Section: Microbiology

Original Research Article

RESISTANCE AND VIRULENCE IN CA-MRSA: CLINICAL AND MICROBIOLOGICAL SPECTRUM OF COMMUNITY-ACQUIRED SSTIs

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Received *: 10/01/2026*
Received in revised form *: 02/03/2026*
Accepted *: 19/03/2026*

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DOI: 10.70034/ijmedph.2026.2.18

Source of Support: Nil,
Conflict of Interest: None declared

Int J Med Pub Health
2026; 16 (2); 97-101

ABSTRACT

Background: Skin and soft tissue infections (SSTIs) are a major clinical burden, with community-acquired methicillin-resistant Staphylococcus aureus (CA-MRSA) increasingly implicated. These strains often combine resistance determinants with virulence factors such as Panton-Valentine leukocidin (PVL), complicating management. The aim is to investigate the clinical profile, microbiological spectrum, genotypic characteristics, and antibiotic resistance patterns of CA-SSTIs, with emphasis on CA-MRSA.

Materials and Methods: A prospective cross-sectional study was conducted on 350 clinically diagnosed CA-SSTI cases over two years. Samples were processed for culture, phenotypic identification, antibiotic susceptibility testing, and PCR-based genotypic analysis.

Results: The mean patient age was 37.9 years, with a slight male predominance (56%). Abscesses (46%) and cellulitis (34%) were the most common presentations. Culture positivity was 61%, with S. aureus as the predominant isolate (43%). MRSA accounted for 16% of cases. Genotypic analysis revealed mecA positivity in 86% and PVL gene presence in 79% of MRSA isolates. Antibiogram showed high resistance to ciprofloxacin (59%), gentamicin (59%), and erythromycin (53%), moderate resistance to clindamycin (33%) and tetracycline (34%), while all isolates remained sensitive to linezolid and vancomycin.

Conclusion: CA-MRSA strains in this cohort demonstrated both multidrug resistance and high PVL prevalence, underscoring their dual threat of resistance and virulence. Linezolid and vancomycin remain reliable therapeutic options, while clindamycin may retain partial utility. Continuous molecular surveillance and antibiotic stewardship are essential to guide rational therapy and curb the spread of resistant, virulent clones.

Keywords: Community-acquired SSTIs, MRSA.

INTRODUCTION

Skin and soft tissue infections (SSTIs) represent a significant burden in both outpatient and inpatient settings, ranging from mild superficial infections to severe necrotizing fasciitis. Globally, Staphylococcus aureus has emerged as the predominant pathogen, with methicillin-resistant Staphylococcus aureus (MRSA) increasingly implicated in community-acquired infections over the past two decades.[1] The epidemiological shift from hospital-associated MRSA (HA-MRSA) to community-acquired MRSA (CA-MRSA) has altered the clinical landscape, as CA-MRSA strains often harbor virulence determinants such as the Panton-Valentine leukocidin (PVL) gene, contributing to abscess formation, tissue necrosis, and recurrent infections.[2] The prevalence of CA-MRSA varies geographically, but reports consistently highlight its role in abscesses, cellulitis,

and other purulent SSTIs.[3] Molecular studies have demonstrated that the mecA gene confers methicillin resistance, while PVL-positive strains are associated with aggressive clinical presentations and higher rates of complications.[4] These dual attributes of resistance and virulence pose challenges in clinical management, particularly in resource-limited settings where empirical therapy often relies on older antibiotics. Antibiotic resistance trends further complicate treatment strategies. Increasing resistance to fluoroquinolones, aminoglycosides, and macrolides has been documented, while agents such as linezolid and vancomycin remain reliable but are costly and require careful stewardship.[5] The emergence of clindamycin resistance in certain regions underscores the need for continuous surveillance of local antibiograms to guide therapy.[6] Given this background, the present study was undertaken to investigate the clinical profile, microbiological spectrum, genotypic characteristics, and antibiotic resistance patterns of CA-SSTIs, with a special focus on CA-MRSA. By analyzing demographic distribution, types of SSTIs, culture positivity, genotypic markers, and antibiogram profiles, this study aims to provide evidence for rational antibiotic use and highlight the importance of molecular surveillance in community settings

Aim & objectives

Aim: To investigate the clinical profile, microbiological spectrum, genotypic characteristics, and antibiotic resistance patterns of community-acquired skin and soft tissue infections (CA-SSTIs), with a special focus on methicillin-resistant Staphylococcus aureus (CA-MRSA).

