Abstract

**Background:** Community-acquired methicillin resistant *Staphylococcus aureus* (CA-MRSA) is an emerging pathogen, responsible for infections of varying severity. The molecular properties, antibiotic susceptibility pattern and clinical profile of these infections vary in different regions.

**Objectives:** The present study was aimed at studying the bacteriological, clinical and molecular properties of CA-MRSA.

**Methods:** The present cross sectional study was conducted on 553 cases of community-acquired infection. The community-acquired infection was defined by CDC guidelines. Clinical specimens and specimens from anterior nares were processed by standard methods and MRSA was identified by cefoxitin disc diffusion method and detection of *meca* gene by PCR. Antibiotic susceptibility testing was performed by Kirby-Bauer disk diffusion method based on CLSI guidelines. D-test was used to detect MLS_B phenotypes. MIC of vancomycin was determined by agar dilution method. Multiplex PCR was used for the detection of *meca* and *pvl* genes and SCCmec typing.

**Results:** The prevalence of MRSA was 21.5% (119/553) among community-acquired infections. The mean age of individuals with CA-MRSA infection was 34.75 ± 2.23. Rate of CA-MRSA infection was significantly more among individuals belonging to the age group 1-20 (43/119, 36.1%). Pyoderma (91.5%) was more common compared to invasive infection. Among pyoderma, primary pyoderma was significantly high (76/109, 63.9%). Antibiotic susceptibility pattern showed that all CA-MRSA were sensitive to linezolid, teicoplanin and vancomycin. Resistance was high to ciprofloxacin (50/119, 42%) compared to other non-β-lactam agents. Resistance to erythromycin and clindamycin in disk diffusion test was seen in 4/119 (3.3%) CA-MRSA indicating cMLS_B phenotypes Results of D-test showed 23/119 (19.3%) iMLS_B and 1/119 (0.8%) were MS_B phenotypes. Non-β-lactam multidrug resistance was seen in 13.5% CA-MRSA. All CA-MRSA were positive for *meca* gene. SCCmec V was seen 84% (100/119), SCCmec
IVa – 2/119 (1.7%), SCCmec IVd – 1/119 (0.8%) and 16/119 (13.4%) nontypable among CA-MRSA.

Conclusion: The results of the present cross-sectional study show that MRSA is a significant pathogen in community acquired infections. The present study demonstrated that CA-MRSA mostly causes SSTI in persons ages < 20 years. Less commonly it caused invasive infections such as bacteremia. More number of CA-MRSA were resistant ciprofloxacin compared to other non-β-lactam antibiotics. Inducible clindamycin resistance is a problem, therefore we recommend D-test before selecting clindamycin for the treatment of CA-MRSA infections. All CA-MRSA were susceptible to linezolid, teicoplanin and vancomycin. SCCmec V was the commonest SCCmec type among CA-MRSA isolates. pvl gene was present in 55.5% of CA-MRSA. pvl was significantly associated with the strains that caused primary pyoderma.

The present study had some limitations. The CDC epidemiological definition was used to identify CA-MRSA. Sixteen CA-MRSA isolates from the clinical specimens and 9 isolates from nasal swabs were nontypable with the primers used in the present study. This could mean that, they belong to some other SCCmec type which needs to be identified by including other primers in PCR. We used only SCCmec typing for the molecular typing of CA-MRSA. Molecular typing methods such as MLST, spa typing and/or PFGE are needed to understand the molecular epidemiology of CA-MRSA and their origin.