1.0 INTRODUCTION

*Staphylococcus aureus* is essentially a human pathogen causing superficial skin and soft tissue infections to deep systemic infections leading to illness. *S. aureus* is a nosocomial pathogen causing serious infections such as bacteremia, meningities, endocardities, pneumonia and sepsis. Penicillin and other beta-lactum group of antibiotics were the treatment for *S. aureus* infections (Lowy, 1988).

With the introduction of penicillin in 1940, *S. aureus* strains resistant to this antibiotic developed. To combat these developing antibiotic resistant strains, semi-synthetic penicillins such as methicillin, dicloxacillin, nafcillin and oxacillin were introduced in the 1960s into clinical use (Chambers, 1997, 1988).

Methicillin-resistant *Staphylococcus aureus* (MRSA) is a resistant variation of the *S. aureus*. It has evolved to an ability to survive treatment with beta-lactum antibiotics and other classes of antimicrobials giving it the name ‘superbug’ (Barber 1961; Jevons 1961). Vancomycin, a glycopeptide antibiotic, is the treatment of choice for serious MRSA infections.

MRSA is a worldwide concern because of their increasing frequency in health-care settings leading to morbidity and mortality. Risk factors for infections with health-care associated MRSA include hospitalization, residence in long-term facility, infancy, older age, implanted devices, peripheral and central lines, and catheters, feeding tubes and exposure to antimicrobial agents (Chambers, 1997, 1998).

MRSA is the most commonly identified antibiotic-resistant pathogens in many parts of the world, including Europe, the Americas, North Africa, the Middle East, and East Asia. In recent decades, MRSA rates have been increasing worldwide, including in the Nordic
countries and the Netherlands, where MRSA rates have been low and stable for many years (Fridkin, 2002; Tiemersma et al., 2004; Turnidge and Bell, 2000).

There has been a steady increase in the prevalence of MRSA in hospitals in the United States over the years such that now approximately 25 per cent of nosocomial isolates of *S. aureus* are methicillin resistant (Shopsin and Kreiswirth, 2001).

In India also there have been reports of increasing rates of MRSA. 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 and Lucknow in 1994, respectively and was of the same order in Mumbai, Delhi and Bangalore in 1996 and in Rohtak and Mangalore in 1999 (Mathur et al., 1994; Pulimood et al., 1996; 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).

Therefore, to reduce these rates it is important to accurately identify the organism from clinical specimens and decide in time on isolations procedures and antimicrobial treatment. Moreover, early diagnosis of MRSA prevents their cross-transmission in the wards, decreases morbidity, helps to determine appropriate antimicrobial therapy, shortens patient’s hospital stay and lowers hospital costs (Bootsma et al., 2006; Diekema et al., 2004).

The epidemiology of MRSA is changing constantly. Two new stages of MRSA evolution have occurred during recent years; emergence of MRSA strains with reduced susceptibility or with resistance to glycopeptides antibiotics (GISA or GRSA strains, respectively) and community-acquisition of MRSA by persons without known risk factors (CDC 1998, 2002). Community-associated methicillin-resistant *Staphylococcus aureus* (CA-MRSA) cause infections such as boils, abscess, carbuncle, folliculities, impetigo etc (Lowy 1998). CA-MRSA infections affect young healthy sports persons (Herold et al., 1998; Chambers, 2001; Naimi et al., 2003), who share towels and athletic equipments; intravenous
Pulsed-field gel electrophoresis (PFGE) demonstrated that MRSA strains causing community-associated infections were different than those causing hospital or healthcare-associated infections (McDougal et al., 2003) in that they carry the gene that encodes the Panton-valentine leukocidin (PVL), a bicomponent \((lukF-PV\) and \(lukS-PV\)) pore-forming leukotoxin. (Vandenesch et al., 2003; Baba et al., 2002; Miller et al., 2005; Moran et al., 2006) Currently, there is a controversy in the role of PVL in the pathogenesis of infections caused by these CA-MRSA strains. Epidemiologic studies and a study by Labandeira-Rey et al., 2007, suggest that PVL is associated with virulence and causes the necrosis characteristic of infections with these strains (Labandeira-Rey et al., 2007). On the other hand, a study by Voyich et al., 2006, found no difference in virulence between the wild-type parent strains and the isogenic knockout strains that did not produce PVL (Voyich et al., 2006). In addition, a study in United States revealed that MRSA strains, USA300 and USA400, causing community-associated infections typically have the staphylococcal cassette chromosome (SCC) mec type IV, not the SCCmec type II carried by most USA100 and USA200 which cause hospital associated infections (Soderquist et al., 2006).

CA-MRSA are generally known to cause Skin and Soft tissue infections (SSTIs) (Niami et al., 2003; Moran et al., 2006; Fridkin et al., 2005) especially in patients with no established health-care risk factors (Campbell et al., 2002; Herold et al., 1998) and HA-MRSA are involved with serious invasive diseases in health-care facilities (Seyold et al., 2006; Francis et al., 2005). But recent reports based on genotype evidence have suggested that there is an in-flow of community strains into health-care settings causing serious hospital or health-care associated infections (e.g., bacteraemia, pneumonia) thereby blurring the line between CA-MRSA and HA-MRSA (Popovich et al., 2008).
CA-MRSA have become a major problem in US hospitals already dealing with high levels of hospital-associated MRSA (HA-MRSA). Although the prevalence of HA-MRSA has been described in some Indian hospitals, the prevalence of CA-MRSA in India is not well known. Few studies have been carried out in the community in rural areas (Alvarez-Uria and Reddy, 2012) but data on the prevalence of CA-MRSA in health-care settings is still unknown. Early detection of HA-MRSA and CA-MRSA from clinical isolates is imperative to determine the appropriate antimicrobial therapy (Bootsma et al., 2006; Diekema et al., 2004).

Rapid methods for the identification of MRSA from clinical specimens are a current need as the conventional methods of their detection take around 48 to 96hrs (Strulens and Denis, 2006). Further, conventional methods for identification of MRSA, such as disc susceptibility tests take more time and are influenced by environmental conditions like temperature, pH, salt concentration and incubation. Additionally, phenotypic expression of methicillin resistance is known to be heterogeneous leading to borderline MICs which are difficult to identify by conventional tests (Chambers, 1988, 1997).

Molecular methods like PCR are rapid and highly sensitive but not cost-effective and also technically demanding. Not all clinical laboratories can afford this technique for routine diagnosis. These factors emphasize the need to develop a rapid, standardized, accurate, highly sensitive and cost-effective method for detection of methicillin resistance in Staphylococci which is not dependent on growth conditions and can be used in routine diagnostic laboratory.

The Center for Disease Control (CDC) has established various surveillance systems for MRSA in health-care settings and community to control the infection. In India, few studies have been undertaken to determine the epidemiology of HA-MRSA and CA-MRSA.
in health-care settings and community. A network of microbiology laboratories (Indian Network for Surveillance of Antimicrobial Resistance - INSAR) at premier medical colleges and hospitals in India was formed with support from the World Health Organization. The network aims to monitor antimicrobial resistance and to review the magnitude of its problem in India. Initially, a few organisms of public health importance have been chosen for monitoring their prevalence and antimicrobial resistance patterns, with *S. aureus* being chosen among the Gram-positive organisms.

All participating laboratories shared their antimicrobial susceptibility data and provided technical support to other members. The present study provides an initiative to understand emerging trends of antimicrobial resistance among clinical isolates of *S. aureus* and provides a platform to initiate epidemiological studies for staphylococcal infections in our set up.