



RESEARCH ARTICLE

**OCCURENCE OF STAPHYLOCOCCUS AUREUS AND SALMONELLA SPECIES IN RAW BEEF**

**Latha, C., Anu, C.J., Sunil, B., Ajaykumar, VJ. And Deepa Jolly**

Department of Veterinary Public Health College Of Veterinary and Animal Sciences, Mannuthy, Thrissur, Kerala-680651

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**ABSTRACT**

*Staphylococcus aureus* and *Salmonella* are major food borne pathogens of great public health concern worldwide. In the study PCR protocol was standardized for the detection of these organisms using oligonucleotide primers targeted against *nuc* gene of *S.aureus* and *inv A* gene of *Salmonella* spp. Specificity of primers was tested using reference strains (MTCC 1144 and MTCC 98) and other bacterial strains including *E.coli*, *E.coli* O157:H7 and *V. parahaemolyticus*. PCR detection on artificially inoculated beef samples showed a sensitivity value up to 1 cfu/g for both organisms. Out of 190 beef samples, 99 (52.10%) tested positive by culture method and 109 (57.36%) by PCR for *S. aureus*. With respect to *Salmonella* spp., rate of occurrence was 29.47% (n=56) and 36.31% (n=66) by culture method and PCR respectively. The high percentage of occurrence of *S. aureus* and *Salmonella* spp. highlights the need to improve the sanitation and hygiene procedures at all levels from production to the consumption of meat.

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**INTRODUCTION**

Food-borne pathogens are the leading cause of disease and mortality in developing countries, causing death of approximately 1.8 million people annually (Iyer *et al.*, 2013). Changes in eating habits, mass catering complexes and lengthy food supply procedures with increased international movement and poor hygienic practices are major contributing factors for the occurrence of food poisoning (Hedberg *et al.*, 1992). *Staphylococcus aureus* and *Salmonella* spp. are the frequently recognized bacterial food borne pathogens responsible for food poisoning and food related intoxications.

*Staphylococcus aureus* is a Gram-positive, catalase-positive commensal bacterium colonizing both humans and animals. 'The organism' is known for causing food poisoning through the production of enterotoxins. It is responsible for causing a variety of animal diseases such as mastitis, arthritis and urinary tract infections and a prominent cause of food borne intoxications due to poor hygienic practices (Akbar *et al.*, 2013). *Staphylococcus* food poisoning is commonly associated with fresh and ready-to-eat foods particularly meat products. This is considered as the third largest cause of food related illness worldwide (Aydin *et al.*, 2011).

Food borne Salmonellosis is recognized as a global zoonosis and constitutes a serious public health threat due to its endemic nature, high morbidity and association with a wide range of foods (Moussa *et al.*, 2012). Consumption of raw and under cooked meat and meat products remain the principal source of *salmonella* but it has been also associated with dairy products and vegetables (Robles *et al.*, 2008). Improper cooking, inadequate storage, cross-contamination and use of raw ingredients in the preparation of foods are the most common factors contributing to outbreaks.

Monitoring the presence of foodborne pathogens in foods is the primary tool for the implementation of food safety systems. It is necessary to monitor the prevalence of food borne

pathogens for effective food safety planning and targeted interventions. Recently, with the development of molecular techniques, polymerase chain reaction (PCR) has become an important tool for detecting pathogenic microorganisms in food products by replacing the time-consuming culture-based classical techniques (Xu *et al.*, 2006). They are rapid, easy to handle, sensitive and specific and constitute very valuable tools for microbiological applications. The objective of this study is to investigate the occurrence of *S. aureus* and *Salmonella* spp. in raw beef using PCR and culture techniques and to compare the results.

**MATERIALS AND METHODS**

**Reference strain and preparation of inoculums**

*Staphylococcus aureus* (MTCC 1144) and *Salmonella enterica* Typhimurium (MTCC 98) were procured from Microbial type culture collection and Gene bank (MTCC), Institute of Microbial Technology (IMTECH), Chandigarh. Cultures were grown in Tryptic soy broth with yeast extract (TSBYE) at 37°C for 18h. Then, tenfold serial dilutions were prepared in normal saline solution to obtain dilutions containing 10<sup>0</sup> to 10<sup>4</sup> cfu/ml.

