Medical Science Journal for Advance Research

Vol. 6, No. 3, September 2025
e-ISSN: 2774-4892

Prevalence and Distribution of Methicillin-Resistant *Staphylococcus aureus* in Clinical Samples from Patients in Diyala Province Hospitals

Falah H. Abbas[1], and Adnan H. Aubaid[2]

[1,2] *Department of Microbiology, College of Medicine, University of Al-Qadisiyah, Iraq.*

Email: adnan.uobed@qu.edu.iq

ABSTRACT

Background: *Methicillin-resistant Staphylococcus. aureus (M.R.S.A) strains have emerged as an emerging worldwide healthcare problem, as well as Staphylococcus aureus is a prominent human pathogenic organism that causes a broad spectrum of diseases. It is essential to comprehend the allocation as well as the frequency of M.R.S.A in various medical specimens to direct antibacterial management initiatives as well as focused therapies.* ***Objectives****: The purpose of the present research was to examine the incidence as well as distribution of antibiotic-resistant strains of S. aureus, including MRSA, that were isolated from a variety of medical samples obtained from hospitalized-patients inside Diyala-Iraq, including throat-swabs, urine-specimens, wound-swabs, as well as burn-specimens.* ***Methods****: A total of 301 medical specimens were gathered between September 2024 and January 2025. The VITEK-2 automated-system, as well as conventional microbiology methods, have been utilized to isolate, identify, as well as analyze for resistance to antibiotics among bacteria.* ***Results****: Out of the 301 clinical samples, 56 (18.60%) showed positive results for S.aureus, with the highest prevalence observed in throat swabs (21.05%) and burn samples (21.88%). Antimicrobial susceptibility testing revealed high rates of resistance to various antibiotic classes, including universal resistance (100%) against β-lactams (penicillins & cephalosporins). Macrolides (erythromycin) as well as lincosamides (clindamycin) also exhibited high resistance rates (78.6% as well as 73.2%, respectively), particularly in throat and wound isolates. Glycopeptides (vancomycin) demonstrated strong efficacy, with 100% susceptibility in throat as well as urine isolates, though worrisome intermediate resistance (28.6%) was detected in burn samples as well as full resistance (18.2%) in wound isolates. Fluoroquinolones (ciprofloxacin, levofloxacin) showed variable resistance (48.2% overall), with urine isolates displaying higher susceptibility (61.1%) but wound isolates exhibiting strong resistance (63.6%). Notably, last-resort antibiotics (tigecycline, linezolid) remained 100% effective across all isolates.*

Conclusion*: The epidemiological study of S.aureus, including M.R.S.A, in hospitalized individuals in Diyala-Iraq, is better understood thanks to the current research. The substantial threat this infection poses to the community's safety is highlighted through the widespread distribution of antibiotic-resistant strains, the appearance of vancomycin-intermediate as well as resistant-isolates, as well as the co-existence of many M.R.S.A-lineages.*

Keywords: Prevalence, Distribution, Clinical Samples, Diyala Province Hospitals.

Article Information

Received: June 12, 2025; Revised: July 28, 2025; Online: September 2025

https://doi.org/10.46966/msjar.v6i3.295

INTRODUCTION

Globally, *Staphylococcus aureus* is a common as well as adaptable bacterium that is a major contributor to infections-acquired in civilian environments as well as clinical settings [1],[2],[3]. This Gram-positive bacteria is well-known for producing a broad spectrum of medical signs, including minor-infections of the skin-tissues as well as soft-tissues to serious invasive illnesses like necrotic-pneumonia, bacteremia, as well as endocarditis[4],[5],[6].

Methicillin-resistant *Staphylococcus.aureus* (M.R.S.A) species are now prevalent as well as spread quickly, providing serious obstacles for the successful treatment with antibiotics as well as infection-management strategies. This has developed into an important issue for the community [7],[8],[9]. *Staphylococcus aureus* that is susceptible to methicillin as well as other semi-synthetic penicillins, including oxacillin as well as nafcillin, is known as M.R.S.A [10].

