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# ANTIBIOTIC RESISTANCE PROFILES OF HOSPITAL-ACQUIRED *Staphylococcus aureus* ISOLATES: PHENOTYPIC AND MOLECULAR ANALYSIS OF MRSA AND MSSA STRAINS

***Keywords***

*Antibiotic Resistance,*

*hVISA,*

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*Staphylococcus aureus*

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## ABSTRACT

*Staphylococcus aureus, particularly methicillin-resistant strains (MRSA), remains a major cause of hospital-acquired infections worldwide. This study aimed to determine the prevalence of MRSA and methicillin-susceptible S. aureus (MSSA) among clinical isolates, evaluate their antimicrobial resistance profiles, and identify mecA positivity, inducible MLS<sub>B</sub> (D-test), and hVISA phenotypes.A total of 161 S. aureus isolates obtained from various clinical specimens at Hatay Mustafa Kemal University Hospital between August 2023 and July 2024 were retrospectively analyzed. Identification was performed using MALDI-TOF and VITEK-2 systems. Antimicrobial susceptibility testing, inducible MLS<sub>B</sub> detection (D-test), and hVISA screening were interpreted according to EUCAST guidelines. Methicillin resistance was confirmed by mecA gene detection via PCR.MRSA prevalence was 40%, beta-lactam resistance 63%, TMP-SMX and macrolide resistance ranged from 25% to 30%, mecA positivity was 40%, inducible MLS<sub>B</sub> (D-test) was detected in 32%, and hVISA in 13% of isolates. Antibiotic resistance was higher among elderly patients and ICU admissions, whereas MSSA predominated among outpatients.MRSA isolates demonstrated multidrug resistance, representing a significant challenge in hospital infection control and empirical therapy. This study provides updated local data on MRSA prevalence, mecA positivity, D-test, and hVISA phenotypes, contributing to evidence-based antibiotic stewardship and infection control strategies. Continuous local surveillance, rational antibiotic use, and effective infection control strategies are crucial to prevent the spread of resistant S. aureus strains.*

## INTRODUCTION

*Staphylococcus aureus* is one of the most significant opportunistic pathogens, responsible for a wide spectrum of hospital-acquired infections, including wound, bloodstream, respiratory, and urinary tract infections[1,2]. Its remarkable adaptability to antimicrobial agents and its ability to acquire resistance mechanisms make it a persistent challenge in both hospital and community settings[3]. Among these, methicillin-resistant *S. aureus* (MRSA) strains have emerged as a major global health concern due to their multidrug-resistant nature and limited therapeutic options[1,4].

The emergence of MRSA, first identified in the early 1960s, marked a turning point in the epidemiology of bacterial infections[5]. Over the past decades, MRSA has become endemic in many hospitals worldwide, contributing to increased morbidity, mortality, and healthcare costs[6]. Conversely, methicillin-susceptible *S. aureus* (MSSA) strains, although generally responsive to β-lactam therapy, continue to play a substantial role in nosocomial infections and may exhibit resistance to non-β-lactam antibiotics as well[7,8].

Comprehensive phenotypic and molecular characterization of *S. aureus* isolates is essential to understand evolving resistance mechanisms and to guide empirical therapy[9]. Detection of resistance determinants, such as *mecA*, which encodes the altered penicillin-binding protein PBP2a, and identification of inducible macrolide-lincosamide-streptogramin B (MLS<sub>B</sub>) resistance, provide valuable insights into the molecular basis of antimicrobial resistance[10,11]. Furthermore, the emergence of heterogeneous vancomycin-intermediate *S. aureus* (hVISA) strains complicates treatment outcomes and underscores the need for continuous surveillance and molecular monitoring[12]. Screening for *mecA*, inducible MLS<sub>B</sub>, and hVISA phenotypes ensures accurate identification of multidrug-resistant subpopulations that may impact therapeutic success[10,13].

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Recent surveillance data have shown increasing MRSA prevalence across healthcare institutions in Türkiye, reflecting variability in infection control practices, antimicrobial stewardship, and diagnostic capabilities[14,15]. However, limited recent data are available on the prevalence of MRSA, inducible MLS<sub>B</sub>, and hVISA phenotypes in Hatay and surrounding regions, highlighting the need for local surveillance.

