

Short communication

Multiplex-PCR Assay for detection of *Salmonella typhimurium* and *Salmonella enteritidis* in poultry feedstuffs

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Abstract

Multiplex polymerase chain reaction (M-PCR), the concurrent amplification of two or more polymerase chain reaction (PCR) products in the same reaction tube, can be applied to the rapid detection of pathogenic microorganisms in animal feedstuffs. Poultry feedstuffs has been implicated as important established source of infection to specific *Salmonella* serovars. Poultry feedstuffs can be an origin for transfer bacteria. In this study, 30 feedstuffs samples were collected from feed stocks of broiler chicken farms in Kermanshah province in the west of Iran. In order to isolate *Salmonella*, conventional cultural methods including pre-enrichment, enrichment and selective agar plating tests were performed. To confirm the identification of isolated colonies as *Salmonella*. and determining as typhimurium and Enteritidis serovars, a M-PCR assay, using three pairs of primers were employed, S141 and S139 for InvA gene, specific for the genus of *Salmonella* spp. Fli15 and Tym for FliC gene, specific for Typhimurium serovar and Sef167 and Sef478 for sefA gene, specific for Enteritidis serovar. M-PCR results indicated that 3.3% of samples were contaminated with *Salmonella* spp. and confirmed that all contaminated samples belong to *Salmonella typhimurium* serovar and no contamination with *Salmonella enteritidis* has been detected. In conclusion, it is recommended that M-PCR method can be used as a viable alternative to traditional cultural methods for detection of poultry feedstuffs contamination by *Salmonella* serovars.

Key words: *Salmonella typhimurium*, *Salmonella enteritidis*, Multiplex PCR, Poultry feedstuffs

Introduction

Salmonella species have been considered as one of the most important food borne pathogens all around the world (Gillespie et al., 2003; Malorny et al., 2003a). Poultry are the principal reservoir of this pathogen (Winfield and Groisman, 2003). Food from animal sources such as poultry meat have been proved to carry these pathogens (Gillespie et al., 2003). Poultry products have been recognized as a major source of human illness caused by these pathogens (Amavisit et al., 2001). *Salmonella* enteritidis and typhimurium serovars are the most frequently isolated serovars from foodborne outbreaks throughout the world (Herikstad et al., 2002). Therefore, it is necessary to discriminate *Salmonella* serovars from poultry origins in order to ensure that if this origins are contaminated (Lim et al., 2003). Conventionally, *Salmonella* was isolated by cultural methods which are based on non-selective pre-enrichment medias followed by selective enrichment and on selective and differential agars (Van Kessel et al., 2003). Generally, these techniques take longer time, since they give only presumptive results after 3-4 days and definitive results after 5-6 days (Malorny et al., 2003b). For this reason, rapid detection methods such as DNA or RNA probing, immune-detection methods and nucleic acid hybridization have been developed, but they do not have enough sensitivity and specificity (Zhu et al., 1996). In vitro amplification of DNA by the PCR methods is a powerful tool in microbiological diagnostics (Malorny et al., 2003b). Several genes have been used to detect *Salmonella* in natural environmental samples. Virulence chromosomal genes including; *invA* (Malorny et al., 2003a; Malorny et al., 2003b), *sefA* (Szabo and Mackey, 1999), *fliC* (Itoh et al., 1997; Soumet et al., 1999) are target genes for PCR amplification of *Salmonella* species. The flagellin gene *fliC* encodes the major component of the flagellum in *Salmonella* typhimurium (Aldridge et al., 2006). The *invA* gene of *Salmonella* spp. contain sequence unique to this genus and has been proved as a suitable PCR target, with potential diagnostic applications (Rahn et al., 1992). This study was aimed to detect contamination of poultry feedstuffs with *Salmonella* in poultry farms around the Kermanshah city.

Materials and methods

In this study, a total of 30 poultry feedstuff samples, were collected from broiler chicken farms located around the Kermanshah. 50 g feed stocks of each farm randomly sampled and referred to the laboratory and kept at -20° C until analysis. Then, 10 g of each feedstuff samples rinsed in 50cc pepton buffer and incubated at 37°C for 24h. Following then, 10cc of the pre-enrichment rinsed in 100cc tetrastat broth and incubated at 37°C for 48h. 1cc pre-enrichment rinsed in 9cc selenite cystine broth and incubated at 37°C for 24h. The DNA from the enriched culture was obtained by a DNA extraction kit (CinnaGen Co. Tehran-Iran) and the purified DNA was used as a template for the PCR assay. Three primers pairs (CinnaGen Co. Tehran-Iran) were used. The sequence of primers used in this study is shown in Table1.

