A total of 202 animal samples (167 milk and 35 pus/exudate samples from cattle and buffalo) were collected and examined from dairy cattle and buffaloes. Simultaneously, 100 nasal swabs were collected from the closely associated personnel and farm workers. Out of these, the Staphylococcus spp. were isolated from 86 (42.57%) animal and 62 (62%) human samples. Of these, total 9 isolates from animals and 20 isolates from human were identified as MRS positive. Out of 9 and 20 MRS isolates from animal and human, 1 (11.11%) and 2 (10%) isolates were Methicillin-Resistant Coagulase Positive Staphylococcus (MRCoPS), whereas 8 (88.89%) and 18 (90%) isolates were Methicillin-Resistant Coagulase Negative Staphylococcus (MRCoNS), respectively. The SCCmec typing of 16 and 40 MRS (Including departmental isolates) isolates from animal and human were carried out. Out of these, the study revealed 18.75% (3/16) and 25% (10/40) isolates were classified as hospital associated methicillin-resistant staphylococci (HA-MRS), whereas 68.75% (11/16) and 45% (18/40) isolates were classified as community associated methicillin resistant staphylococci (CA-MRS) and 12.5% (2/16) and 30% (12/40) MRS isolates remained untypable, respectively. The overall percentage of CA-MRS (63.04%) was higher as compare to HA-MRS (28.26%) among both the species.
Introduction

*Staphylococcus aureus* is one of the most extensively studied bacteria of genus *Staphylococcus*. During recent years, Coagulase Negative Staphylococci (CNS) referred as “Environmental Staphs” have become the most common bovine mastitis isolates in many countries and are regarded as emerging mastitis pathogens (Jakee et al., 2013).

Amongst the Staphylococci group, *Staphylococcus aureus* strains are more dangerous to dairy animals and are of greatest attention for scientific community worldwide as they have ability to resist antibiotic therapy due to production of beta-lactamases a group of enzymes that inactivate penicillin and closely related antibiotics. To overcome infections caused by beta-lactamase producing Staphylococci, narrow spectrum semi-synthetic penicillin (methicillin) was introduced. However, soon after introduction, Methicillin-resistant *Staphylococcus aureus* (MRSA) strain was identified. Initially, MRSA strains were encountered only in the hospitals, but in the late 1990s first virulent community-acquired MRSA (CA-MRSA) clones, characterized by the presence of the toxin Panton-Valentine Leukocidin (PVL), appeared rapidly and unexpectedly. They quickly spread worldwide, initially only in the community, but later on also in the healthcare facilities, displacing in some countries typical HA-MRSA. For this reason, nowadays, distinction between CA-MRSA and mostly multi resistant HA-MRSA become challenging (Chambers and Deleo, 2009).

MRSA needs to be identified below the species level by rapid and reliable typing methods. Staphylococcal cassette chromosome *mec* (SCCmec) typing accompanied with overall genotyping has already provided strong evidence for the independent origins of healthcare associated MRSA and community acquired MRSA (Naimi et al., 2003). To date, eleven different types of SCCmec (I–XI) have been defined on the basis of the combination of *ccr* and *mec* complexes, but only type I–V are globally distributed, while others appear to exist as local strains in the country of origin (Zhang et al., 2009). Among this five types, SCCmec types I, II and III are mainly associated with healthcare associated MRSA (HA-MRSA) strains, whereas SCCmec type IV and V are associated with community associated MRSA (CA-MRSA) strains, as well as with the Pediatric clone MRSA strains (Shore et al., 2005).

The literature reviewed that there are lots of reports on staphylococcal cassette chromosome *mec* (SCCmec) types in Methicillin-resistance Staphylococci of human origin across the globe including India, but in compare to human, few reports on SCCmec typing have been published from animals across the globe and still very few from India. The identification and molecular SCCmec typing and epidemiological studies have been conducted from pig and human, but scanty of references available regarding animal and human SCCmec types, epidemiological studies and their relationship in the world and in India.