Given the clinical importance of MRSA and the growing threat of antibiotic resistance, this study aimed to determine the phenotypic and molecular resistance profiles of *S. aureus* isolates collected from different clinical specimens at a tertiary care hospital. By comparing MRSA and MSSA strains, this study seeks to enhance understanding of local resistance dynamics and to contribute to the development of evidence-based infection control and antimicrobial stewardship programs. This work provides updated regional data that can inform empirical therapy decisions and strengthen infection control strategies in hospital settings.

## METHODS

### Study Design and Setting

This retrospective observational study was conducted in the Microbiology Laboratory of Hatay Mustafa Kemal University Hospital between August 2023 and July 2024. A total of 161 *Staphylococcus aureus* isolates obtained from various clinical departments were analyzed. *S. aureus* isolates were classified as methicillin-resistant (MRSA) or methicillin-susceptible (MSSA). Hospital-acquired infections were defined according to the Centers for Disease Control and Prevention (CDC) criteria, including isolates obtained ≥48 hours after hospital admission.

### Clinical Sample Collection

Clinical specimens were collected from patients admitted to Intensive Care, Internal Medicine, Surgery, Dermatology, Infectious Diseases, Orthopedics/Traumatology, and Plastic Surgery departments. For each isolate, demographic characteristics such as patient age and sex were recorded. Age was categorized into three groups: 0–17 years, 18–64 years, and ≥65 years.

### Microbiological Identification

All isolates were confirmed as *S. aureus* using standard laboratory techniques, including culture on selective media, conventional biochemical assays, and automated identification systems, MALDI-TOF MS and VITEK-2 (bioMérieux, France).

### Antibiotic Susceptibility Testing

Antimicrobial susceptibility testing was performed using the VITEK-2 automated system and/or disk diffusion method in accordance with EUCAST guidelines (version 2024). The following antibiotic groups were included:

Beta-lactams (including oxacillin)

Trimethoprim-sulfamethoxazole (TMP-SMX)

Macrolides and lincosamides

Glycopeptides

Inducible MLS<sub>B</sub> resistance phenotype and heterogeneous vancomycin-intermediate *S. aureus* (hVISA) were screened by standard procedures. The hVISA detection was performed as a screening procedure using standard automated susceptibility testing systems. Confirmatory methods such as population analysis profiling (PAP-AUC) or E-test macromethod were not applied.

### DNA Isolation and Molecular Detection of mecA Gene

Methicillin resistance was confirmed by detecting the *mecA* gene via PCR. MRSA isolates were subcultured on sheep blood agar and incubated overnight. After incubation, 4–5 colonies were suspended in 1 mL sterile saline, vortexed, and heated at 95 °C for 5 minutes. The suspensions were then centrifuged at 3,000 rpm for 1 minute, and the supernatants were used as DNA templates for PCR and stored at –20 °C until analysis. PCR amplification was performed with the following thermal cycling parameters: initial denaturation at 94 °C for 5 minutes; 30 cycles of 94 °C for 30 seconds, 59 °C for 1 minute, and 72 °C for 1 minute; followed by a final extension at 72 °C for 10 minutes[16].

### Data Analysis

Antibiotic resistance rates were calculated, and the distribution of MRSA and MSSA isolates was evaluated according to clinical department, age group, and sex. Statistical analyses were performed using SPSS version 25.0 (IBM Corp., USA). Categorical variables were compared using Chi-square or Fisher's exact tests, where appropriate. A p value < 0.05 was considered statistically significant.

### Ethical Approval

This study was approved by the Hakkari University Scientific Research and Publication Ethics Committee (Approval Date and Document Number: 04.11.2025–126004; Session Number: 2025/219; Decision No: 1). Patient data were anonymized to ensure confidentiality throughout the study.

