1. Introduction

*Staphylococcus aureus* is a major pathogen causing different kinds of infections both in healthcare and community settings (1). *S.aureus* accounted for over 10% of healthcare – associated infections in the United States in 2014 (2). Infection caused by *S.aureus* varies from superficial pyogenic lesion (folliculitis, furuncle, abscess) and deep infections (bacteremia, septicemia, osteomyelitis, endocarditis) (1). The success of *S.aureus* as a versatile pathogen depends on rapid multiplication, ability to survive in different environments, transmission through contact, ability to emerge resistant to antimicrobial agents and production of several virulence factors (adherence factors, capsule, toxins and enzymes). *S.aureus* can also receive genes from other bacteria such as enterococci (1). Patients and carriers are important source of infection for hospitalized patients. Endogenous infection also occurs (1).

Antimicrobial resistance was not a problem with *S.aureus* before 1960 (3). First methicillin resistant *S.aureus* (MRSA) emerged in England in 1961, just one year after the introduction of methicillin for clinical use (3). Since then MRSA has been recognized as a major cause of healthcare – associated infections these are known as healthcare – associated MRSA (HA-MRSA). In 1980s MRSA infections were noticed in young persons in the community without prior exposure to hospitals. This MRSA is known as community - associated MRSA or community – acquired MRSA (CA-MRSA) (2).

Methicillin resistance in *S.aureus* is due to the production of altered penicillin binding protein PBP2a, encoded by *mecA* gene located in mobile genetic element, Staphylococcal Cassette Chromosome *mec* (SCCmec) (4). PBP2a no more acts as receptor for penicillin and methicillin and the bacterium becomes resistant to these antibiotics.

One or more of several molecular techniques are available for genotyping of MRSA. The important ones are pulse field gel electrophoresis (PFGE), multilocus sequence typing (MLST), staphylococcal protein A (spa) typing and SCCmec typing (5,6). Different studies have used different kinds of molecular typing methods and comparison of these results are quite difficult.
HA-MRSA normally belongs to SCC\textit{mec} type I/II/III, demonstrates resistance to multiple antimicrobial agents and is normally Panton Valentine Leukocidin (PVL) negative. CA-MRSA normally belongs to SCC\textit{mec} type IV/V, is more susceptible to antimicrobial agents other than β lactam agents and is PVL positive (2). However, recent studies have shown that properties of HA-MRSA and CA-MRSA overlap (7-9). Literature on molecular epidemiology of HA-MRSA in India is scarce. Multilocus sequence typing (MLST), pulse field gel electrophoresis (PFGE) and staphylococcal protein A (spa) typing are useful in studying molecular features and epidemiology of MRSA (5,6).

Resistance to multiple antimicrobial agents is common among HA-MRSA. Vancomycin is the antimicrobial agent of choice for treatment of serious infections caused by MRSA. In addition to this, there have been several reports on reduced susceptibility and resistance to vancomycin (10,11). First strain of MRSA with reduced vancomycin susceptibility was isolated in Japan in 1997 (12). This strain had moderately increased minimum inhibitory concentration (MIC 3 – 8µg/ml) of vancomycin. This is known as Vancomycin Intermediate \textit{S.aureus} (VISA). Some strains of MRSA have heterogeneous population, containing vancomycin resistant subpopulation in the frequency of 1 X 10\textsuperscript{6} (13). These strains are known as heterogeneous VISA (hVISA).

Infections caused by VISA and hVISA are associated with treatment failure, prolonged duration of treatment, hospitalization, increased morbidity and mortality (14). Considering these, Clinical and Laboratory Standards Institute (CLSI) lowered the vancomycin MIC breakpoints from ≤ 4 µg/ml to ≤ 2 µg/ml for vancomycin sensitive and from ≥ 32 µg/ml to ≥ 16 µg/ml for vancomycin resistance in 2006 (15). Mutation appears to be the mechanism behind VISA (16). First vancomycin resistant \textit{S.aureus} (VRSA) appeared in the USA in 2002 (17). VRSA carries transposon Tn1546 that codes for \textit{vanA} gene (16,17). If the infection is caused by VISA, hVISA or VRSA vancomycin cannot be used for treatment, posing problems in selection of antimicrobial agents.
HA-MRSA has the ability to cause several kinds of superficial and deep infections. Predisposing factors play a significant role in pathogenesis of deep infection. The understanding of role played by virulence factors such as biofilm, enterotoxin B and PVL in the pathogenesis of these infections needs further study. Antimicrobial resistance in HA-MRSA varies in different hospitals and countries. Knowledge regarding antimicrobial resistance pattern will help in selection of appropriate antimicrobial agent for early effective treatment. Genotypic studies are needed to understand the molecular epidemiology of infections and relationship between HA-MRSA strains prevalent in different countries.