**Artificial inoculation of meat samples**

Meat samples were purchased from retail market and aseptically transferred to the laboratory in sterilized polythene bags and kept frozen at -20<sup>0</sup> C. The samples were tested microbiologically for the presence of organisms under study. After ensuring the absence of the organisms, twenty five grams of meat was weighed and different concentrations of *S. aureus* and *Salmonella* spp. *i.e.*, 1cfu, 10 cfu, 10<sup>2</sup> cfu and 10<sup>3</sup>cfu/g were inoculated individually with 225ml of sterile Tryptic Soy Yeast extract broth (TSBYE) and pummeled in a stomacher (AES Chemiuex, France) for two minutes. An uninoculated sample was also included as control to ensure the sterility. Samples were then incubated at 37°C for 18h.

\* Corresponding author: Latha, C.

Department of veterinary public health College of veterinary and animal sciences, Mannuthy, thrissur, kerala-680651

**Microbiological analysis**

Microbiological analysis was carried out by the method demonstrated by APHA, 2001. Pre-incubated samples (0.1 ml) in TSBYE were spread on the surface of Baird-Parker agar medium (Himedia, India) supplemented with Egg Yolk Tellurite Emulsion (Himedia), selective media for *S. aureus* and incubated further at 37°C for 48 h. Black colonies surrounded by opaque halo on Baird-Parker agar were considered as presumptive *S. aureus*. For the isolation of *Salmonella* spp., 0.1 ml of enriched samples were spread on the surface of Brilliant green sulphur agar medium (Himedia, India), selective media for *Salmonella* and incubated at 37°C for 24 h. Pink coloured colonies were counted as *Salmonella* spp. and isolated colonies were subjected to series of biochemical tests for confirmation.

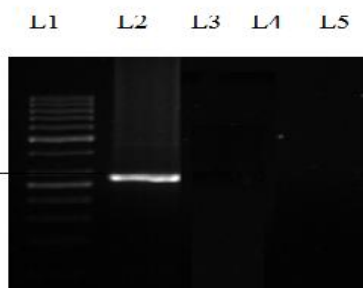
**Polymerase chain reaction**

Extraction of DNA was carried out by boiling and snap chilling method (Lee *et al.*, 2009). Target genes that were detected by PCR, primer sequences, amplicon size and the references thereof are summarized in Table.1.

**Table 1** Primers used in the study

Organism	Target gene	Sequence	Amplicon size	Reference
<i>S. aureus</i>	<i>nuc</i>	Forward GCGATTGATGGTGATACGGTT	270bp	Brakstad <i>et al.</i> (1992)
		Reverse AGCCAAGCCTTGACGAATAAAGC		
<i>S. enterica</i> Typhimurium	<i>inv A</i>	Forward GGTGGCAAGGGAATGAA	284bp	Rahn <i>et al.</i> (1992)
		Reverse CGCAGCGTAAAGCAACT		

PCR amplifications were conducted in a reaction mixture containing 2.0µl PCR buffer (10x, Sigma), 2.0µl MgCl<sub>2</sub> (2.5mM, Sigma), 0.5µl dNTPs (2mM each, Fermentas), 0.5µl of each primer sets (10pM, Sigma), 0.2µl Taq Polymerase (5U/µl, Sigma) and 2µl of template DNA, in a final volume of 25µl. Amplification conditions were 2 min. at 95°C, 35 cycles of 15sec. at 95°C, 30sec. at 60°C and 60sec. at 72°C and a final extension of 10 min. at 72°C. Reactions were carried out in a Master cycler (Eppendorf, Germany). After PCR reaction, 3µl of the PCR product was resolved on 1.5% agarose gel. The gels were stained with Ethidium bromide (0.2µg/ml) and photographed under UV transillumination in gel documentation system (Synoptics, UK). To evaluate the specificity of primers used in the study, PCR was carried out using the DNA prepared from the common cross-reacting bacterial species such as *E.coli*, *E.coli* O157:H7, and *V. parahaemolyticus*.



**Figure 1** Specificity of PCR using *nuc* primer(L1-Marker, L2-*S. aureus*, L3- *E.coli*, L4- *E.coli* O157:H7 and L5- *V. parahaemolyticus*)

**Screening of samples**

A total of 190 beef samples were collected from retail markets in Mannuthy (n=22), Thrissur (n=63), Calicut (n=20),

Ernakulam (n=66) and Wayanad (n=19). Samples were collected aseptically and transported to the laboratory under chilled condition. All samples were investigated for the presence of *S.aureus* and *Salmonella* spp. using in parallel the microbiological method and PCR. Samples were considered positive when the suspected colonies were confirmed by biochemical identification and PCR amplification with specific primers.

