing plants and retail outlets in Finland [13].

In conclusion, we have developed an easy and rapid triplex PCR method for the simultaneous detection of Salmonella, Listeria monocytogenes and Shigella with high specificity and sensitivity. Our results demonstrate that three common foodborne bacterial pathogens are prevalent in raw poultry products in Tai’an, China, and indicate the necessity to screen bacterial pathogens routinely during the poultry processing procedures in order to reduce the potential risk of foodborne disease outbreaks.

Acknowledgement

This study was funded by the “Twelfth Five-Year” Major National Research Projects (No. 2012BAK17805 and No. 2012BAD28803). Study sponsors played no role in study design; in the collection, analysis, and interpretation of data; in the writing of the report; and in the decision to submit the paper for publication. We appreciate the thoughtful comments of Dr. Qijing Du. We would like to thank Yanjun Jiang for her assistance.

References

1. National Institute of Allergy and Infectious Diseases. Understanding Foodborne Diseases.
5. Greig JD, Ravel A. Analysis of foodborne outbreak data reported internationally for source attribution. Int J Food Microbiol. 2009; 130: 77-87.