The main process that confers resistance to methicillin within *S.aureus* involves the acquisition of the mecA-gene, resulting in a modified penicillin-binding-protein (P.B.P.2a) with decreased-affinity for β-lactam antimicrobia[4],[11],[12]. Healthcare-associated M.R.S.A (HA-MRSA) as well as community-associated M.R.S.A (CA-MRSA) are the two main epidemiology groups into which M.R.S.A strain may be generally divided. Although CA-MRSA is more frequently linked to infectious diseases in communities as well as seems to possess a different virulent profile, HA-MRSA is usually connected alongside medical centers such as hospitals as well as long-term care-institutions, as well as can frequently be described by multidrug-susceptibility [13],[14] . M.R.S.A's worldwide expansion has proven to be a serious problem; reports of the infection have come from both industrialized as well as developing nations [15]. According to estimates, M.R.S.A causes more than 300.000 healthcare-associated-infections in the U.S each year, leading to significant death, complications, death, as well as financial impact [16],[17]. Similarly, in Europe, M.R.S.A has been identified as a leading cause of healthcare-associated infections, with prevalence rates varying widely among different countries [18],[19]. M.R.S.A is frequently more common in poorer as well as middle-income nations, which is indicative of difficulties with infection management, restricted availability of potent antibiotics, as well as inadequate diagnosis skills [4]. There were a few studies on the epidemiological basis of MRSA in Iraq. The majority of the publications have concentrated on certain areas or medical institutions. A comprehensive analysis conducted discovered that hospitalized patients in Iraq had an MRSA incidence ranging from 20% to 70%, underscoring the substantial burden of this infection in the nation. Nevertheless, little is known about the prevalence and patterns of antibiotic resistance of MRSA in several medical specimen resources, such as burn, wound, urine, as well as throat infections[20],[21]. It is essential to comprehend the spreading as well as frequency of M.R.S.A in diverse clinical specimens to direct antibacterial management initiatives as well as focused therapies. Determining the resistant profiling of M.R.S.An isolation can help design suitable treatment plans as well as guide empirical antibiotic therapy [22]. Additionally, describing the genetic diversity as well as the molecular epidemiology of M.R.S.A strain might offer important information on the dynamics of transmission as well as the appearance of new or dangerous clones in a particular area [15],[23],[24].

The purpose of the present research was to examine the incidence and distribution of antibiotic-resistant strains of *Staphylococcus aureus*, involving MRSA, that were isolated from a variety of medical specimens obtained

from hospitalized patients in Diyala-Iraq, including throat-swabs, urine-specimens, wound-swabs, as well as burn-specimens.

MATERIALS AND METHODS

Specimens Collecting

This cross-sectional during the current research that carried out at Diyala city hospitals, Iraq, from December 2024 to April 2025. A total of 301 clinical samples, including burn-wound swabs (*n*=32), wound-swabs (*n*=65), urine-swabs (*n*=109), as well as throat-swabs (*n*=95). After being aseptically collected, every specimen was brought to the microbiological lab for analysis, where collected from patients presenting with suspected Staphylococcus aureus infections.

Bacterial Isolation and Identification

Throat swab samples were obtained by gently rubbing a sterile cotton-tipped swab against the posterior pharynx and tonsil areas. Urine samples were collected as clean-catch mid-stream specimens. Wound samples were acquired by swabbing the exudates or tissue from the infected site, while burn samples were obtained by swabbing the affected burn area. Each of the specimens went through processing right away for bacterium isolation as well as designation after being delivered to the microbiological lab in suitable, sterilized containers. Mannitol-Salt-Agar (M.S.A), a selective as well as differential-medium for *staphylococci* isolation, was used to cultivate-medical specimens. For 24 hours, plates were incubated at 37°C. The existence of clusters of Gram-positive cocci, which are indicative of Staphylococcus species, was confirmed by Gram-staining colonies that displayed typical morphological features such as golden-yellow coloring or yellow-zones on M.S.A [**25**].