Objectives

1. To study the demographic distribution (age, gender) of patients with CA-SSTIs.
2. To categorize the types of SSTIs (abscess, cellulitis, furuncle, necrotizing fasciitis, impetigo, carbuncle, folliculitis).
3. To determine culture positivity rates, identify predominant pathogens& to detect genotyping status of CA-MRSA using PCR.
4. To evaluate resistance and sensitivity profiles of CA-MRSA isolates against commonly used antibiotics.

MATERIALS AND METHODS

Study Design and Setting: This was a cross-sectional prospective study conducted in the Department of Microbiology at a tertiary care hospital over a period of two years (December 2016 – November 2018). Approval was obtained from the Institutional Ethics Committee, and written informed consent was taken from all participants prior to enrollment.

Study Population: A total of 350 clinically diagnosed cases of community-acquired skin and soft tissue infections (CA-SSTIs) were included, based on predefined inclusion and exclusion criteria.

Inclusion criteria:

1. Patients attending OPD with SSTIs.
2. Patients presenting with SSTIs within 48 hours of hospital admission.

Exclusion criteria:

1. SSTIs developing after 48 hours of admission.
2. Previous hospitalization within 1 year.
3. Patients on dialysis.
4. Patients with indwelling catheters.

Sample Collection and Transportation

A. Types of samples: Pus aspirates or pus swabs (two swabs when aspirate was not possible).
B. Timing: Samples were collected aseptically, preferably before initiation of antibiotics. If patients were already on antibiotics, samples were collected just prior to the next dose.
C. Transport: Well-labelled samples were immediately transported in sterile containers to the microbiology laboratory.

Laboratory Processing

1. **Direct Microscopy:** Gram staining (Jensen's modification) was performed to detect pus cells and organisms.
2. **Culture:** Specimens were inoculated on Blood agar and MacConkey agar. Plates were incubated aerobically at 37°C for 18–24 hours. Colonies were identified based on morphology, pigmentation, hemolysis, and biochemical reactions.
3. **Phenotypic Identification of Staphylococcus aureus:**
   a. Biochemical tests: Catalase, oxidative-fermentative test, coagulase (slide and tube), mannitol fermentation, phenolphthalein phosphatase, and heat-stable nuclease tests.
   b. MRSA detection: Cefoxitin (30 µg) disc diffusion method (CLSI 2018). Zone of inhibition ≤ 21 mm was considered MRSA.
   c. Control strains: ATCC S. aureus (25923, negative control) and ATCC MRSA (43300, positive control).
4. **Antibiotic Susceptibility Testing (AST):** Performed by modified Kirby-Bauer method on Mueller-Hinton agar as per CLSI 2018 guidelines. Inoculum prepared to 0.5 McFarland turbidity. Antibiotic discs used: Ciprofloxacin (5 µg), Gentamicin (10 µg), Clindamycin (2 µg), Erythromycin (15 µg), Linezolid (30 µg), Vancomycin (30 µg), Tetracycline (30 µg). Zone diameters were measured and interpreted as sensitive or resistant.
5. **Genotypic Study:** All CA-MRSA isolates were subjected to PCR analysis using multiplex MRSA detection kit (HiMedia). Target genes: Staphylococcus aureus (16S rRNA), Fem-A, Mec-A (methicillin resistance), and luk-PVL (virulence). PCR products were analyzed by agarose gel electrophoresis.

Statistical Analysis: Data were analyzed using SPSS version 20. Results were expressed as mean ± SD, frequencies, and percentages (N, %). Appropriate statistical test were applied to evaluate significance.

A p-value < 0.05 was considered statistically significant.

RESULTS

Table 1: ?

