

Characterization of *Staphylococcus aureus* of Goat Mastitis Milk Origin for *cap* and *clfA* Genes

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***Staphylococcus aureus* is major pathogen causing mastitis in dairy milch animals including goats. The present study was carried out on 27 *S. aureus* isolates of milk origin from goats with clinical mastitis which included characterization of isolates for two important virulence associated genes namely *clfA*, responsible for clumping factor and *cap*, responsible for capsule. All the isolates were genotypically identified by 23S rRNA ribotyping in which a species-specific amplicon of 1250 bp was obtained. Of the 27 isolates 17 (68.38%) showed single amplicon of approximately 350 bp representing presence of *cap5K* gene responsible for capsular type 5 whereas nine (34.61%) of the isolates produced amplicons of approximately 200bp representing presence of *cap8K* genes responsible for production of capsular type 8, whereas one isolate was non-typable for any of the two genes. In the present investigation each of the 25 isolates produced single amplicon of 1050 bp indicating no polymorphism in *clfA* gene while two isolates did not produce any PCR amplicon. Epidemiological investigation of these genes is significant in terms of vaccine design and control of mastitis from the study area.**

Key words: *Staphylococcus aureus*, *cap*, *clfA*, goat, mastitis.

Goat is one of the oldest domesticated species which is used for milk, meat, hair, hide, and manure. It is very important animal species especially in western Rajasthan where most of the land area is arid and rearing is done almost on zero input. Mastitis is one of the important diseases of goat wherein due to improper or delayed diagnosis and no/or improper treatment, they are ultimately rendered useless for purpose of milk production.

The disease is multi-etiological complex in which *Staphylococcus aureus* has been found to be the most important pathogen worldwide for clinical as well as subclinical forms in dairy small ruminants (Bergonier *et al.*, 2003; Aras *et al.*, 2012).

A variety of virulence factors are produced by this organism which are involved in the pathogenesis of mastitis (Poutrel *et al.*, 1988; O'Riordan and Lee, 2004; Momtaz *et al.*, 2010), however, all factors are not produced by each strain (Balaban and Rasooly, 2000). Capsular polysaccharides produced by *S. aureus* isolates are considered important virulence factors in the

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pathogenesis of Staphylococcal infections. Of the many capsular types cap5 and cap8 have been considered important in pathogenesis and hence in vaccine development (Risley *et al.*, 2007; Tuchscher *et al.*, 2008). These capsular polysaccharides are surface bound and promote bacterial colonization and persistence on mucosal surfaces. Clumping factor A (ClfA) is a cell wall-anchored *S. aureus* surface protein that has been shown to enhance staphylococcal virulence in animal infection models (Moreillon *et al.*, 1995; Wolz *et al.*, 2002) and has been suggested as a vaccine potential candidate (Josefsson *et al.*, 2001; Nour El-Din *et al.*, 2006) and as a target for passive immunization approaches (Domanski *et al.*, 2005; Patti, 2004; Vernachio *et al.*, 2003).

Both of the virulence factors have also been suggested to be potential vaccine candidates (Risley *et al.*, 2007). In one study, Tuchscher *et al.* (2008) showed that antibodies to *clfA* enhanced the protection against infection provided by capsular polysaccharides antibodies. Caprine mastitis has been recorded in different countries by different authors (Moroni *et al.*, 2005; Ayedin *et al.*, 2009) but data from India are scarce. The present paper reports characterization of *S. aureus* of goat milk origin for capsular and clumping factor genes.

MATERIALS AND METHODS

Isolation and identification of bacteria

Isolation of *S. aureus* was carried out from milk samples of Marwari goats native to Bikaner with clinical mastitis. The organisms were isolated and identified as per the methods described by Cowan and Steel, (1975). Further they were genotypically identified by ribotyping based on 23S rRNA gene (Straub *et al.*, 1999) using species-specific primer-1 (5'-ACGGAGTTACAAAGGACGAC-3') and primer-2 (5'-AGCTCAGCCTTAACGAGTAC-3'). The amplification products were electrophoresed for 1.5 h at 100 V and then gel was visualized using a UV transilluminator.

cap gene amplification:

