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Detection of Virulence Genes in Salmonella Species Isolated from Chevon and Chicken Meat

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ABSTRACT

The aim of present study was to investigate the detection of virulence factors encoded *Salmonella* enterotoxin (*stn*) and plasmid encoded fimbriae (*pef*) genes in isolates of Salmonellae isolated from chevon and chicken meat samples collected from different districts of Chhattisgarh. A total of 32 *Salmonella* isolates were recovered, among them 18 and 14 isolates were recovered from chevon and chicken meat samples, respectively. All the *Salmonella* isolates were tested for the presence of virulence associated genes *viz.*, *stn* and *pef* by using polymerase chain reaction (PCR) protocols, standardized separately for each gene. All 32 (100%) *Salmonella* isolates were found to carry the enterotoxin determinant *stn* gene where as none of the *Salmonella* isolate was found positive for *pef* gene, indicating that the *stn* gene is widely distributed among the *Salmonella* isolates irrespective of source of sample, species, serovars and location. The *stn* gene in *Salmonella* was found to be highly conserved. Thus, stn gene may be used as a target gene for detection of Salmonellae in different types of field samples.

Keywords: Salmonellosis, *stn*, *pef*, meat, virulence

In India, Salmonella has become leading cause of food borne illnesses viz., food poisoning, acute gastroenteritis, dysentery and other diseases even to death with considerable economic impact. Eggs, chicken, meat and meat products are the most common vehicles of salmonellosis to humans (Maharjan *et al.*, 2006). There are more than 2500 serotypes of Salmonella and new serotypes are emerging every year, most of them have strong pathogenicity to humans and animals (Fang et al., 2010). The outcome of a Salmonella infection is determined by the status of the host and of the bacterium. Age, genetic and environmental factors mainly determine the status of the host whereas virulence factors determines the status of the bacterium (Van Asten and Van Dijk, 2005). Virulence factors responsible for pathogenicity in enteric bacteria are often plasmid encoded, as in E. coli, Yersinia spp. and Shigella spp. However, current evidences suggest that the contribution

of virulence plasmids to pathogensis in *salmonella* is less important (Muthu *et al.*, 2014) and dictated by an array of factors that act in tandem and ultimately manifest in the typical symptoms of salmonellosis. Virulence genes encode products that assist the organisms in expressing its virulence in the host cells. Some genes *viz.*, *sef*, *pef*, *spv* or *inv* are known to be involved in adhesion and invasion of *Salmonella* into the host cell; whereas other *mgt*C genes are associated with the survival in the host system and *sop*, *stn*, *pip* A, B, D genes are involved in the actual manifestation of pathogenic processes. Other virulence factors of *Salmonella* include production of endotoxins and exotoxins, and presence of fimbrie and flagella (Van Asten and Van Dijk, 2005).

Therefore, present study was planned to determine the virulence factors encoded by *Salmonella* enterotoxin (*stn*)



Table 1. Primer sequences for polymerase chain reaction

Target Virulence Gene	Primer Sequence (5'-3'	Amplicon Size (bp)	Reference	
Stn	(F*): TTGTGTCGCTATCACTGGCAACC	617		
	(R**): ATTCGTAACCCGCTCTCGTCC	017	Murugkar et al. (2003)	
Pef	(F*): TGTTTCCGGGCTTGTGCT	700		
	(R**): CAGGGCATTTGCTGATTCTTCC	700		

^{*} Forward Primer, ** Reverse Primer

and plasmid encoded fimbriae (*pef*) genes of *Salmonella* in isolates recovered from chevon and chicken meat samples collected from different districts of Chhattisgarh.

MATERIALS AND METHODS

Bacterial isolation

During the study period from September 2013 to August 2014, a total of 32 *Salmonella* isolates were recovered from chevon and chicken meat samples collected from different districts of Chhattisgarh. Among the 32 *salmonella* isolates, 18 and 14 isolates were recovered from chevon and chicken meat samples, respectively. All the isolates were available and maintained with the Department of Veterinary Public health and Epidemiology, College of Veterinary Science and A.H., Anjora, Durg (C.G.).

Polymerase Chain Reaction (PCR) for stn and pef genes

All the *Salmonella* isolates were tested for the presence of virulence associated *stn* and *pef* genes using PCR protocols standardized separately for each gene. Template DNA of *Salmonella* isolates incorporated in PCR reactions was

prepared by boiling and snap chill method (Nagappa et al. 2007). Briefly, all Salmonella isolates were grown in 10 ml Luria Bertani (LB) broth (HiMedia, India) and incubated at 37°C for 24 hrs. Thereafter, one ml of the test culture were taken in a 1.5 ml microcentrifuge tube and centrifuged at 8000 rpm for 10 min. The pellet was washed twice with sterile saline solution and finally re-suspended in 300 ul sterilized DNAse and RNAse-free milliO water (Millipore, USA). All the Salmonella isolates were vortexed and boiled for 10 min and then were immediately kept on ice. Suspensions were centrifuged at 12000 rpm for 10 min and 3µl of the supernatant was used as a DNA template in PCR mixtures. The PCR analysis for stn and pef genes was carried out as per the protocol described by Murugkar et al. (2003) with suitable modifications. The primers sets of stn and pef genes used in this study were synthesized from Imperial Life Sciences (P) Limited, Gurgaon, Haryana, India. The primer sequence of target virulence genes used in this study are presented in Table 1 and PCR cycling conditions are mentioned in Table 2.