Materials and Methods

The present investigation was carried out to optimize and standardize uniplex PCR for various types of Staphylococci SCCmec types from MRS prevalent in this region in animals and closely associated human beings that will facilitate the study of epidemiological correlation between human and animal isolates on the basis of hospital acquired methicillin resistance staphylococci (HA-MRS) or community acquire methicillin resistance staphylococci (CA-MRS).
Collection of samples from milk, pus/exudate (abscess) from animal and human nasal swabs

A total of 202 animal samples (167 milk and 35 pus/exudate samples from cattle and buffalo) were collected and examined from dairy cattle and buffaloes. Simultaneously, 100 nasal swabs were collected from the closely associated personnel and farm workers aseptically as per the guidelines given by Peacock et al., (2001). The milk samples were collected from clinical and sub clinical mastitis as per the guidelines laid by European Food Safety Authority (EFSA, 2009). Simultaneously, the isolates of Staphylococci previously recovered from subclinical and clinical mastitic milk from bovines and human nasal swabs and maintained at the Department of Veterinary Microbiology, Junagadh Agricultural University, were included in the study for SCCmec typing.

The isolates presumably identified as Staphylococcus spp. based on cultural, colony and biochemical characteristics (Result not shown) and amplified with different pairs of 4 primers by m-PCR for the identification of Methicillin-Resistance coagulase positive staphylococci (MRCoPS) or Methicillin-Resistance coagulase negative staphylococci (MRCoNS).

The isolates were confirmed as methicillin resistant staphylococci (MRS) using mecA-positive gene amplification. The isolates confirmed as MRS were further subjected to SCCmec typing using four primer-pairs designed to identify the five main known SCCmec types.

Isolation of bacterial genomic DNA from bacterial culture by Proteinase K-SDS method

The genomic DNA of staphylococci from bacterial broth culture was extracted according to Parayre et al., (2007) with minor modifications.

Molecular detection of MRSA isolates from animal and humans

Four predominant genes (16S rRNA, Nuc, Coa & MecA gene targets) (Table 1) identified based on the outcome of phenotype-based speciation were considered to be included for detection by m-PCR. From all genes, 16S rRNA was used to identify genus i.e. Staphylococci, Nuc gene encodes for thermonuclease was used to identify species i.e. Staphylococcus aureus, Coa gene encodes for coagulase was used as pathogenicity indicator and mecA gene target encodes for modified penicillin binding protein 2B was used for genotypically identification of methicillin resistance in Staphylococcus spp. Five microliters of the extracted DNA were used as a template in a 25 μL PCR mixture containing 14.25μL of 2X PCR master mix (Thermoscientific) (0.05 U/μL Taq DNA polymerase, reaction buffer,4 mM MgCl2, 0.4 mM of each dNTP (dATP, dCTP, dGTPand dTTP), 0.5 μL of each forward and reverse primer except mecA (1.25 μL of each forward and reverse primers) and 0.1 μLTaq Polymerase (5U/ μl) (Thermo scientific).

The reference strain of Staphylococcus aureus ATCC 43300 and ATCC 25923 (Himedia Pvt. Ltd., Mumbai) was used as negative and positive control, respectively for mecA gene. The Steps and cycling conditions for m-PCR were Initial denaturation at 94 °C for 5 min followed by 40 cycle of Denaturation at 94 °C for 30 sec, Annealing at 52 °C for 1 min., Extension at 72 °C for 1 min and Final extension at 72 °C for 10 min in m-PCR. Using m-PCR Methicillin Resistant Coagulase Positive Staphylococci (MRCoPS) as well as Methicillin Resistant Coagulase Negative Staphylococci (MRCoNS) were identified in one single reaction.
Molecular detection of SCC\textit{mec} types from methicillin-resistant staphylococci from animal and humans

Four primer sets were used to ensure amplification of two DNA targets from SCC\textit{mec} type IV and two targets from SCC\textit{mec} type V. The targets were chosen so that one target would be amplified from each of SCC\textit{mec} types I–III (Table 2). The PCR of MRS colonies was carried out in final reaction volume of 25 µl in thermal cycler (verity, Applied Biosystems by life technology, Singapore).

