2. Background

*S. aureus* is a frequent source of skin infections, which can usually be treated without antibiotics, but it can also cause serious surgical wound infections, bloodstream and bone infections, or pneumonia. The burden of such infections, according to recent studies by Centers for Disease Control and Prevention is close to 2 million nosocomial infections annually resulting in nearly 20,000 deaths and associated costs close to $50 billion. Physicians are particularly concerned about *S. aureus* because of its ability to survive in the presence of antibiotics designed to kill it. In 1972, according to the Centers for Disease Control, only two percent of *S. aureus* infections were drug-resistant. By 2004, 63 percent were resistant to the antibiotics commonly used to treat them [Archer 1998]. As more strains develop resistance to existing drugs, treating the infections is becoming increasingly challenging [Lowy 1998].

Indian literature shows that MRSA incidence was as low as 6.9 per cent in 1988 and reached to 24 and 32.8 per cent in Vellore (Pulimood et al 1996) and Lucknow (Mathur et al 1994) in 1994, respectively and was of the same order in Mumbai, Delhi and Bangalore in 1996 and in Rohtak and Mangalore in 1999 (Verma et al 2000). However, in some of the centres, it was as high as 80 per cent and in India the isolation varied from 20-40 per cent (Geha et al 1994). In Kerala no such studies have been reported so far.

In India the prevalence and spread of MRSA has been recognized late which led to its emergence as a real threat to community and hospital settings. Prevalence of MRSA has widely been reported in several parts of India where MRSA has become a major nosocomial pathogen and few states have even reported the emergence of VISA and VRSA strains. Studies on MRSA have been conducted in almost all the Southern states except Kerala where no such reports are available so far. So we have undertaken this study to determine the antimicrobial susceptibility pattern and the molecular characteristics of MRSA obtained in Kerala. Genotyping of strains isolated in Kerala have not been done till now. The aim of this study was to determine the genetic diversity of methicillin resistant *Staphylococcus aureus* strains isolated in Kerala over a three year period.
In the present study 104 isolates of MRSA were analysed. Phenotypic characterization by antibiogram analysis and phage typing and genotypic characterization based on molecular analysis of resistance genes have been carried out. Molecular typing was carried out using plasmid profiling, staphylococcal cassette chromosome typing, pulse field gel electrophoresis (PFGE) and microsatellite marker studies.

**Objectives**

The aim of the present study is

i. To determine the antimicrobial susceptibility patterns of the isolates and minimum inhibitory concentrations of commonly used antibiotics.

ii. Plasmid profile analysis to determine the position of resistance determinants.

iii. Transformation studies to determine whether the resistance determinant mecDNA could be transformed into susceptible isolates.

iv. Epidemiological typing of the isolates by phage typing.

v. Isolation and amplification of the genes involved in multi drug resistance viz. mecA, femA, femB, blaZ and aac6’-aph2” genes.

vi. Sequence analysis of the central determinant for methicillin resistance, mecA, femA and femB.

vii. Molecular typing of isolates by Staphylococcal Cassette chromosome (SCCmec) typing and Pulsed field gel electrophoresis (PFGE).

viii. Analysis of hypervariable region to study the presence of microsatellite markers to determine the clonal diversity of strains.