Sr No	Variables	Number of cases n	Percentage %
1	Age (Years) Mean ± SD	 37.88±16.00	 -
2	Gender n (%) a. Male b. Female	 194 156	 56 % 44 %
3	Diagnosis of skin and soft tissue infections (SSTI) a. Abscess b. Cellulitis c. Furuncle/boil d. Necrotizing fasciitis e. Impetigo f. Carbuncle g. Folliculitis	 159 117 26 22 11 8 7	 46 % 34 % 7 % 6 % 3 % 2 % 2 %

The study enrolled 350 participants with a mean age of 37.88 ± 16 years, indicating that SSTIs affected a wide age range, predominantly young to middle-aged adults. Males constituted 56% (194 cases), while females accounted for 44% (156 cases), showing a slight male predominance.

Table 2: ?

Sr No	Culture status	Number of cases n	Percentage %
1	Culture positivity	214	61 %
	a. Staphylococcus aureus	151	43 %
	1. MRSA	58	16 %
	2. MSSA	53	15 %
	3. CONS (MS)	23	7 %
	4. CONS(MR)	17	4 %
	b. Other organism	63	18 %
2	No growth	136	39 %
Total N (%)		350	100

Out of 350 cases, 214 (61%) showed culture positivity, while 136 (39%) had no growth. Staphylococcus aureus was the predominant isolate (151 cases, 43%). Among these, MRSA accounted for 58 cases (16%), while MSSA was 53 cases (15%). Coagulase-negative staphylococci (CONS) were also detected, with methicillin-sensitive (7%) and methicillin-resistant (4%) strains. Other organisms contributed to 18% of positive cultures, reflecting polymicrobial involvement in some SSTIs.

Table 3: Methicillin-Resistant Staphylococcus aureus Genotype status

Sr No	Genotype status	Number of cases 58	Percentage %
1	Staphylococcus aureus identification		
	a. 16S rRNA gene positivity	53	91 %
	b. Fem-A gene. Positivity	53	91 %
	c. Non-specific Amplification	5	8 %
2	Methicillin-Resistance detection		
	a. Mec-A gene	50	86 %
	b. Luk-PVL gene	46	79

Molecular testing confirmed 16S rRNA and Fem-A gene positivity in 91% of isolates, validating Staphylococcus aureus identification. Mec-A gene, the hallmark of methicillin resistance, was detected in 86% of MRSA isolates. Luk-PVL gene, associated with virulence and tissue necrosis, was present in 79%, suggesting that a majority of CA-MRSA strains carried potent virulence factors.

Table 4: Antibiogram of CA-MRSA

Sr No	Antibiotics	Sensitive n (%)	Resistant n (%)
1	Ciprofloxacin (CIPRO)	24 (41.37%)	34 (58.62%)
2	Gentamicin (G)	24 (41.37%)	34 (58.62%)
3	Clindamycin (CD)	39 (67.24%)	19 (32.75%)
4	Erythromycin (E)	27 (46.55%)	31 (53.44%)
5	Linezolid (LZ)	58 (100%)	0 (0%)
6	Vancomycin (VA)	58 (100%)	0 (0%)
7	Tetracycline (TE)	38 (65.51%)	20 (34.48%)

The antibiogram revealed significant resistance trends. High resistance was noted tociprofloxacin (59%), gentamicin (59%), and erythromycin (53%). Moderate resistance was seen with clindamycin (33%) and tetracycline (34%).Complete sensitivity (100%) was observed to linezolid and vancomycin, making them the most reliable therapeutic options. Clindamycin and tetracycline retained partial efficacy, while fluoroquinolones and aminoglycosides showed poor activity against CA-MRSA.