Three microliters of the extracted DNA were used as a template in a 25 µL PCR mixture containing 12.5 µL of 2X PCR master mix (Thermoscientific) (0.05 U/µL Taq DNA polymerase, reaction buffer, 4 mM MgCl2, 0.4 mM of each dNTP (dATP, dCTP, dGTP, and dTTP), 1 µL of each forward and reverse primer and 7.5 µl nuclease free water.

The steps and cycling conditions for PCR were Initial denaturation at 94 °C for 4 min followed by 30 cycle of Denaturation at 94 °C for 30 sec, Annealing at 55 °C for 30 sec, Extension at 72 °C for 60 sec and Final extension at 72 °C for 4 min for different primer pairs described by Boye et al., (Boye et al., 2007). The reference strain of \textit{E. coli} (MTCC-522) strain was used as SCC\textit{mec} types negative.

PCR products (5 µL) were analyzed by electrophoresis on agarose 1.5% w/v gel followed by staining with ethidium bromide. The SCC\textit{mec} type was determined on the basis of the band pattern obtained (Table 3).

Isolates with no visible bands, or with a band pattern that was not in agreement with one of the five predicted band patterns, were classified as non typeable (NT).

Results and Discussion

\textbf{m-PCR for the detection of MRSA from animal and human isolates}

The 202 animal samples (milk, pus/exudate) and 100 human nasal swabs were processed for isolation of bacteria as per standard procedures (Quinn et al., 1994). Out of total 202 animal and 100 human samples collected 86 (42.57%) and 62 (62%) isolates, respectively were identified as \textit{Staphylococcus} spp. based on phenotypic, biochemical growth patterns (Result not shown) and molecular characterization.

The m-PCR was carried out for detail classification and characterization of presumably identified staphylococci. Out of total 202 animal samples, 86 isolates were identified as staphylococci based on amplification of 16S rRNA gene. Of these, 74 isolates were identified as Coagulase Negative Staphylococci (CoNS) based on amplification of only 16S rRNA gene and 12 isolates were identified as Coagulase Positive Staphylococci (CoPS) based on amplification of both 16S rRNA and \textit{Coa} gene. Based on amplification of three genes 16S rRNA, \textit{Coa} and \textit{mecA}, 8 isolates were identified as Methicillin-resistant Coagulase Negative Staphylococci (MRCoNS) and 1 isolates were Methicillin-Resistant Coagulase Positive Staphylococci (MRCoPS), whereas only one isolate was identified (based on all four gene amplification pattern) as Methicillin-Resistant Coagulase Negative \textit{Staphylococcus aureus} (MRCoNSA) from the animal samples (Table 4). Based on amplification of genes 16S rRNA and \textit{mecA} gene, 9 isolates were identified as positive for Methicillin-Resistant Staphylococci (MRS) (Figure 1).

The 100 samples were collected from the human nasal swabs which had remained in contact with these animals. Of these, 62
isolates were identified as *Staphylococcus* based on amplification of 16S rRNA gene and 50 isolates were identified as Coagulase Negative Staphylococci (CoNS) based on amplification of only 16S rRNA gene and 12 isolates were identified as Coagulase Positive Staphylococci (CoPS) based on amplification of both 16S rRNA and Coa gene. Based on amplification of three genes 16S rRNA, Coa and mecA, 18 isolates were identified as Methicillin-Resistant Coagulase Negative Staphylococci (MRCoNS) and 2 isolates were identified as Methicillin-Resistant Coagulase Positive Staphylococci (MRCoPS) from the human samples (Table 4). Based on amplification of genes 16S rRNA and mecA gene, 20 isolates were identified MRS positive.

