Conclusions

Healthcare-associated infections caused by MRSA remain significant threat to humankind into the second decade of 21st century. The present study supports this statement. The significant risk factors for HA-MRSA infections are exposure to antibiotics within last 6 months and prior hospitalization. HA-MRSA mostly causes infection in patients with one or more risk factors. Multidrug resistance is a common problem among HA-MRSA, posing problems in the selection of appropriate antibiotic for treatment. Inducible clindamycin resistance should be detected by performing D-test. This should be done before selecting clindamycin for treatment of infections caused by HA-MRSA strains that appear resistant to erythromycin but susceptible to clindamycin in routine antibiotic susceptibility test. Emergence of VISA (4 cases in this study) in tertiary care hospitals is a cause of concern. Prior hospitalization, prior treatment with antibiotics during previous 6 months and diabetes mellitus are the risk factors for VISA. Antibiotic susceptibility testing by disk diffusion method does not differentiate VISA from VSSA. Proper identification of VISA strains needs determination of MIC by dilution tests or Etest. Since Etest can determine MIC values in intermediate range, it can be used for studying vancomycin MIC creep. MIC values generated by Etest are 0.5 – 1 µg/ml more compared to those generated by agar dilution method. Most (72%) HA-MRSA strains carry SCCmec III, are multidrug resistant and PVL negative. pvl gene is absent in large number of HA-MRSA indicating that these strains are less virulent. Our study documents the emergence of HA-MRSA SCCmec IV/V (24.8%) in tertiary care hospitals in Mangaluru, costal Karnataka.

Further studies using Pulse Field Gel Electrophoresis (PFGE), Multilocus Sequence Typing (MLST) and Staphylococcal Protein A (spa) typing for genotyping HA-MRSA strains will identify the clones and help understanding the molecular epidemiology of healthcare associated infections caused by MRSA. It is quite possible that hVISA could be present among HA-MRSA strains and they should be detected by performing Population Analysis Profile/ Area Under the Curve (PAP/AUC).