The PCR was performed using thermocycler (Mastercycler, Eppendorf, Germany) in a final reaction volume of 25 μ l containing 2.5 μ l of 10X Taq Buffer, 1.5 mM MgCl₂, 50 μ M of each deoxyribonucleotide triphosphate (dNTP), 10

Table 2. Polymerase chain reaction conditions

Primers	Initial Denaturation	C Denaturation	ycling Conditions Annealing	Extension	Final Extension
Stn (F*)	0400 6 5 :	94°C for 1min	59°C for 1 min	72°C for 1 min	7200 6 10 :
Stn (R**)	94°C for 5 min	Repeated for 30 Cycles			72°C for 10 min
$pef(F^*)$	0400 6 5	94°C for 1min	55°C for 1 min	72°C for 1 min	72°C for 10 min
<i>pef</i> (R**)	94°C for 5 min	Repeated for 25 Cycles			72°C 101°10 min

^{*} Forward Primer, ** Reverse Primer

Table 3. Distribution of virulence genes among Salmonella isolated from chevon and chicken meat samples.

Source/Sample type	Number of isolates tested		of isolates positive for virulence genes n Pef	
Chevon	18	18 (100%)	-	
Chicken Meat	14	14 (100%)	-	
Total	32	32 (100%)	-	

pmol of each primers, 1U Taq Polymerase, 3 µl of template DNA and nuclease free water to make up the total volume 25 μl. After completion of PCR reaction cycles, amplified products were analysed using submarine agarose gel electrophoresis by running along with DNA ladder. The final PCR product was electrophoresed on 1.5% (w/v) agarose gel prepared in 1X Tris- Borate EDTA (TBE) buffer, visualized by ethidium bromide (0.5µg/ml) stain under UV transilluminator (Biometra) and documented by Gel Documentation System (Gel Doctm XR, Biorad, USA). All the biologicals required for molecular work were procured from Thermo Scientific (USA), Genetix (India) and Bangalore Genei (India).

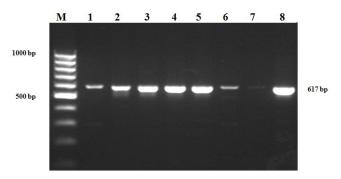


Figure 1. Agarose gel electrophoresis showing amplified PCR product of stn gene. Lane M: 100 bp DNA Ladder, Lane 1-8: Salmonella isolates with stn positive amplicons (617 bp)

RESULTS AND DISCUSSION

In the present study, all 32 (100%) Salmonella isolates were found to carry the enterotoxin determinant stn gene (Table 3). The amplified PCR products of all salmonella isolates on agarose gel electrophoresis yielded a 617 bp product in the *stn* gene segment (Figure 1).

Present study revealed that stn gene was present in all the isolates (100%) irrespective of source of sample and region of sampling. Salmonella induced diarrhoea is a complex phenomenon involving several pathogenic mechanisms including production of enterotoxin (Baloda et al., 1983) which is mediated by the stn gene (Chopra et al., 1987). The findings of present study are in agreement with Ezzat et al. (2014), wherein they reported the presence of stn gene in all salmonella isolates (100%) isolated from broiler chicken's liver, caecum, heart blood, spleen & kidney samples. The stn gene was found in 41 faecal isolates of Salmonella including 34 isolates of S. Typhimurium and 7 isolates of S. Enteritidis of calves, piglets and poultry (Barman et al., 2013) and in 95 Salmonella strains belonging to Salmonella enterica, isolated from man and animals (Murugkar et al., 2003). Prager et al. (1995) reported that stn gene could be detected in all the strains of Salmonella Enterica but not in Salmonella Bongori. The gene stn is reported to be absent in S. bongori strains as well as in other members of Enterobacteraceae or Vibrio families harbouring enterotoxigenic potential (Murugkar et al., 2003). Makino et al. (1999) also reported that the presence of even a single organism per gram of meat sample was detectable by PCR on the basis of detection of stn gene. Shi et al. (2013) reported the presence of stn gene in 45 out of 47 strains of salmonella had a chicken source origin and revealed that the enterotoxin stn gene carrying rate among Salmonella strains was 95.7%. Findings of present study revealed that the stn gene is widely distributed among the Salmonella isolates irrespective of source of sample, species, serovars and region of sampling. stn gene in Salmonella is highly conserved and it is expected to be a new target gene for detection of Salmonellae in field samples.

In the present study, none of the Salmonella isolates were found to be positive for pef gene. Results of our study are in agreement with Muthu et al. (2014) who also couldn't find pef gene among any of the Salmonella isolates recovered from human clinical samples. In contrary, Murugkar et al. (2003) reported the presence of pef gene in 85 of the 95 Salmonella isolates and revealed that there was no serotype specific presence or absence of this gene. The pef gene expresses plasmid-encoded fimbriae that contribute in adhesion and invasion of host cells.

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