Mastitis associated pathogenic attributes of *S. aureus* and genetic component of cattle and buffaloes investigated shown considerable variations. Strains of *S. aureus* showed diverse characteristics on testing, and the biochemical assays were by and large successful in their identification. However, unusual biochemical patterns were also seen in some of the isolates and identification of atypical isolates was confirmed by molecular identification. It was emphasized that isolates with unusual patterns should be excluded only after molecular identification as misidentification could lead to a decrease in the true number of isolates in the study. Further, the prevalence of considerable proportion of coagulase, bio-film, slime, capsule formation, clumping factor and hemolysins indicated importance in establishment of mastitic infection.

The antibiogram provided the status of resistance in isolates of mastic animal of the herd. Resistance to some of the routine antimicrobials (gentamicin, tetracycline, streptomycin, kanamycin, erythromycin, penicillin-G, ampicillin, etc.) was severely high in isolates of all the breeds. However, commonness of resistance by strains to some of the antibiotics (lincomycin, cephalexin, cefixime, ofloxacin, etc.) those are not frequent in use was also seen and indicated probability of dissemination of these isolates in animals from milk-man/farmer/herd worker. Detection of multiple antibiotic-resistances MRSA in mastitic cattle and buffaloes represents a risk to public health. Further, molecular detection of antibiotic-resistant determinants revealed higher proportion of *MsrA*, *MsrB*, *LinA*, *TetK* and *Aac*A-D genes in the obtained isolates and remained higher in clinical isolates. Hence, culling of animals infected with strains consisting high number of such genes should be preferred to reduce the dissemination antibiotic-resistance determinants. Further, the generated information also revealed variation in phenotypic and genotypic antibiotic-resistance assays. Therefore, observations emphasized that prevention and control of mastitis caused by antibiotic-resistant *S. aureus* should be preferred based on detection of phenotypic and genotypic tests, instead of broadening the selection of antimicrobials for treatment.

Apart to antibiotic-resistance, strains of *S. aureus* revealed virulence factors and had large variations (*Coa*, *Clf*A and *Ig*-binding) in the expression of these genes and were more prevalent in clinical as compared to subclinical isolates. The longer
Conclusions

fragments of ClfA and Ig-binding genes were prevalent in the isolates. Inferences were drawn that the longer fragment could be helpful to establish the mastitis. The presence of coagulase gene patterns in the clinical as well as in a few subclinical isolates advocates the probable transfer of infection or spread of pathogens amongst animals.

Higher prevalence of Hla, Enol, FnbA, Nuc, Ehp, Fib and Map genes emphasized their importance in virulence of S. aureus in mastitis. These genes might be playing a central role in pathogenesis of bovine IMI; however, their presence cannot predict strain-specific virulence. Genetic determinants of the FnbB were found in less proportion of isolates. However, FnbB gene was more prevalent in clinical isolates. The unusual appearance of Bhp and Cna genes does not seem to influence mastitic infection. The absence of some virulence factors in strains of mastitic cases signifies that causative agent or isolates possibly could be from skin microbiota or opportunistic micro-flora. Additionally, presence of limited toxins in the mastitis pathogenicity stressed that these genes play minor role in the dissemination and pathogenesis of bovine IMI. Hence, it is inferred that typing of these genetic determinants might be useful to generate information on the clonal association and discrimination of pathogenic and non-pathogenic isolates. A considerable variation (3-12R) was observed in X-region of SpA gene of isolates. The prevalence of toxins and pathogenic genes was found significantly higher in isolates consisting of SpA<7R. Similarly, SpA<7R remained higher in clinical isolates. Eventually, it is concluded that SpA genotypes have the potential to distinguish the virulence, clonal association, origin and host specificity, and outbreak of mastitis.

Genetic evaluation of IgG3 gene revealed a considerable variation in mastitic animals. Variation in genotypes observed in Murrah, Karan Fries and Sahiwal indicated their phylogenetic distance and uniqueness in genetic architecture. Genotypes of IgG3 gene in mastitis resistance/susceptible animals associated with determinants of SpA gene of S. aureus strains showed the probability of use of molecular markers in animal breeding evaluation programs.