For definitive identification of the Staphylococcus isolates, the VITEK-2 automated-system (bio.Mérieux-France) was utilized. This platform performs a series of biochemical tests, including coagulase production, catalase activity, and carbohydrate utilization patterns, for differentiation of *Staphylococcus aureus* from other *staphylococcal species*. Isolates confirmed as coagulase-positive were identified as *Staphylococcus aureus* [**26**].

Antimicrobial Susceptibility Testing:

The VITEK 2 system was used to conduct antibacterial resistance examination by the Clinical & Laboratory-Standards Institute's-recommendations [**27**],[**28**]. Several antibacterial medications, such as penicillins, Cephalosporins, glycopeptides, aminoglycosides, macrolides, tetracyclines, Fluoroquinolones, as well as others, have been utilized to assess the resistance profiling of the *Staphylococcus aureus* isolates. The C.L.S.I breakpoints were utilized to interpret data to determine susceptibility (S), intermediary (I), or resistance (R).

Ethical-Consideration:

The Ethics Studies Commission of Al-Qadisiyah-University's Medicine-College gave its approval to the researchers' methodology. Additionally, everyone who participated, as well as the controllers, gave verbal understanding permission.

RESULTS

Bacterial isolation

The *Staphylococcus aureus* was isolated from 301 clinical specimens from various sources, including throat swabs (95 samples), urine (109 samples), wounds (65 samples), and burns (32 samples). The bacterial isolation of *Staphylococcus aureus* was performed using selective-medium (Mannitol-Salt-Agar (M.S.A), which is differential for *S.aureus* due to its ability to ferment mannitol, producing yellow-colonies. This step ensured the

preferential growth of staphylococci while inhibiting other microbiota. Suspect colonies exhibiting typical morphology (golden-yellow pigmentation on blood-agar or yellow-zones on M.S.A) were further purified as well as subjected to Gram-staining, revealing Gram-positive cocci in clusters as shown in **Figure (1)**. For definitive identification, the isolates were analyzed using the VITEK-2 automated-system, a widely recognized platform for microbial-identification as well as antibacterial-susceptibility testing. The VITEK-system employs a series of biochemical-tests, including coagulase-production, catalase-activity, as well as carbohydrate-utilization patterns, to differentiate *S.aureus* from other staphylococci. Coagulase-positive isolations have been confirmed as *S.aureus*, ensuring high specificity in the results.

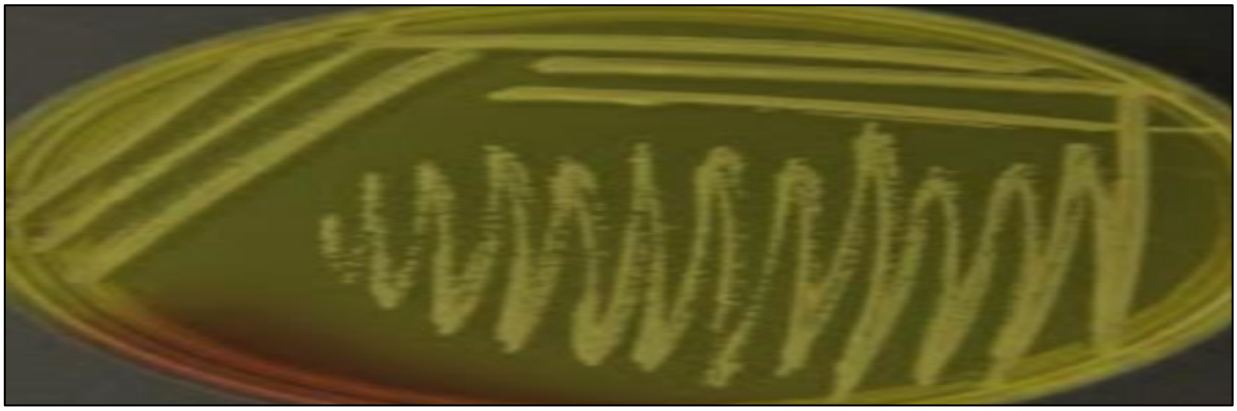

Figure (1): Cultural characteristic of *Staphylococcus aureus* on Mannitol-Salt-Agar (MSA) Show In Yellow Colonies.