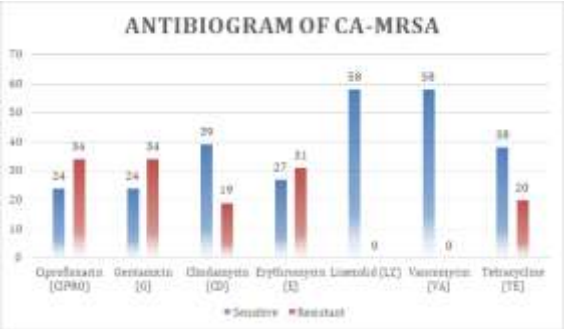

Figure 1: Antibiogram of CA-MRSA

DISCUSSION

The present study highlights the epidemiological and microbiological profile of community-acquired skin and soft tissue infections (CA-SSTIs), with particular emphasis on methicillin-resistant Staphylococcus aureus (CA-MRSA). The mean age of 37.88 years with a predominance of abscesses (46%) and cellulitis (34%) reflects the typical burden of CA-SSTIs in young to middle-aged adults. Similar age distribution and clinical spectrum have been reported in Indian and Southeast Asian cohorts, where abscesses remain the most common presentation of CA-MRSA infections.[7] Male predominance (56%) in our study also aligns with prior observations, possibly attributable to greater occupational exposure and minor trauma in males.[8] Culture positivity was 61%, with S. aureus being the predominant isolate (43%). MRSA accounted for 16% of total cases, which is lower than some North American studies reporting CA-MRSA prevalence exceeding 30%,[9] but comparable to Indian surveillance data showing rates between 12–20%.[10] The relatively lower MRSA burden in our cohort may reflect regional differences in antibiotic usage and community transmission dynamics. Coagulase-negative staphylococci (CONS) and other organisms contributed to 18% of isolates, underscoring polymicrobial involvement in SSTIs, consistent with findings from European studies.[11] Molecular analysis revealed Mec-A gene positivity in 86% of MRSA isolates and Luk-PVL gene presence in 79%. The high prevalence of PVL mirrors global reports where CA-MRSA strains frequently harbor PVL, contributing to tissue necrosis and recurrent abscesses.[12] The coexistence of resistance (Mec-A) and virulence (PVL) determinants explains the aggressive clinical course observed in CA-MRSA infections. Mechanistically, PVL induces leukocyte lysis and local tissue destruction, while Mec-A confers resistance to β-lactams, limiting therapeutic options.[13] The antibiogram demonstrated high resistance to ciprofloxacin (59%), gentamicin (59%), and erythromycin (53%), with moderate resistance to clindamycin (33%) and tetracycline (34%). These findings are consistent with recent Indian surveillance studies reporting rising resistance to fluoroquinolones and aminoglycosides.[14] Complete sensitivity to linezolid and vancomycin underscores their continued reliability, though cost and stewardship concerns limit widespread use. Interestingly, clindamycin retained partial efficacy, supporting its role as a potential oral agent in selected cases, provided inducible resistance is excluded.[15] The observed resistance trends may be attributed to Selective pressure from widespread empirical use of fluoroquinolones and aminoglycosides in outpatient settings, Horizontal gene transfer among staphylococcal species, facilitating dissemination of resistance determinants & Clonal expansion of PVL-positive CA-MRSA strains, which combine virulence with multidrug resistance. Given the dual challenge of resistance and virulence, future strategies should emphasize Molecular surveillance to track emerging CA-MRSA clones and their resistance determinants, Antibiotic stewardship programs to rationalize fluoroquinolone and aminoglycoside use & Exploration of novel agents such as ceftaroline and newer oxazolidinones, which may offer alternatives in resistant cases.[16] Community-level interventions including hygiene education and early drainage of abscesses to reduce transmission.

CONCLUSION

This study highlights the significant role of CA-MRSA in community-acquired skin and soft tissue infections, particularly among young to middle-aged adults presenting with abscesses and cellulitis. The coexistence of mecA-mediated resistance and PVL-associated virulence in the majority of isolates explains the aggressive clinical course and therapeutic challenges. Rising resistance to fluoroquinolones, aminoglycosides, and macrolides limits empirical options, while linezolid and vancomycin remain consistently effective. Clindamycin retains partial efficacy but requires careful monitoring for inducible resistance. These findings emphasize the urgent need for molecular surveillance, rational antibiotic use, and community-level interventions to reduce transmission and improve outcomes in CA-SSTIs.

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