3. SCOPE AND PLAN OF THE STUDY

3.1. Methicillin Resistant coagulase-negative staphylococci (MR-CoNS) have emerged as an important causative agent of nosocomial and community acquired infections worldwide especially in hospitalized and immunocompromised patients. Nasal carriage of MR-CoNS among patients and healthy volunteers from hospital and community settings has been recognized as a potential source for infection. End-Stage Renal Disease (ESRD) patients receiving hemodialysis will be in constant flux with both the hospital and community environment and have a significantly higher risk of colonization by invasive staphylococcal population than normal population. Further, there is a paucity of data on the molecular epidemiology and prevalence of MR-CoNS from different populations in our country. Hence, the primary objective of this study was to determine the prevalence of MR-CoNS among hospitalized patients, immunocompromised patients (HIV infected), patients with constant community hospital interaction (ESRD patients undergoing Hemo Dialysis) and carriers from various closed community settings at risk of MR-CoNS infection.

3.2. A great concern related to MR-CoNS is their ability to develop resistance to various antibiotics and serve as a reservoir of antimicrobial resistance to S. aureus, the more infective and virulent species of staphylococci. In general, MR-CoNS are resistant to all the beta-lactam antibiotics and are found to be multidrug resistant. The transmissible resistance to macrolides, fluoroquinolones and aminoglycosides and to reserved antibiotics
such as, mupirocin, fusidic acid, linezolid and glycopeptides are increasing and pose a major threat to the treatment of MR-CoNS infections. There are reports on the significant difference in antibiotic resistance pattern between hospital and community acquired MR-CoNS. Hence, antibiotic susceptibility testing was carried out for the MR-CoNS isolates from hospital and community settings to detect their antibiotic resistance profile followed by PCR to characterize the drug-resistance determinants among MR-CoNS from hospital and community settings.

3.3. Staphylococcal cassette chromosome mec (SCCmec) typing has proved to be an important tool to study the molecular epidemiology of MR-CoNS particularly MRSE. MR-CoNS are opportunistic pathogens and serve as a large reservoir of SCCmec and have shown to be transferable among staphylococcal species. Recent studies highlighting the community spread of MR-CoNS have raised concerns, because of the probable role of MR-CoNS as a source of SCCmec for Community Acquired-MRSA. Characterization of SCCmec in MR-CoNS from patients and healthy volunteers from different settings might generate useful information on the mobilization and evolution of this element. Hence in this study, SCCmec typing was carried out for the assessment of the molecular epidemiology of MR-CoNS isolates from hospital and community settings.

3.4. The most frequently encountered CoNS species associated with human infections is Staphylococcus epidermidis, which poses an array of virulence factors including icaAD, aap, atlE, MSCRAMMs and IS256 that promote their colonization, invasion and pathogenesis. Biofilm forming strains of Methicillin-Resistant S. epidermidis (MRSE) have become a very serious clinical problem. Further, many of the above-mentioned
resistant genes are not reported from other species of CoNS. Moreover, there is a paucity of data on the virulence factors of MRSE in Indian settings. **In the present study, phenotypic and genotypic detection of virulence determinants were carried out to compare their prevalence among MRSE isolates from hospital and community settings.**

3.5. Besides SCCmec, other mobile elements have been described in staphylococci that transport important survival or virulence genes, such as arginine catabolic mobile element (ACME), a novel genomic island that may contribute to the enhanced capacity of this species to colonize the human skin and mucosal surfaces. However, presently, there is no data regarding the distribution of the ACME gene among MRSE strains in India. **Hence, the present study was designed to study the prevalence of Arginine catabolic mobile element (ACME) among MRSE isolated from hospital and community settings.**

3.6. MLST - a sequence based method involving seven housekeeping genes is a robust, highly discriminatory, molecular epidemiological tool for understanding the molecular basics of the pathogen. It is a long term evolutionary analysis and has provided additional insights into the population structure of MRSE isolates from hospital and community settings. There are no published reports from India on MLST analysis of MRSE so far. Hence, **MLST analysis was carried out for representative MRSE isolates and grouped as MLST clonal complexes in order to find the major clonal complexes circulating in our geographic location.**