**Molecular characterization of major SCCmec types among MRS from animal and humans**

The occurrence of staphylococcal cassette chromosome mec types (SCCmec types) were investigated from MRS isolates obtained from animal and human samples. Out of total 133 and 102 *Staphylococcus* spp. isolates (47 and 40 departmental staphylococci isolates from animal and human were included, respectively), 16 and 40 isolates from animal and human were identified as Methicillin-resistant staphylococci, respectively. Of these 16 animal MRS isolates, 14 isolates having one of the SCCmec types (SCCmec type I, 2; SCCmec type II, 0; SCCmec type III, 1; SCCmec type IV, 5; SCCmec type V, 6), whereas 2 isolates were untypable, whereas 40 human MRS isolates, 28 isolates having one of the SCCmec types (SCCmec type I, 7; SCCmec type II, 0; SCCmec type III, 3; SCCmec type IV, 9; SCCmec type V, 9), whereas 12 isolates were Untypable (Table 5 and Figure 2).

During the current study, 18.75% (3/16) isolates were classified as hospital associated methicillin-resistant staphylococci (HA-MRS) (SCCmec type I, 2; SCCmec type III, 1), whereas 68.75% (11/16) isolates were classified as community associated methicillin resistant staphylococci (CA-MRS) (SCCmec type IV, 5; SCCmec type V, 6) and 12.5% (2/16) isolates remained untypable from animal MRS isolates.

**Table.1** Nucleotide sequences of primers used for m-PCR along with their product size and references

<table>
<thead>
<tr>
<th>Sr. No.</th>
<th>Name of primer</th>
<th>Primer sequence (5’-- 3’)</th>
<th>Product size</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>TStaG422F1</td>
<td>5’- GGC CGT GTT GAA CGT GGT GCT CAA ATC A-3’</td>
<td>370 bp</td>
<td>(Martineau et al., 2001)</td>
</tr>
<tr>
<td></td>
<td>TStaG765R1</td>
<td>5’- TIA CCA TTT CAG TAC CCT CTG GTA A-3’</td>
<td></td>
<td></td>
</tr>
<tr>
<td>2</td>
<td>Nuc F</td>
<td>5’- GGC ATT GAT GGT GAT ACG GTT -3’</td>
<td>280 bp</td>
<td>(Brakstad et al., 1992)</td>
</tr>
<tr>
<td></td>
<td>Nuc R</td>
<td>5’- ACG CAA GCC TTG ACG AAC TAA AGC -3’</td>
<td></td>
<td></td>
</tr>
<tr>
<td>3</td>
<td>Coa F1</td>
<td>5’- GTA GAT TGG GCA ATT ACA TTT TGG AGG -3’</td>
<td>117 bp</td>
<td>(Moon et al., 2007)</td>
</tr>
<tr>
<td></td>
<td>Coa R1</td>
<td>5’- CGC ATC AGC TTT GGT ATC CCA TGT A -3’</td>
<td></td>
<td></td>
</tr>
<tr>
<td>4</td>
<td>mecA F1</td>
<td>5’- ’GAGT TGT AGT TGT Cgg Gtt TGG-3’</td>
<td>454 bp</td>
<td>(Malik et al., 2006)</td>
</tr>
<tr>
<td></td>
<td>mecA R1</td>
<td>5’- ’GGG CAA TTC CAT ATT Gtt TC-3’</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
Table 2: Nucleotide sequences of primers used for the identification of SCC\textit{mec} types of MRS