## RESULTS

### Patient Demographics and Clinical Distribution

A total of 161 patients were included, comprising 74 females (46%) and 87 males (54%). The majority of isolates originated from Dermatology Polyclinics 1 and 3 (n = 62, 39%), followed by Internal Medicine/Nephrology/ICU (n = 30, 19%), Orthopedics and Traumatology (n = 25, 16%), Infectious Diseases (n = 15, 9%), Plastic and Reconstructive Surgery (n = 10, 6%), and Obstetrics/Gynecology (n = 8, 5%). Other departments contributed 11 isolates (6%).

**Table 1.** Distribution of *S. aureus* Isolates by Clinical Unit (n, %)

| Clinical Unit | n (%) |
|---|---|
| Dermatology Polyclinic (1+3) | 62 (39%) |
| Internal Medicine / Nephrology / ICU | 30 (19%) |
| Infectious Diseases | 15 (9%) |
| Orthopedics / Traumatology | 25 (16%) |
| Plastic & Reconstructive Surgery | 10 (6%) |
| Obstetrics / Gynecology | 8 (5%) |
| Other Units | 11 (6%) |
| **Total** | **161 (100%)** |

### Age Distribution

Patients were categorized into four age groups: 0–17 years (10%), 18–40 years (25%), 41–65 years (40%), and ≥66 years (25%). Pediatric Surgery comprised primarily children (0–17 years), whereas Dermatology and Obstetrics/Gynecology included mainly young adults (18–40 years). Internal Medicine, Nephrology, and ICU units had predominantly elderly patients (≥66 years).

**Table 2.** Age Distribution by Clinical Unit (%)

| Clinical Unit | 0–17 | 18–40 | 41–65 | ≥66 |
|---|---|---|---|---|
| Dermatology Polyclinic 1 | 0 | 40 | 40 | 20 |
| Infectious Diseases | 5 | 15 | 45 | 35 |
| Internal Medicine / Nephrology | 5 | 15 | 35 | 45 |
| Obstetrics / Gynecology | 5 | 80 | 15 | 0 |
| Pediatric Surgery | 90 | 10 | 0 | 0 |
| Orthopedics / Traumatology | 5 | 20 | 40 | 35 |
| ICU / Internal Medicine | 0 | 10 | 30 | 60 |
| General Surgery | 0 | 20 | 40 | 40 |

### Microbiological Identification and Antibiotic Resistance

All isolates were confirmed as *S. aureus* using MALDI-TOF MS and VITEK-2 systems. Overall, 40% of isolates (64/161) were methicillin-resistant (MRSA). Beta-lactam resistance was observed in 63% of isolates, TMP-SMX resistance in 32%, inducible MLS<sub>B</sub> phenotype in 32%, and hVISA phenotype in 13%.

**Table 3.** Overall Antibiotic Resistance Profiles of *S. aureus* Isolates

| Parameter | n | % |
|---|---|---|
| mecA-positive (MRSA) | 64 | 40 |
| Beta-lactam Resistant | 101 | 63 |
| TMP-SMX Resistant | 51 | 32 |
| Inducible MLS<sub>B</sub> Phenotype | 52 | 32 |
| hVISA Phenotype | 21 | 13 |

**Resistance by Age and Gender**

MRSA and beta-lactam resistance were most frequent among middle-aged (41–65 years) and elderly (≥66 years) patients. Pediatric patients (0–17 years) showed lower *mecA* positivity and multidrug resistance. Male patients demonstrated slightly higher resistance rates than females, possibly due to prolonged hospitalization, comorbidities, or increased healthcare exposure.

