7. Conclusion

The advances in genome sequencing, analytical instrumentation, computing power, and user-friendly software tools have irrevocably changed the practice of biology. The results of this study demonstrated that majority of the *S. aureus* strains isolated from Kerala were multidrug resistant. The central resistance determinant mecA gene was sequenced and analysed. Based on sequence alignment with well studied structures of PBP2a, the *mecA* gene sequences obtained in the present study showed >90% sequence identity to the A chain of Penicillin binding protein 2a [PDB ID: 1VQQ_A] with a root mean square deviation of 0.46Å° in the main chain atoms which is not significant enough to implicate a change in the function of the penicillin binding protein PBP2a.

In conclusion, the MRSA infections in Kerala were found to be due to an endemic clone and the isolates were genetically homogenous. Grouping of isolates with a common genetic background will help in understanding the spread of multidrug resistant strains of MRSA and at the same time, it may be predictive of the emergence of even more serious strains such as VRSA. If preventive measures can be taken at the initial stages, spread of VRSA could be controlled. The reluctance of health care workers in accepting the prevalence of MRSA in some hospitals is an important factor that obstructs the prompt institution of preventive measures. Regular surveillance of hospital associated infections, including monitoring of antibiotic sensitivity patterns of MRSA and formulation of definite antibiotic policy may help in reducing incidence of MRSA infection.

In a setting where an MRSA strain is highly endemic, encounters with other patients or healthcare personnel harboring this strain during previous hospitalizations may result in transmission and spread. As this is the first study on molecular subtyping of MRSA in Kerala, the DNA fingerprints obtained will provide a baseline for tracking the spread of this endemic clone. This study will enable epidemiologists to understand the nature of MRSA isolates in this part of India. Moreover, molecular characterization of the genes encoding these resistance determinants would help in developing strategies to prevent rapid emergence and spread of resistant organisms.