**Statistical analyses**

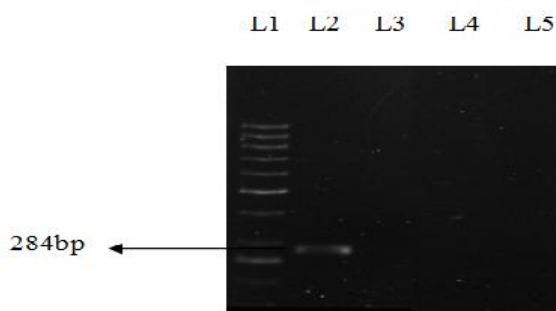
All data were analysed by Mc Nemar’s test using SPSS version 22.0. Evaluation of PCR and culture techniques was done by calculating sensitivity, specificity, efficiency and predictive values.

**RESULTS AND DISCUSSION**

Despite improvements in meat processing hygiene practices in recent years, the occurrence of pathogenic organisms is a major cause of food borne diseases and highlights the need for a rapid and accurate identification of these food borne pathogens (Guan *et al.*, 2013). In the present study,

cultural and PCR techniques were employed to investigate the occurrence of *S. aureus* and *Salmonella* spp. in raw beef.

In the recent years, PCR protocol is emerged as a rapid, easy to handle, sensitive and specific technology for detecting food-borne pathogens. Implementation of these methodologies to the routine laboratory analysis still needs more data on their application in naturally contaminated food, as well as, their validation with the currently accepted procedures (Alarcon *et al.*, 2005). PCR protocol was standardized using the primers targeting the *nuc* gene of *S. aureus* and *inv A* gene of *Salmonella* spp.



**Figure 2** Specificity of PCR using *inv A* primer(L1-Marker, L2-*Salmonella* spp., L3- *E.coli*, L4- *E.coli* O157:H7 and L5- *V. parahaemolyticus*)

**Specificity assay of PCR**

The standardized PCR protocol for each organism was carried out individually using other competing organisms like *E. coli*, *L. monocytogenes*, and *V. parahaemolyticus* for checking the specificity of *nuc* and *inv A* primers separately. The result showed that the primers were specific for targeting the region of their respective organisms. No nonspecific reactions with other species were obtained in PCR reaction (Figure 1 and 2).

The PCR protocol standardized by Pinto *et al.* (2005) also showed high specificity of *nuc* primers. Santos *et al.* (2001) observed high specificity of *inv A* gene for the *Salmonella* detection.

**Sensitivity assay of PCR**

When PCR assay was performed using artificially contaminated beef samples after enrichment, upto 1 cfu/g of initial concentration could be detected for both pathogens within 24 h. (Figure 3 and 4). The culture technique was also able to detect same level, but result was obtained after 96 h. of analysis in case of *S. aureus* and 72 h. for *Salmonella*. A study by Alarcon *et al.* (2005) reported that they could detect only 10<sup>3</sup>cfu/g of *S. aureus* directly from the homogenized sample without enrichment. Cocolin *et al.* (1998) reported that they could detect *Salmonella* upto 1-10 cfu/25g after 18h. in selenite cysteine broth and 10<sup>2</sup>-10<sup>3</sup> cfu/g without enrichment.

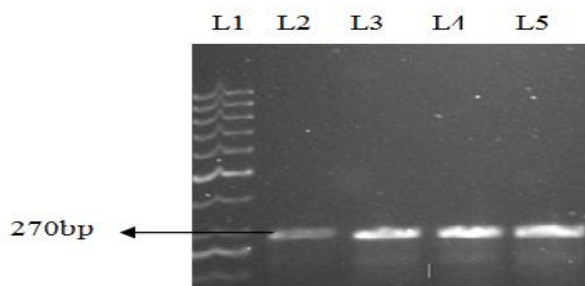


Figure 3 Sensitivity of PCR for *S. aureus*(L1-Marker, L2-1cfu/g, L3- 10cfu/g, L4- 10<sup>2</sup>cfu/g and L5- 10<sup>3</sup>cfu/g)