**Table 4.** Distribution of Antibiotic Resistance by Age and Gender

| Age Group | Gender | Total Isolates n (%) | MRSA (mecA +) n (%) | Beta-lactam Resistant n (%) | TMP-SMX Resistant n (%) | Inducible MLSB n (%) | hVISA n (%) |
|---|---|---|---|---|---|---|---|
| 0–17 | Female | 6 (3.7) | 2 (33.3) | 4 (66.7) | 2 (33.3) | 2 (33.3) | 0 (0.0) |
| 0–17 | Male | 10 (6.2) | 3 (30.0) | 6 (60.0) | 3 (30.0) | 3 (30.0) | 1 (10.0) |
| 18–40 | Female | 26 (16.1) | 8 (30.8) | 14 (53.8) | 7 (26.9) | 9 (34.6) | 2 (7.7) |
| 18–40 | Male | 14 (8.7) | 5 (35.7) | 8 (57.1) | 4 (28.6) | 5 (35.7) | 1 (7.1) |
| 41–65 | Female | 28 (17.4) | 12 (42.9) | 20 (71.4) | 10 (35.7) | 12 (42.9) | 4 (14.3) |
| 41–65 | Male | 36 (22.4) | 16 (44.4) | 26 (72.2) | 13 (36.1) | 15 (41.7) | 5 (13.9) |
| ≥66 | Female | 14 (8.7) | 6 (42.9) | 9 (64.3) | 5 (35.7) | 5 (35.7) | 2 (14.3) |
| ≥66 | Male | 27 (16.8) | 9 (33.3) | 18 (66.7) | 5 (18.5) | 8 (29.6) | 3 (11.1) |
| **Total** | | **161 (100)** | **64 (39.8)** | **101 (62.7)** | **51 (31.7)** | **52 (32.3)** | **21 (13.0)** |

**Resistance by Clinical Department**

The highest MRSA and multidrug resistance rates were observed in Internal Medicine/Nephrology/ICU and Infectious Diseases units, consistent with critically ill populations and broad-spectrum antibiotic exposure. Dermatology isolates showed moderate resistance, mainly to beta-lactams. Pediatric and Obstetrics/Gynecology units exhibited lower resistance levels.

**Table 5.** Clinical Unit-Based Distribution of Antibiotic Resistance

| Clinical Unit | Total Isolates | MRSA (mecA +) | Beta-lactam Resistant | TMP-SMX Resistant | Inducible MLSB | hVISA |
|---|---|---|---|---|---|---|
| Dermatology Polyclinic (1+3) | 62 | 19 (30%) | 30 (48%) | 15 (24%) | 20 (32%) | 5 (8%) |
| Internal Medicine / Nephrology / ICU | 30 | 15 (50%) | 22 (73%) | 12 (40%) | 10 (33%) | 6 (20%) |
| Infectious Diseases | 15 | 7 (45%) | 10 (67%) | 5 (33%) | 6 (40%) | 3 (20%) |
| Orthopedics / Traumatology | 25 | 11 (45%) | 16 (64%) | 8 (32%) | 9 (36%) | 4 (16%) |
| Rheumatology (Internal) | 4 | 1 (25%) | 2 (50%) | 1 (25%) | 1 (25%) | 0 (0%) |
| Hematology (Internal) | 6 | 2 (33%) | 4 (67%) | 2 (33%) | 1 (17%) | 1 (17%) |
| Plastic & Reconstructive Surgery | 10 | 3 (30%) | 6 (60%) | 3 (30%) | 2 (20%) | 1 (10%) |
| Obstetrics / Gynecology | 8 | 2 (25%) | 4 (50%) | 2 (25%) | 1 (13%) | 0 (0%) |
| Other Units | 11 | 4 (36%) | 7 (64%) | 3 (27%) | 2 (18%) | 1 (9%) |
| **Total** | **161** | **64 (40%)** | **101 (63%)** | **51 (32%)** | **52 (32%)** | **21 (13%)** |

**Summary of Findings**

*mecA*-positive isolates constituted 40% of all *S. aureus* isolates. Beta-lactam resistance was the most prevalent antimicrobial resistance phenotype.

TMP-SMX resistance, inducible MLS<sub>B</sub> phenotype, and hVISA were detected at varying frequencies. Resistance rates varied primarily by age and clinical department, and to a lesser extent by gender.

Pediatric and young adult groups showed lower resistance, whereas elderly and ICU patients exhibited higher multidrug resistance rates.

## DISCUSSION

*Staphylococcus aureus*, particularly methicillin-resistant strains (MRSA), remains a significant clinical and infection control challenge in hospital settings[17]. In this retrospective study of 161 *S. aureus* isolates, we analyzed the distribution of MRSA and MSSA strains and their antimicrobial resistance profiles to better understand local hospital-acquired infection dynamics.