Staphylococcus aureus Frequency in Clinical Samples

The results of *Staphylococcus aureus* frequency across various clinical specimens (throat, urine, wound, and burn samples) revealed a prevalence rate of **18.60%** (56 out of 301 tested samples). Among the individual sources, throat samples exhibited the highest number of positive isolates (20 out of 95, 21.05%), closely followed by burn samples (7 out of 32, 21.88%), these two sources may be more conducive to *Staphylococcus aureus* colonization or infection compared to others. Urine and wound samples showed slightly lower prevalence rates, with 16.51% (18 out of 109) and 16.92% (11 out of 65), respectively. The findings showed no statistical significance association among the medical specimen's a resource as well as the probability of *S.aureus* positive results, with a *P*-value of 0.82 as well as a Chi-square statistic (χ^2) of 1.03 with three levels of independence. This suggests that instead of resulting from intrinsic variations in a specimen resources, the noticed variances in frequency levels are probably the result of randomized fluctuation. as show in **Table (1) and Figure (2)**.

Table (1) The prevalence of Staphylococcus aureus from clinical infectious specimens.

Source	No. of Tested Samples	No. of Positive Isolates	Prevalence (%)
Throat	95	20	21.05
Urine	109	18	16.51
Wound	65	11	16.92
Burn	32	7	21.88
Total	**301**	**56**	**18.60**

Chi-square test: $\chi^2 = 1.03$, Degrees of freedom df = 3, p-value = 0.82.

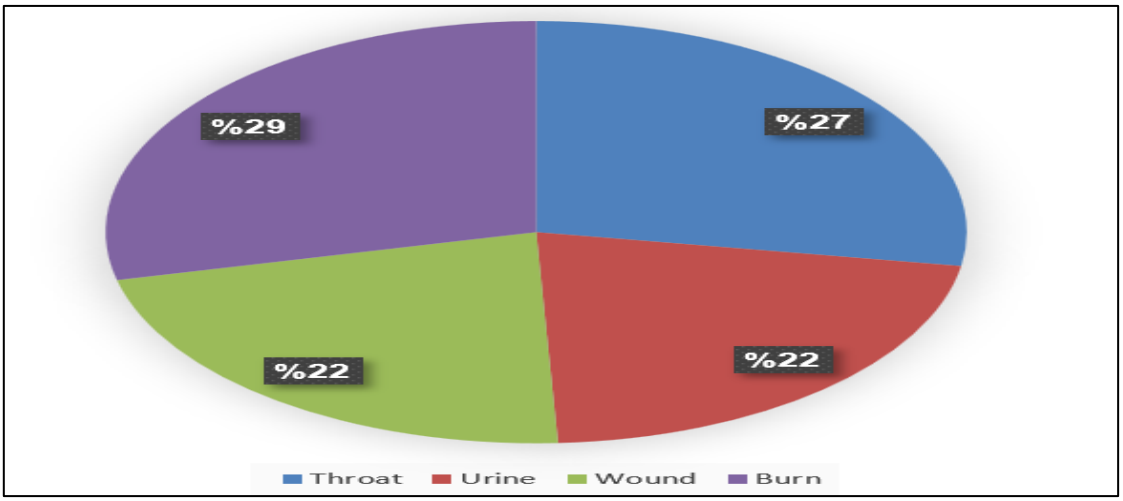

Figure (2): Histogram shows prevalence of Staphylococcus aureus from clinical infectious specimens.