<table>
<thead>
<tr>
<th>Sr. No.</th>
<th>Name of primer</th>
<th>Primer sequence (5'--3')</th>
<th>Product size</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>β F1 α 3 R1</td>
<td>5'-ATTGCGTTTGATAATAGGCCYTCT-3', 5'-TAAAGGCATCAATGCACAAACT-3'</td>
<td>937 bp</td>
<td>(Ito et al., 2001)</td>
</tr>
<tr>
<td>2</td>
<td>ccrCF1 ccrCR1</td>
<td>5'-CGTCTATTACAAGATGTTAAGGATAAT-3', 5'-CCTTTATAGACTGGATTATTCAAAAAT-3'</td>
<td>518 bp</td>
<td>(Ito et al., 2004)</td>
</tr>
<tr>
<td>3</td>
<td>1272F1 1272R1</td>
<td>5'-GCCACTCATACATGGA-3', 5'-CATCCGAGTGAAACCCAAA-3'</td>
<td>415 bp</td>
<td>(Boye et al., 2007)</td>
</tr>
<tr>
<td>4</td>
<td>5RmecAF1 5R431R1</td>
<td>5'-ATAACCCAAACCGACACACTAC-3', 5'-CGGCTACAGTGAACATCC-3'</td>
<td>359 bp</td>
<td>(Boye et al., 2007)</td>
</tr>
</tbody>
</table>

Table 3: Primers used in SCC\textit{mec} typing PCR and the resulting gel band patterns of SCC\textit{mec} types I-V

<table>
<thead>
<tr>
<th>Sr. No.</th>
<th>Name of primer</th>
<th>Product size</th>
<th>Target Gene</th>
<th>SCC\textit{mec} type</th>
<th>I</th>
<th>II</th>
<th>III</th>
<th>IV</th>
<th>V</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>β F1 α 3 R1</td>
<td>937 bp</td>
<td>ccrA2-B</td>
<td>√</td>
<td>√</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>2</td>
<td>ccrCF1 ccrCR1</td>
<td>518 bp</td>
<td>ccrC</td>
<td>√</td>
<td></td>
<td>√</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>3</td>
<td>1272F1 1272R1</td>
<td>415 bp</td>
<td>IS1272</td>
<td>√</td>
<td></td>
<td></td>
<td>√</td>
<td></td>
<td></td>
</tr>
<tr>
<td>4</td>
<td>5RmecAF1 5R431R1</td>
<td>359 bp</td>
<td>meca- IS431</td>
<td>√</td>
<td></td>
<td></td>
<td></td>
<td>√</td>
<td></td>
</tr>
</tbody>
</table>

√-Desired amplification of gene.

Table 4: Coagulase Negative (MRCoNS) and coagulase positive (MRCoPS) MRS isolates from animal ad humans

<table>
<thead>
<tr>
<th>Sample origin</th>
<th>No. of samples collected</th>
<th>No. of sample found positive for \textit{Staphylococcus} spp. No. (%)</th>
<th>Methicillin-Resistant \textit{Staphylococcus} (out of positive \textit{Staphylococcus}) No. (%)</th>
<th>No. (%) Methicillin-Resistant \textit{Staphylococcus}</th>
</tr>
</thead>
<tbody>
<tr>
<td>Animals (Milk+Pus)</td>
<td>202</td>
<td>86 (42.57)</td>
<td>9 (10.47)</td>
<td>8 (88.89)</td>
</tr>
<tr>
<td>Human (Nasal swabs)</td>
<td>100</td>
<td>62 (62)</td>
<td>20 (32.26)</td>
<td>18 (90)</td>
</tr>
</tbody>
</table>

MRCoNS – Methicillin-Resistant Coagulase Negative \textit{Staphylococcus}
MRCoPS – Methicillin-Resistant Coagulase Positive \textit{Staphylococcus}
Table 5 Occurrence and correlation between SCCmec type isolates based on HA-MRS and CA-MRS among animal and human MRS isolates