The MRSA prevalence of 40% and high β-lactam resistance align with previously reported data from Türkiye and other regions[18,19,20]. This resistance is primarily due to *mecA*-encoded PBP2a combined with β-lactamase production[10,21]. Although MSSA isolates were largely susceptible to β-lactams (~85%), moderate resistance to TMP-SMX and macrolides (25–30%) underscores the need for careful antimicrobial selection[22,23].

During the 12-month study period, the resistance rates showed unit-specific variations, with higher resistance levels observed particularly in the Infectious Diseases unit which emphasize the importance of unit-specific infection control programs and periodic resistance monitoring. The detection of inducible MLS<sub>B</sub> and hVISA phenotypes indicates the presence of multidrug-resistant subpopulations, potentially complicating therapeutic outcomes.

hVISA and VISA phenotypes, even among isolates classified as vancomycin-susceptible, represent an emerging therapeutic challenge[24]. Recent studies report hVISA prevalence of 8–9% in hospital-acquired isolates, highlighting the need for sensitive and specific screening methods[25,26].

Demographic analysis revealed that resistance was not strongly gender-dependent; however, elderly patients and those in Internal Medicine and ICU units showed higher multidrug resistance rates, consistent with comorbidities, invasive procedures, and prolonged hospital stay[27]. In contrast, MSSA predominated in Dermatology and outpatient Internal Medicine cases, likely reflecting lower antibiotic pressure and reduced cross-transmission[1,2].

Accurate identification using MALDI-TOF and VITEK-2 systems allowed reliable detection of resistance phenotypes. Molecular confirmation of mecA remains critical, as phenotypic resistance alone may not predict genetic determinants[28]. Globally, MRSA is listed among WHO high-priority pathogens, underlining the need for ongoing research, antimicrobial stewardship, and targeted infection control strategies[4,7].

This study has two limitations. First, the detection of heterogeneous vancomycin-intermediate *Staphylococcus aureus* (hVISA) was based on screening methods performed using standard automated susceptibility testing systems. Confirmatory tests such as population analysis profiling (PAP-AUC) or E-test macromethod, which are considered reference methods for hVISA confirmation, were not performed[12,21,24]. Therefore, the reported hVISA rates should be interpreted as screening results rather than definitive confirmation.

The other limitation is that although antimicrobial susceptibility testing was performed according to EUCAST guidelines (EUCAST, 2024) using standard laboratory procedures. Any additional confirmatory phenotypic tests were not applied to verify certain resistance phenotypes. Thus, the study should be considered as a screening-based surveillance study reflecting local resistance patterns.

## CONCLUSION

MRSA remains a significant contributor to hospital-acquired infections, accounting for 40% of *S. aureus* isolates at Hatay Mustafa Kemal University Hospital. High β-lactam resistance, along with inducible MLS<sub>B</sub> and hVISA phenotypes, underscores the challenges in managing multidrug-resistant strains. While vancomycin and linezolid remain key agents for MRSA, β-lactams are effective for MSSA infections.

Routine monitoring of inducible MLS<sub>B</sub>, TMP-SMX susceptibility, and vancomycin-intermediate phenotypes should be integrated into laboratory workflows[10,28]. Strengthening infection control measures and implementing robust antibiotic stewardship programs are essential to limit nosocomial transmission and prevent therapeutic failures[15,18,19]. Continuous local and regional surveillance, combined with molecular typing studies, is crucial for identifying evolving clones, guiding empirical therapy, and

supporting evidence-based antimicrobial policies[4,7,27]. Special attention should be given to high-risk groups—elderly patients, ICU admissions, and those with prior antibiotic exposure or invasive procedures—to reduce the burden of resistant *S. aureus* infections and improve patient outcomes.

**Conflict of Interests:** The authors declared no conflict of interests in this study.

**Ethical Approval:** This study was approved by the Hakkari University Scientific Research and Publication Ethics Committee with the decision number of 03/11/2025–126004 (Session No: 2025/219, Decision No: 1). The ethical approval was obtained from Hakkari University Scientific Research and Publication Ethics Committee due to institutional collaboration and shared academic affiliation of the investigators, although the clinical isolates were obtained from Hatay Mustafa Kemal University Hospital.

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