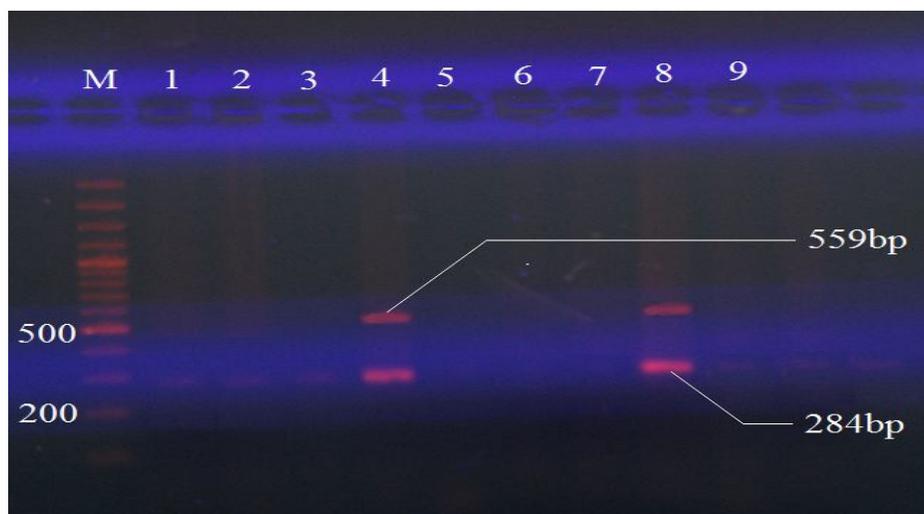
Table1: Sequences of primer pairs used in the Multiplex-PCR

Primer	Sequence	Target gene	Amplicon fragment(bp)	Reference
S139-F	GTGAAATTATCGCCACGTTCCGGCAA	invA	284 bp	Malorny et
S141-R	TCATCGCACCGTCAAAGGAACC			
Fli15-F	CGGTGTTGCCAGGTTGGTAAT	fliC	559bp	Soumet et al.
Tym-R	ACTCTTGCTGGCGGTGCGACTT			
Sef167-F	AGGTTCAAGCAGCGGTTACT	sefA	312 bp	Soumet et al.
Sef478-R	GGGACATTTAGCGTTCTTG			

Reactions were carried out in a 25 μ l amplification mixture consisting of 12.5 μ l mastermix, 0.2 μ l (containing 75 ng) extracted DNA. Amplification was performed in a Bio-Rad gradient thermocycler. The cycling condition was as follows: an initial denaturation at 95°C for 10 minutes, followed by 35 cycles of denaturation at 94°C for 30 seconds, annealing at 56°C for 1 minutes, elongation at 72°C for 1 minutes, and final extension period for 10 minutes at 72°C. Amplified products were run in 1 % agarose gel and a 100bp DNA ladder was used as a size reference. Deionized distilled water was used as a template for negative control and *S. typhimurium* was used as a positive control.

Results

Multiplex-PCR assay for 30 samples of poultry feedstuffs, using three primer pairs (Table 1), showed that 3.33% of samples were contaminated with *Salmonella typhimurium*. No contamination has been detected for *Salmonella enteritidis* serovar (Figure 1).

**Figure1.** Multiplex-PCR was carried out by three sets of primers

The 284 bp amplified product from *invA* gene specific for *Salmonella enteritidis*, and 559 bp from *fliC* gene specific for *S. typhimurium*. Lane (M): 100bp molecular weight marker, Lane (8) *S. typhimurium* as positive control, Lane (4) positive sample for *S. typhimurium*, Lane (4) positive samples for *Salmonella* spp.

Discussion

Culture techniques are universally recognized as the standard methods for the detection of bacterial pathogens, such as *Salmonella* in feedstuffs (Whyte et al., 2002). These techniques generally take longer time (Malorny et al., 2003b) and are less sensitive compared to PCR based methods (Oliveira et al., 2002). In an international research project for the validation and standardization of PCR for the detection of five major foodborne pathogens including *Salmonella* showed that the most selective primer set was found to be *invA* gene which used in the current study. These specific primer assay, which was validated in that project, showed high selectivity on 242 *Salmonella* strains (sensitivity 99.6%). The amplification of the *invA* gene has been proposed as an international standard for genus of *Salmonella* detection (Malorny et al., 2003a). The *fliC* and *fliB* genes in *Salmonella* spp. encode the phase-1 and phase-2 flagellins, respectively. These genes are found at two different locations (Soumet et al., 1999; Joys 1985), The fimberie encoding gene named *sefA*. The *sefA* gene used for *Salmonella enterieidis* (Doran et al., 1996). In this study, specific detection of *Salmonella typhimurium* in M-PCR assay was performed using *Fli15* and *Tym* primers targeting the *fliC* gene. Oliveira et al. (2002) reported that the Multiplex-PCR assay using *invA* gene for detection of *Salmonella* and *fliC* gene for identification of *S. typhimurium* from poultry-related samples has 100% specificity.

In consistent with present results, other investigations also indicated that PCR methods is a rapid and specific test for detection of Salmonellas in animal feed samples (Rahn et al., 1992; Hoorfar et al., 2000; Lofstrom et al., 2004; Malorny et al., 2008). Maciorowski et al. (2000) showed that PCR based method could be applied to detection of Salmonellas from poultry rations. Jarquin et al. (2009) reported that development of bead-based DNA microarray coupled with flow cytometry and PCR amplification would be ideal for simultaneous detection and differentiation of *Salmonella* serovars commonly associated with poultry breeder feed contamination. It is usefulness to use multiplex-PCR method that could be considered as an appropriate alternative to conventional culture method for detection of *Salmonella* serovars (Jamshidi et al., 2009). This

Selective and/or non-selective enrichment medias combined with PCR have been applied to the detection of many bacterial pathogens (Schrank et al., 2001) to improve sensitivity and dilution of PCR inhibitory substances (Fluit et al., 1993). In this study, tetratonat broth and selenite cystine broth were used for pre-enrichment and enrichment stages and *Salmonella* serovars were diagnosed using M-PCR method. The results of this study showed that M-PCR is a rapid and synchronous method for detection of *Salmonella* SP. from poultry feedstuffs.

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