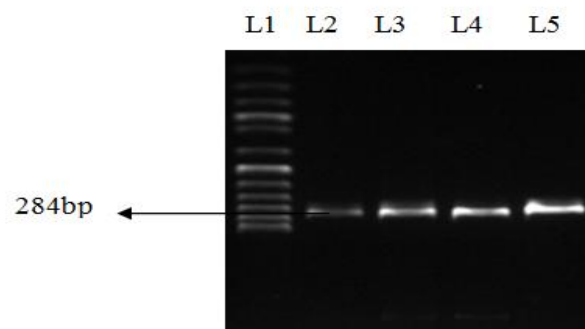


Figure 4 Sensitivity of PCR for *Salmonella* spp.(L1-Marker, L2-1cfu/g, L3- 10cfu/g, L4- 10<sup>2</sup>cfu/g and L5- 10<sup>3</sup>cfu/g)

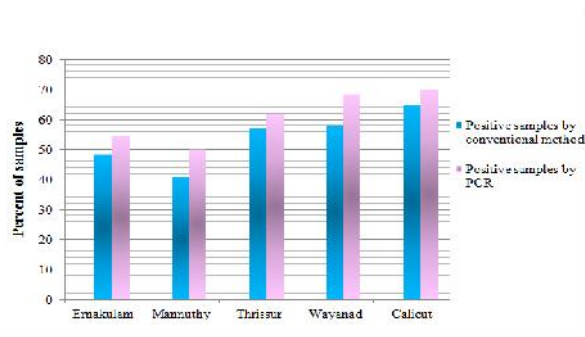


Figure 5 Occurrence of *S. aureus* in beef

**Screening of samples**

A total of 190 beef samples were analyzed for the presence of *S. aureus* and *Salmonella* spp. by using culture method and PCR. The distribution of the occurrence of both pathogens in

meat samples from various sources is presented in Figures 5 and 6.

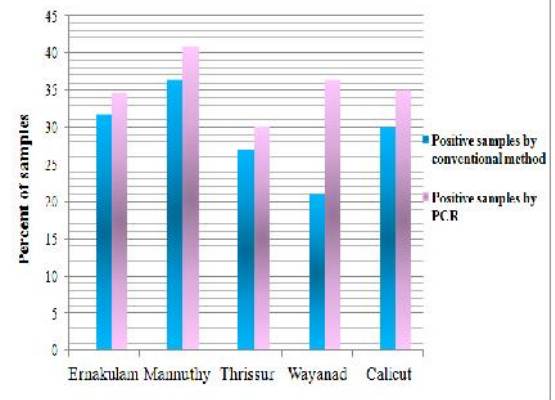


Figure 6 Occurrence of *Salmonella* spp. in beef

Out of 190 beef samples, 99 (52.10%) per cent. samples were tested positive by culture method and 109 (57.36%) by PCR for *S. aureus*. Yemisi *et al.* (2011) reported that occurrence of *S. aureus* in meat samples was 46 per cent. A study by Jackson *et al.* (2013) reported 63 % of *S. aureus* contamination of beef samples. A high occurrence rate was reported by Rahimi *et al.* (2013), who found 76.3 % *S. aureus* contamination in beef. With respect to *Salmonella* spp., rate of occurrence was 29.47 per cent (n=56) and 36.31 per cent (n=69) by culture method and PCR respectively. According to Iyer *et al.* (2013), occurrence of *Salmonella* spp. was 45 per cent in beef purchased from butcher shops. Khan *et al.* (2013) reported a low prevalence rate (4%) of *Salmonella* spp. by PCR and cultural techniques in beef samples.

The comparative study using Mc Nemar’s test showed that PCR has sensitivity of 87.88 per cent and 80.36 per cent for *S. aureus* and *Salmonella*, respectively. *Staphylococcus aureus* showed 82.11 % agreement (kappa value = 0.640) between the PCR and cultural methods whereas, *Salmonella* spp. Showed 83.68 per cent agreement (kappa value = 0.625). 93.3 per cent of agreement between PCR and cultural technique was reported for the detection of *S. aureus* by Alarcon *et al.* (2005). Fratamico (2003) reported that there was a good to excellent agreement (kappa value = 0.6824) between both methodologies for the detection of *Salmonella*.

**CONCLUSION**

In the present study, direct PCR was shown to be very effective in the detection of the pathogens from meat sample homogenates indicating that it is a robust method for rapid detection in comparison with culture technique which provide a significant contribution to both regulatory agencies and the meat industries. The high percentage of occurrence of *S. aureus* highlights the need to improve the sanitation and hygiene procedures at all levels from production to the consumption of meat.

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