<table>
<thead>
<tr>
<th>SCCmec types of MRS</th>
<th>MRS isolates from Animal</th>
<th>MRS isolates from Human</th>
<th>MRS type</th>
<th>No. (%) Positive for HA-MRS/CA-MRS</th>
<th>MRS type</th>
<th>No. (%) Positive for HA-MRS/CA-MRS</th>
</tr>
</thead>
<tbody>
<tr>
<td>SCCmec type I</td>
<td>Positive for SCCmec type No. (%)</td>
<td>MRS type</td>
<td>No. (%) Positive for SCCmec type (No.)</td>
<td>MRS type</td>
<td>No. (%) Positive for SCCmec type (No.)</td>
<td></td>
</tr>
<tr>
<td>SCCmec type I</td>
<td>2 (12.5)</td>
<td>HA-MRS</td>
<td>3 (18.75)</td>
<td>7 (17.5)</td>
<td>HA-MRS</td>
<td>10 (25)</td>
</tr>
<tr>
<td>SCCmec type II</td>
<td>0</td>
<td>-</td>
<td>0</td>
<td>0</td>
<td>-</td>
<td>10 (25)</td>
</tr>
<tr>
<td>SCCmec type III</td>
<td>1 (6.25)</td>
<td>HA-MRS</td>
<td>3 (7.5)</td>
<td>HA-MRS</td>
<td>18 (45)</td>
<td></td>
</tr>
<tr>
<td>SCCmec type IV</td>
<td>5 (31.25)</td>
<td>CA-MRS</td>
<td>11 (68.75)</td>
<td>9 (22.5)</td>
<td>CA-MRS</td>
<td></td>
</tr>
<tr>
<td>SCCmec type V</td>
<td>6 (37.5)</td>
<td>CA-MRS</td>
<td>9 (22.5)</td>
<td>CA-MRS</td>
<td>12 (30)</td>
<td></td>
</tr>
<tr>
<td>UT</td>
<td>2 (12.5)</td>
<td>-</td>
<td>2 (12.5)</td>
<td>12 (30)</td>
<td>-</td>
<td>12 (30)</td>
</tr>
<tr>
<td>Total</td>
<td>16</td>
<td>-</td>
<td>40</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Figure 1 PCR amplicons of Methicillin-resistant coagulase negative/positive Staphylococcus aureus by mPCR (16S rRNA gene = 370bp, MecA = 454bp, Coa= 280bp and Nuc = 117bp) from animal isolates
Similarly, study revealed 25% (10/40) isolates were classified as hospital associated methicillin resistant staphylococci (HA-MRS) (SCCmec type I, 7; SCCmec type III, 3), whereas 45% (18/40) isolates were classified as community associated methicillin resistant staphylococci (CA-MRS) (SCCmec type IV, 9; SCCmec type V, 9) isolates and 30% (12/40) isolates remained untypable from human MRS isolates. The overall percentage of CA-MRS (63.04%) was higher as compared to HA-MRS (28.26%) among both the species (Figure 2).

In many countries, the presence of MRSA in animal and human is of veterinary and public health concern. Nasal carriage has an important role in the epidemiology and pathogenesis of MRSA infection in human and animal (Kluytmans et al., 1997). Several reports showed the prevalence of MRSA in cattle with mastitis (Bhagat et al., 2017). In a study made in farm animals, the nasal MRSA prevalence was found to be 0.3 % and 1 % in 400 cattle and 300 calves, respectively (Huber et al., 2010) which was lower as compared to present findings. In comparison to current finding, higher rates of MRSA were reported by, Erdem and Turkyilmaz (Erdem and Turkyilmaz, 2013) reported 7.14% (4/56) bovine and 17.64% (6/34) human nasal isolates were positive for MRSA. In another study from Turkey, Methicillin resistant was detected in 26.8 % (15/56) and 62.8 % (22/35) of bovine nasal and human nasal isolates, respectively (Inegol and Turkyilmaz, 2012). Garipcin and Seker, (Garipcin and Seker, 2015) revealed the nasal carriage rates of MRSA in 150 humans and 250 cattle at the rate of 8.7 % and 1.2 % respectively.