The method of Verdier *et al.* (2007) was used for the amplification of *cap5K* and *cap8K*

genes using the primer sets: The sequences for two primers used for *cap5K* gene were: Primer-1: 5'-GTCAAAGATTATGTGATGCTACTGAG-3' and Primer-2: 5'-ACTTCGAATATAAACTTGAATCAATGTTATACAG-3', the sequences for two primers used for *cap8K* gene were: Primer 1: 5'-GCCTTATGTTAGGTGATAAACC-3' Primer 2: 5'-GGAAAAACACTATCATAGCAGG-3'. The PCR mixture (total volume 30 µl) was prepared by mixing 1.0 µl of primer-1 (75 pmol/µl), 1.0 µl of primer-2 (75 pmol/µl), 3.5 µl of 10x *Taq* buffer A (containing 15mM MgCl₂), 1 unit of *Taq* polymerase (5 U/µl), 2.0 µl of dNTP mix (10 mM/µl), 21.0 µl of deionised water, and 2.5 µl of DNA template (25 ng/µl). The PCR was performed using following cycling parameters: Cycle 1: Denaturation at 94°C for 5 min, Primer annealing at 55°C for 30 s, Primer extension at 72°C for 1 min; Cycle 2-25: Denaturation at 94°C for 30 s, Primer annealing at 55°C for 30 s, Primer extension at 72°C for 1 min; Cycle 26: Denaturation at 94°C for 30 s, Primer annealing at 55°C for 30 s, Primer extension at 72°C for 5 min.

clfA gene amplification

The method of Stephan *et al.* (2001) was used for the amplification of *clfA* gene using the primers set (Primer 1: 5'-GGCTTCAGTGCTTGTAGG-3'; Primer 2: 5'-TTTTTCAGGGTCAATATAAGC-3'). The PCR mixture (total volume 30 µl) was prepared by mixing 1.25 µl of primer-1 (75 pmol/µl), 1.25 µl of primer-2 (75 pmol/µl), 2.5 µl of 10x *Taq* buffer containing MgCl₂ (25mM), 0.3 µl of *Taq* polymerase (5 U/µl), 2.5 µl of dNTP mix (10 mM/µl), 17.20 µl of deionised water and 2.5 µl of DNA template (25 ng/µl). The PCR was performed in Palmcycler (Corbett Research, Australia) using following cycling parameters:- Cycle 1: Preheating at 94°C for 4 min; Cycle 2-36: Denaturation at 94°C for 1 min, Primer annealing at 57°C for 1 min, Primer extension at 72°C for 1 min; final extension at 72°C for 5 min.

The PCR products, after addition of 2 µl of trekking dye were resolved in 1.2% agarose gels prepared in 1.0 x TBE buffer containing 0.5 µg/ml of ethidium bromide and 100 bp DNA ladder was used as molecular marker. The amplification products were electrophoresed for 1 h 30 min at 100 V. The gel was then visualized under U.V. transilluminator.

RESULTS AND DISCUSSION

23S rRNA gene based confirmation

All the 27 isolates on 23S rRNA ribotyping produced a single PCR product of 1250 base pairs confirming them to be *S. aureus*. This method was found 100% specific in genotypic identification of *S. aureus*.

cap genotyping

Seventeen of the 27 (68.38%) isolates showed single amplicon of approximately 350 bp representing presence of *cap5K* gene responsible for capsular type 5 (fig. 1) whereas nine (34.61%) of the isolates produced amplicons of approximately 200bp representing presence of *cap8K* genes responsible for production of capsular type 8 (fig. 2). In our study one of the 27 isolates was non-typable for CP5 or CP8.

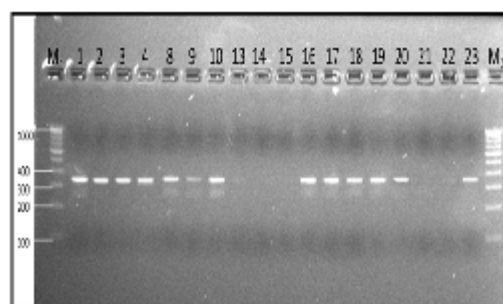
clfA genotyping

In the present investigation 25 isolates produced single amplicon in each isolate whereas two of the isolates did not produce any PCR amplicon. The size of the amplicon product obtained in the present study was 1050 bp indicating no polymorphism in *clfA* gene (fig. 3).

Mastitis is one of the most important diseases of dairy animals globally leading to severe financial losses to dairy industry. Among dairy animal species goat has its own important place in many of the countries. In India also goat rearing is practiced by marginal farmers for their livelihood. *Staphylococcus aureus* has been identified as the most important udder pathogen in small ruminants (Bergonier *et al.*, 2003). This organism doesn't demonstrate host specificity and is responsible for many different infections in animals as well as humans. Aires-de-Sousa *et al.* (2007) characterized *S. aureus* from buffalo, cattle, sheep and goat milk samples by phenotypic and genotypic methods and they concluded that a major clonal type is responsible for mastitis in different regions which does not demonstrate host specificity among the different animal species and seems to be capable of both infection and colonization. Mastitis caused by *S. aureus* should be eliminated because of the risk of contamination of milk products by the thermo-stable toxins (Contreras *et al.*, 2007).