Antibacterial-Susceptibility-Test (A.S.T) results

The VITEK-2 automated-system, an accurate foundation for detecting bacteria as well as antimicrobial-resistant characterization, was utilized to conduct antibiotic- susceptibility testing in this investigation. The data were interpreted by the criteria provided by Clinicals as well as Laboratory-Standards-Institute (C.L.S.I). A total of 56 *Staphylococcus aureus* isolates from burn-swabs (7), wounds-swabs (11), urine-specimens (18), as well as throat-swabs (20) were included during analysis. Concerning resistant patterns were shown by classifying the susceptibility-profiles for each antimicrobial class as susceptible (S), intermediate (I), or resistant (R), as shown in **tables (2) through (6)**. The inefficiency of *β*-lactams, which include Cephalosporins as well as penicillins, was highlighted by the observation of universal resistance (100%) to these first-line antibiotics.

Additionally, lincosamides (clindamycin) and macrolides (erythromycin) showed substantial resistance rates (78.6% and 73.2%, respectively), especially in isolates from the neck and wounds, where resistance approached 100%. Although concerning intermediate resistance (28.6%) was found in burn samples and complete resistance (18.2%) in wound isolates, indicating developing tolerance, glycopeptides (vancomycin) showed remarkable effectiveness, with 100% susceptibility in throat and urine isolates. Total resistance to Fluoroquinolones (ciprofloxacin, levofloxacin) was 48.2%; urine-isolates were more resistant (61.1%), whereas wound-isolates had the most resistance (63.6%). Notably, all isolates showed 100% efficacy with last-resort antimicrobial (tigecycline, linezolid), confirming their use in treating infections that are extensively drug-resistant (XDR) as well as multidrug-resistant (MDR). Mechanisms of resistance have been expanded by statistical studies.

A chi-square test (χ^2=5.82, df=3, P=0.12) revealed no None-statistically significant relationship among the MDR-XDR frequencies as well as the specimen's resource **(burn-swap, wound-swap, urine-specimen, or throat-swap**), indicating that resistance is broad rather than source-dependent. Summary information, nevertheless, showed glaring differences: wound-isolates from other resources were 80-85.7% MDR/XDR, whereas 100% were. Fisher's-exact-test revealed no None-statistically significant relationship between urine-isolates as well as wound-isolates (*P*=0.29); however, the high total MDR/XDR burden of 85.7% highlights a serious public health issue. Just 14.3% of the isolates were non-MDR, whereas 57.1% of the resistance categorization was MDR (three to five antibiotic classes), as well as 28.6% XDR (six or more classes), **Table 6 and Figure 3**.

Table (2): Antibiotic susceptibility profiles in Burn isolates.

Antimicrobial-Class	Antimicrobial-Agent	Susceptible.(S)	Intermediate.(I)	Resistant.(R)
Penicillin's	Oxacillin	0 (0%)	0 (0%)	7 (100%)
	Benzylpenicillin	0 (0%)	0 (0%)	7 (100%)
Cephems	Cefotaxime	0 (0%)	0 (0%)	7 (100%)
	Ceftriaxone	0 (0%)	0 (0%)	7 (100%)
Glycopeptides	Cefepime	0 (0%)	0 (0%)	7 (100%)
Lipoglycopeptides	Vancomycin	5 (71.43%)	2 (28.57%)	0 (0%)
Aminoglycosides	Teicoplanin	5 (71.43%)	0 (0%)	2 (28.57%)
Macrolides	Gentamicin	4 (57.14%)	0 (0%)	3 (42.86%)
Tetracycline	Erythromycin	2 (28.57%)	0 (0%)	5 (71.43%)
	Tetracycline	2 (28.57%)	0 (0%)	5 (71.43%)
	Tigecycline	7 (100%)	0 (0%)	0 (0%)
Fluoroquinolones	Doxycycline	2 (28.57%)	0 (0%)	5 (71.43%)
	Ciprofloxacin	4 (57.14%)	0 (0%)	3 (42.86%)
	Levofloxacin	4 (57.14%)	0 (0%)	3 (42.86%)
Lincosamides	Moxifloxacin	5 (71.43%)	0 (0%)	2 (28.57%)
Folate pathway antagonists	Clindamycin	0 (0%)	0 (0%)	7 (100%)
Ansamycin	Trimethoprim-sulfamethoxazole	2 (28.57%)	0 (0%)	5 (71.43%)
Oxazolidinones	Rifampicin	4 (57.14%)	0 (0%)	3 (42.86%)
	Linezolid	7 (100%)	0 (0%)	0 (0%)

Table (3): Antibiotic susceptibility profiles in Throat swab isolates.