Amplification of all these primers in accordance with presence of respective genes gives identification of presence of Methicillin-resistant Coagulase Negative Staphylococci (MRCoNS) or Methicillin-
Resistant Coagulase Positive Staphylococci (MRCoPS). Similar to present study Nimavat, (Nimavat, 2015) and Hetal, (Hetal, 2016) applied multiplex PCR assay using same primer pairs used in this study and characterized the staphylococci as similar fashion as characterized in this study.

The study revealed higher percentage of CA-MRSA isolates as compare to HA-MRSA in animal as well as in human, indicating emergence of CA-MRSA strains in this geographical area. Inegol and Turkyilmaz (Inegol and Turkyilmaz, 2012) revealed higher rate of (67.80%) isolates including type II and III were hospital acquired (HA-MRS) whereas 32.20% isolates including type IV and V were community acquired (CA-MRS), which was lower as compared to present finding, but they had reported similarity of SCCmec types between bovine and human isolates, suggestive of evidence of transmission from animals to humans, or vice versa. Bhutia et al., (Bhutia et al., 2015) reported 25.33% (38/150) isolates met the definition of CA-MRSA and 10% (15/150) of HA-MRSA, which was lower as compare to present study.

During the study, the isolates from animal (Milk, pus/exudate) yielded various SCCmec type (SCCmec type I, III, IV and V), similarly the same SCCmec types were isolated from the human nasal swab of labors/worker/personnel who remain in close contact with this animals. During the current study, the same SCCmec types prevail in animaland human beings attributed the transmission of MRS from animal to human or vice versa indicating potential zoonotic pathogen prevalence in farm animal and their workers.

Simultaneously, we found that the MRSA strains harboured the high and variable prevalence of SCCmec alleles which is an additional pathogenic factor for infections. SCCmec IV and V were the most prevalent alleles in our findings. The CA-MRSA is mainly considered by SCCmec IV and V alleles, while HA-MRSA are recognized by SCCmec I, II and III alleles (De Lencastre, 2007). During the current study, MRS strains were mainly associated with CA-MRSA. In other hand, detection of SCCmec types IV and V suggested the emergence of CA-MRSA strains in this geographical area and occurrence of SCCmec I and II alleles indicated a possible transmission of MRSA from humans to animals. Further studies are needed to establish clonal relation of MRS from animaland farm workers with advance molecular techniques (Pulsed field gel electrophoresis, Staphylococcal Protein A analysis, multilocus sequence typing). The result of these studies may shed light on the clonility and transmission of resistance strain between human and animal. High prevalence of SCCmec types IV and V were also detected by various authors (Havaei et al., 2015).

MRSA infected cattle acts as a reservoir and later transmit the infections to other animals and humans. MRSA colonization in cattle may be an occupational risk to the people in close contact with MRSA infected cattle such as veterinarians, farmers, milkers and people working at slaughterhouses. Transmission of animal MRSA to veterinary personnel has been found and it is more common for large animal personnel than small animal personnel (Wulf et al., 2008).

Although, MRSA has been reported as transmissible diseases of zoonosis as well as humanosis importance, the direction and routes of transmission are superficially understood. Some authors have reported bidirectional transmission of MRSA (Ferreira et al., 2011). Animal to human transmission occurs through direct contact, environmental contamination and through handling of
infected animal product, whereas human to animal transmission is still unclear (Weese, 2010).

The similar SCCmec types in both the groups (Animal and human) suggest co-circulation of MRS isolates between human and animal population which was indication of possible lateral gene transfer between the staphylococcal isolates in this region. Most of the reported SCCmec types (except SCCmec type II) were found in this region. Higher number of CA-MRS associated types IV, V and a marked number of these in animal isolates suggested the possible transfer of resistance from human to animal isolates.

References


University, Junagadh.


Quinn, P. J., Carter, M. E., Markey, B. K. and


How to cite this article:

doi: https://doi.org/10.20546/ijcmas.2019.810.107