Summary
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The present cross-sectional study was carried out to understand the bacteriological, clinical and molecular properties of CA-MRSA isolated from different community-acquired infections and nasal colonization.

The present study included 553 patients based on the CDC epidemiological definition of community-acquired infection. The clinical specimens and nasal swabs were processed using standard methods. MRSA was isolated and identified by colony morphology, grams stain, catalase test, coagulase test, cefoxitin (30 µg) disk diffusion test and meCA gene detection by PCR. Antibiotic susceptibility testing was done by Kirby-Bauer disk diffusion method, MIC of vancomycin was determined by agar dilution method and inducible clindamycin resistance was detected by D-test. pvl gene detection and SCCmec typing was done by multiplex PCR.

Among the 553 patients, S.aureus was isolated from 442 patients. Out of these 442 S.aureus strains, 119 were MRSA. Therefore, the prevalence of MRSA was 21.5% (119/553) among community-acquired infections and the proportion of CA-MRSA among CA-S.aureus was 26.9% (119/442). Patients belonging to the age group 1-20 years were affected more compared to other age groups and this difference was statistically significant. The Male: Female ratio was 1.6. Mean family size of patients infected with CA-MRSA was 5.05 ± 2.20 with an average median family income of 4000 (1500 - 20000). CA-MRSA infections were significantly more among people living below poverty line.

Among the infections caused by CA-MRSA, pyoderma (109 cases) was most common (P<0.05). Primary pyoderma was
significantly more compared to secondary pyoderma ($P<0.05$). Abscess was more common compared to other kinds of pyoderma. Out of 119 patients who had CA-MRSA infections, 27 (22.7%) did not have risk factors. Among those who had risk factors, diabetes mellitus was most common, followed by nasal colonization and elderly individuals aged ≥ 65 years.

The antibiotic resistance pattern showed that all the isolates were susceptible to teicoplanin and linezolid. Among the non-β-lactam antibiotics, maximum resistance was observed to ciprofloxacin, followed by trimethoprim-sulphamethoxazole, gentamicin, erythromycin, tetracycline, clindamycin and rifampicin. MDR to non β-lactam antibiotics (Resistance to 3 or more antibiotics) was detected in 13.5% CA-MRSA of which 7.6% were resistant to 3 antibiotics, 2.5% were resistant to 4 antibiotics and 3.4% were resistant to 5 antibiotics.

Out of 119 CA-MRSA isolated from clinical specimens, 28 were resistant to erythromycin. Among these 28 strains, 4 (3.3%) were resistant to clindamycin also, indicating cMLS$_B$ phenotype. Among the remaining, 24 (20.2%) strains which were resistant to erythromycin but susceptible to clindamycin, 23 (19.3%) were D-test positive, indicating iMLS$_B$ phenotype whereas one strain (0.8%) which was D-test negative was considered MS$_B$ phenotype. All the isolates were susceptible to vancomycin (MIC ≤ 2 µg/ml). Out of 119 isolates, 81 (68.1%) had MIC of 0.5 µg/ml and 38 (31.9%) had MIC of 1µg/ml. MIC$_{90}$ of vancomycin was 1µg/ml and MIC$_{50}$ 0.5µg/ml.

Molecular characterization of CA-MRSA showed that all 119 isolates (100%) were positive for mecA gene. The results of SCCmec showed that 84.1% (100/119) CA-MRSA were SCCmec V, 1.7% was SCCmec IVa and 0.8% was SCCmec IVd. Out of 119 isolates, 16
(13.4%) were nontypable with the primers used in the present study. Among 119 CA-MRSA, 66 (55.5%) carried *pvl* gene.

Correlation of bacteriological and clinical and molecular properties of CA-MRSA showed the following results – Ciprofloxacin resistance was significantly more with isolates from primary pyoderma. *pvl* gene was associated with SSTI. CA-MRSA with SCC*mec* type V was high among primary pyoderma. SCC*mec* V was associated with resistance to ciprofloxacin, erythromycin, gentamicin and trimethoprim-sulphamethoxazole (*P*<0.05). The *pvl* gene was associated with SCC*mec* V.

*S. aureus* was isolated from the swabs collected from anterior nares of 25.7% (142/553) of the total patients. Nasal carriage of CA-MRSA was seen in 5.6% (31/553) of the total patients and 21.8% (31/142) of the patients with *S. aureus* infection. Both CA-MRSA infection and carriage was seen in 17 patients accounting for 3.1% (17/553) of the total patients and 14.3% (17/119) of CA-MRSA infected patients. Majority of the patients with nasal colonization of CA-MRSA belonged to the age group of 41-50 years. The Male: Female ratio was 2.4.

Antibiotic resistance pattern of CA-MRSA isolated from nasal swabs showed higher degree of resistance compared to CA-MRSA isolated from clinical specimens especially for non-β-lactam antibiotics like co-trimoxazole, erythromycin and tetracycline. D-test showed that iMLS*B* phenotype was the predominant phenotype followed by cMLS*B* phenotypes and MS*B* phenotypes. MDR to non β-lactam antibiotics was seen in 29.1% CA-MRSA. Out of 31 nasal isolates of CA-MRSA, 6 (19.4%) were positive for *pvl* gene. SCC*mec* typing showed that 17/31 (54.8%) nasal isolates were SCC*mec* V, 5/31 (16.1%) were SCC*mec* IV and 9/31 (29%) were nontypable.