Antimicrobial Class	Antimicrobial Agent	Susceptible (S)	Intermediate (I)	Resistant (R)
Penicillin's	Oxacillin	0 (0%)	0 (0%)	20 (100%)
	Benzylpenicillin	0 (0%)	0 (0%)	20 (100%)
Cephems	Cefotaxime	0 (0%)	0 (0%)	20 (100%)
	Ceftriaxone	0 (0%)	0 (0%)	20 (100%)
Glycopeptides	Cefepime	0 (0%)	0 (0%)	20 (100%)
Lipoglycopeptides	Vancomycin	20(100%)	0 (0%)	0 (0%)
Aminoglycosides	Teicoplanin	16 (80%)	0 (0%)	4 (20%)
Macrolides	Gentamicin	20 100%)	0 (0%)	0 (0%)
Tetracyclines	Erythromycin	0 (0%)	0 (0%)	20 (100%)
	Tetracycline	8 (40%)	0 (0%)	12 (60%)
	Tigecycline	20(100%)	0 (0%)	0 (0%)
Fluoroquinolones	Doxycycline	16 (80%)	0 (0%)	4 (20%)
	Ciprofloxacin	16 (80%)	4 (20%)	0 (0%)
	Levofloxacin	16 (80%)	4 (20%)	0 (0%)
Lincosamides	Moxifloxacin	12 (60%)	0 (0%)	8 (40%)
Folate pathway antagonists	Clindamycin	4 (20%)	0 (0%)	16 (80%)
Ansamycin	Trimethoprim-sulfamethoxazole	4 (20%)	0 (0%)	16 (80%)
Oxazolidinones	Rifampicin	4 (20%)	0 (0%)	16 (80%)
	Linezolid	20(100%)	0 (0%)	0 (0%)

Table (4): Antibiotic susceptibility profiles in wound isolates.

Antimicrobial Class	Antimicrobial Agent	Susceptible (S)	Intermediate (I)	Resistant (R)
Penicillin's	Oxacillin	0 (0%)	0 (0%)	11 (100%)
	Benzylpenicillin	0 (0%)	0 (0%)	11 (100%)
Cephems	Cefotaxime	0 (0%)	0 (0%)	11 (100%)
	Ceftriaxone	0 (0%)	0 (0%)	11 (100%)
Glycopeptides	Vancomycin	9 (81.81%)	0 (0%)	2 (18.18%)
Lipoglycopeptides	Teicoplanin	9 (81.81%)	0 (0%)	2 (18.18%)
Aminoglycosides	Gentamicin	4 (36.36%)	0 (0%)	7 (63.63%)
Macrolides	Erythromycin	0 (0%)	0 (0%)	11 (100%)
Tetracyclines	Tetracycline	0 (0%)	0 (0%)	11 (100%)
	Tigecycline	11 (100%)	0 (0%)	0 (0%)
	Doxycycline	2 (18.18%)	0 (0%)	9 (81.81%)
Fluoroquinolones	Ciprofloxacin	4 (36.36%)	0 (0%)	7 (63.63%)
	Levofloxacin	4 (36.36%)	0 (0%)	7 (63.63%)
	Moxifloxacin	4 (36.36%)	0 (0%)	7 (63.63%)
Lincosamides	Clindamycin	0 (0%)	0 (0%)	11 (100%)
Folate pathway antagonists	Trimethoprim-sulfamethoxazole	2 (18.18%)	0 (0%)	9 (81.81%)
Ansamycin	Rifampicin	2 (18.18%)	0 (0%)	9 (81.81%)
Oxazolidinones	Linezolid	0 (0%)	0 (0%)	11 (100%)

Table (5): Antibiotic susceptibility profiles in urine isolates.