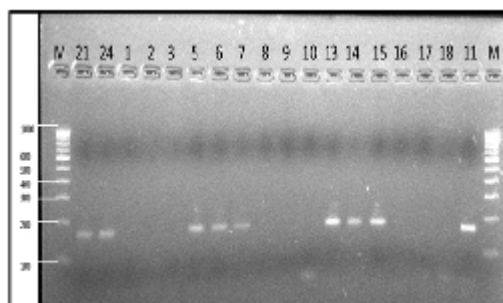
The identification of *S. aureus* strains is important to confirm the epidemiological relationships among them (Aarestrup *et al.*, 1994).

All the isolates in the present study were identified by genotypic method in which 23S rRNA gene was targeted using specific primers. This method is being used for confirmation of *S. aureus* from different sources worldwide (Akineden *et al.*, 2001;



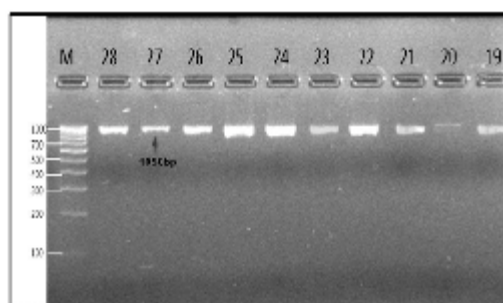
M = Molecular marker (100 bp)
Isolate no. 13, 14, 15, 21 and 22 with no *cap5K* gene amplicon

Fig. 1. Amplification of *cap5K* gene obtained from milk from goats with clinical mastitis



M: Molecular marker (100 bp)
Isolate no. 6, 7, 8, 15, 16, 17, 25, 26 and 27 with no *cap8K* gene amplicon

Fig. 2. Amplification of *cap8K* gene obtained from milk from goats with clinical mastitis



M: Molecular marker (1000 bp)
1050bp size amplicon showing presence of *clfA* gene

Fig. 3. Amplification of *clfA* gene obtained from milk from goats with clinical mastitis

Momtaz *et al.*, 2010; Proietti *et al.*, 2010; Khichar *et al.*, 2012; Suleiman *et al.*, 2012).

Various workers have experimentally elucidated the antigenic properties and possible role of capsular polysaccharides in the generation of vaccines against *S. aureus* infections. The gene cluster for CP5 and CP8 type contains 16 open reading frames (*cap5A* through *cap5P* and *cap8A* through *cap8P*, respectively) the four of which are located in the central region (H - K) and are type specific. In the present study except one isolate (no.22) all other 26 isolates were typable for *cap5K* or *cap8K* gene fragments. Seventeen isolates showed presence of *cap5K* gene whereas nine showed presence of *cap8K* genes. The amplicon sizes obtained in the present study were almost similar to those obtained by Verdier *et al.* (2007), Upadhyay *et al.* (2010) and Khichar, (2011).

Of the 11 CP types CP5 and CP8 are produced by majority of the animal mastitic isolates (Poutrel *et al.*, 1988; Naidu *et al.*, 1991). Likewise, CP5 and CP8 have been reported to be produced by more than 75% of human isolates (Fatton *et al.*, 1996; Lee *et al.*, 1997). The *cap* genes are highly conserved and the capsular polysaccharides have got limited antigenic specificity (O'Riordan and Lee, 2004). Similarly, other studies have also shown that antibodies to capsular polysaccharides have some protective efficacies for preventing infections in experimental animal (Fatton *et al.*, 1996; Lee *et al.*, 1997). The occurrence of *cap5K* or *cap8K* varies in isolates from different geographical regions (Sordelli *et al.*, 2000; Salasia *et al.*, 2004).

In our study one of the 27 (3.7%) isolates was non-typable for *cap5* or *cap8* genes, which is in agreement to the observations of many workers who found a variable percentage of non-typable isolates for these genes. Upadhyay *et al.* (2010) had reported 50% caprine *S. aureus* isolates to be non typable whereas 30% showed presence *cap5K* gene and 20% possessed *cap8K* gene. They did not observe any polymorphism in *cap5K* and *cap8K* genes which is in complete agreement to the present study. However, a very high percentage (86.2%) of non-typable isolates was detected by Sordelli *et al.* (2000) by serotyping. Guidry *et al.* (1998) also recorded 59% of the US isolates and 30% of the isolates from Europe to be CP5 or CP8 negative. Similarly, 30% of *S. aureus* from bovine mastitis were reported not to possess CP5

