6. SUMMARY AND CONCLUSION

- A total of 135 isolates of *S. aureus* were recovered from human patients and confirmed on the basis of morphology, Gram’s staining and biochemical tests in our laboratory.
- The isolates were screened for their susceptibility to 20 different antibiotics belonging to 11 different antibiotic groups such as penicillins, glycopeptides, macrolides, β-lactams, quinolones, sulphonamides, tetracycline, linezolid etc.
- A total of 40.3% isolates were multidrug resistant: 32.6% MRSA and 7.7% MSSA. Of these, 40 MRSA and 20 MSSA isolates were characterized based on amplification of selective virulence genes (*coa*, *spa* and *tst*).
- Amplification was achieved in 36 out of 40 MRSA and 18 out of 20 MSSA and two out of 40 MRSA isolates respectively for *coa*, *spa* and *tst* genes.
- Five distinct restriction patterns of *coa* gene amplicons using *Hae*II were observed in MRSA isolates and a single pattern was observed in case of *spa* gene amplicons using *EcoRII*.
- The amplicons of *coa* and *spa* genes of three isolates each of MRSA and MSSA originating from blood, pus and urine were sequenced for their nucleotides.
- The amplicons of *coa* and *spa* genes of these isolates has been assigned accession numbers by the National Centre for Biotechnology Information (NCBI).
- The MRSA isolates exhibited 88% to 99% homology to the standard MRSA strains whereas it was 89% to 96% in case of MSSA isolates in respect of *coa* gene. In case of *spa* gene amplicon the sequence homologies of 92% to 97% in MRSA and 91% to 100% in MSSA were observed.
- Variability was observed amongst the MRSA and MSSA isolates of different origins.
- The substitutions were observed in the predicted amino acid sequences of *coa* gene at positions 22, 72, 87, 88, 100, 107, 109, 134, 149 and 164. In case of *spa* gene the major amino acids substitutions were found at position 114, 115, 116, 117, 118, 119, 120, 121 and 122.
- 20/37 (54.05%) MSSA isolates were typed by bacteriophage typing while 17/37 (45.94%) were found non-typeable.
It may be concluded that multidrug resistant strains are prevalent in the state of Himachal Pradesh. The typing methods used in the study could differentiate and characterize the multidrug resistant MRSA and MSSA strains in hospital setting and in the community. It might prove helpful in the better management of these infections in light of the therapeutic options based on the study in the state of Himachal Pradesh.