or CP8 by Naidu *et al.* (1991). This finding is almost similar to observations of Khichar, (2011) from the same study area who did not record any of the isolates without *cap* genes in his study involving bovine cattle mastitis isolates. Similarly Singh *et al.* (2011) recorded that only 86.8% (60.7% *cap5K* and 26.1% *cap8K*), 79.0% (56.3% *cap5K* and 22.7% *cap8K*) and 81.1% (22.2% *cap5K* and 18.9% *cap8K*) *S. aureus* isolates from intra-mammary infections in Sahiwal cattle, Karan-Fries cattle and Murrah buffaloes respectively were capsulated.

Khichar, (2011) had also reported capsular typing of cattle mastitic *S. aureus* isolates from the same laboratory and found 92.86% isolates to possess *cap5K* gene while 7.14% isolates to possess *cap8K* gene amplicon with no polymorphism in *cap* genes.

In the present study 68.38% isolates were detected with *cap5K* genes and 34.61% with *cap8K* genes among typeable isolates which is in conformity to observations of Upadhyay *et al.* (2010) who recorded that 60% of mastitis isolates from cattle and goats had *cap5K* genes and 20% had *cap8K* gene. Similarly Khichar, (2011) reported 92.86% isolates with presence of *cap5K* gene and 7.14% isolates with presence of *cap8K* gene. Contrarily, Alves *et al.* (2008) recorded CP type 8 with an overall prevalence of 83.1% in ovine and caprine isolates.

Clumping factor A (*clfA*) is a cell surface bound protein in *S. aureus* which is thought to be essential for colonization and establishment of infections. It is known to participate in the infection process by facilitating bacterial binding via soluble or immobilized fibrinogen (Karahan *et al.*, 2011) and has also been suggested as a potential vaccine candidate. Said *et al.* (2010) also suggested *clfA* typing useful for revealing the clonal nature of mastitis isolate lineage. Risley *et al.* (2007) in a study found that capsular polysaccharide masks *clfA* mediated adherence of *S. aureus* to fibrinogen and platelets and suggested that these findings have important implications in vaccine development.

In the present investigation 25 isolates each produced single amplicon whereas two isolates (Moroni *et al.*, 2005; Aires-de-Sousa *et al.*, 2007) did not produce any PCR amplicon. The observation is in accordance to the finding of Salasia *et al.* (2004), Karahan *et al.* (2011) and

Momtaz *et al.* (2010) who suggested that clumping factor is present in majority of the isolates. The size of the amplicon product obtained in the present study was 1050 bp which is in complete agreement to report of Kalorey *et al.* (2007) who characterized 37 strains of *S. aureus* of bovine milk origin for *clfA* gene and obtained an amplicon of approximately 1042 base pairs in all the isolates. Moroni *et al.* (2005) characterized *S. aureus* isolated from milk from chronically infected Alpine dairy goats and obtained an amplicon of 1030 bp in all 28 isolates by amplification of *clfA* gene. Similarly, Akineden *et al.* (2001) investigated 103 *S. aureus* isolates from milk of mastitic cows for *clfA* gene and obtained a single amplicon with a size of approximately 1000 bp. Salasia *et al.* (2004) also carried out amplification of *clfA* gene and found a single amplicon with a size of approximately 1000 base pairs.

We did not observe any polymorphism in *clfA* gene which is in accordance with the observations of some other workers from various locations viz. Akineden *et al.* (2001) from Germany; Stephan *et al.* (2001) from North-east Switzerland; Salasia *et al.* (2004) from Germany and Momtaz *et al.* (2010) from Iran. Contrarily, polymorphism in *clfA* gene was reported by Fitzgerald *et al.* (2000) who carried out genotyping of 102 Irish and 42 USA *S. aureus* strains of bovine intramammary infection origin and recorded the *clfA* region-R amplicons to vary between 220 and 1180 bp in sizes. Similarly, Reinoso *et al.* (2008) on genotyping of *S. aureus* isolates from different sources for *clfA* revealed an amplicon size of 1000 bp for 40 *S. aureus* whereas four strains from bovine origin and one strain from food origin had an amplicon of 900 bp size. Likewise, Karahan *et al.* (2011) investigated *S. aureus* isolated from sub-clinical bovine mastitis in Turkey and found that 91.3% of the 92 coagulase positive *S. aureus* isolates carried *clfA* gene in which 68 isolates had *clfA* amplicon of 1000 bp and remaining 16 isolates had amplicon of 900 bp, the remaining eight isolates did not possess *clfA* gene.

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