Antimicrobial Class	Antimicrobial Agent	Susceptible (S)	Intermediate (I)	Resistant (R)
Penicillin's	Oxacillin	0 (0%)	0 (0%)	18 (100%)
	Benzylpenicillin	0 (0%)	0 (0%)	18 (100%)
Cephems	Cefotaxime	0 (0%)	0 (0%)	18 (100%)
	Ceftriaxone	0 (0%)	0 (0%)	18 (100%)
	Cefepime	0 (0%)	0 (0%)	18 (100%)
Glycopeptides	Vancomycin	18 (100%)	0 (0%)	0 (0%)
Lipoglycopeptides	Teicoplanin	18 (100%)	0 (0%)	0 (0%)
Aminoglycosides	Gentamicin	18 (100%)	0 (0%)	0 (0%)
Macrolides	Erythromycin	14 (77.77%)	0 (0%)	4 (22.22%)
Tetracycline's	Tetracycline	18 (100%)	0 (0%)	0 (0%)
	Tigecycline	18 (100%)	0 (0%)	0 (0%)
	Doxycycline	18 (100%)	0 (0%)	0 (0%)
Fluoroquinolones	Ciprofloxacin	11 (61.11%)	7 (38.88%)	0 (0%)
	Levofloxacin	11 (61.11%)	7 (38.88%)	0 (0%)
	Moxifloxacin	14 (77.77%)	0 (0%)	4 (22.22%)
Lincosamides	Clindamycin	7 (38.88%)	0 (0%)	11 (61.11%)
Folate pathway antagonists	Trimethoprim-sulfamethoxazole	14 (77.77%)	0 (0%)	4 (22.22%)
Ansamycin	Rifampicin	14 (77.77%)	0 (0%)	4 (22.22%)
Oxazolidinones	Linezolid	18 (100%)	0 (0%)	0 (0%)

Table (6) Antimicrobial Resistance pattern (*n*=56 Isolates).

Antimicrobial Class	Antimicrobial Agent	Susceptible (S)	Intermediate (I)	Resistant (R)
Penicillin's	Oxacillin	0 (0%)	0 (0%)	20 (100%)
	Benzylpenicillin	0 (0%)	0 (0%)	20 (100%)
Cephems	Cefotaxime	0 (0%)	0 (0%)	20 (100%)
	Ceftriaxone	0 (0%)	0 (0%)	20 (100%)
Glycopeptides	Cefepime	0 (0%)	0 (0%)	20 (100%)
Lipoglycopeptides	Vancomycin	20 (100%)	0 (0%)	0 (0%)
Aminoglycosides	Teicoplanin	16 (80%)	0 (0%)	4 (20%)
Macrolides	Gentamicin	20 (100%)	0 (0%)	0 (0%)
Tetracyclines	Erythromycin	0 (0%)	0 (0%)	20 (100%)
	Tetracycline	8 (40%)	0 (0%)	12 (60%)
	Tigecycline	20 (100%)	0 (0%)	0 (0%)
Fluoroquinolones	Doxycycline	16 (80%)	0 (0%)	4 (20%)
	Ciprofloxacin	16 (80%)	4 (20%)	0 (0%)
	Levofloxacin	16 (80%)	4 (20%)	0 (0%)
Lincosamides	Moxifloxacin	12 (60%)	0 (0%)	8 (40%)
Folate pathway antagonists	Clindamycin	4 (20%)	0 (0%)	16 (80%)
Ansamycin	Trimethoprim-sulfamethoxazole	4 (20%)	0 (0%)	16 (80%)
Oxazolidinones	Rifampicin	4 (20%)	0 (0%)	16 (80%)
	Linezolid	20 (100%)	0 (0%)	0 (0%)

Chi-square Test for MDR/XDR Distribution: χ^2=5.82, d.f=3, *P*-value=0.12 (N.S).

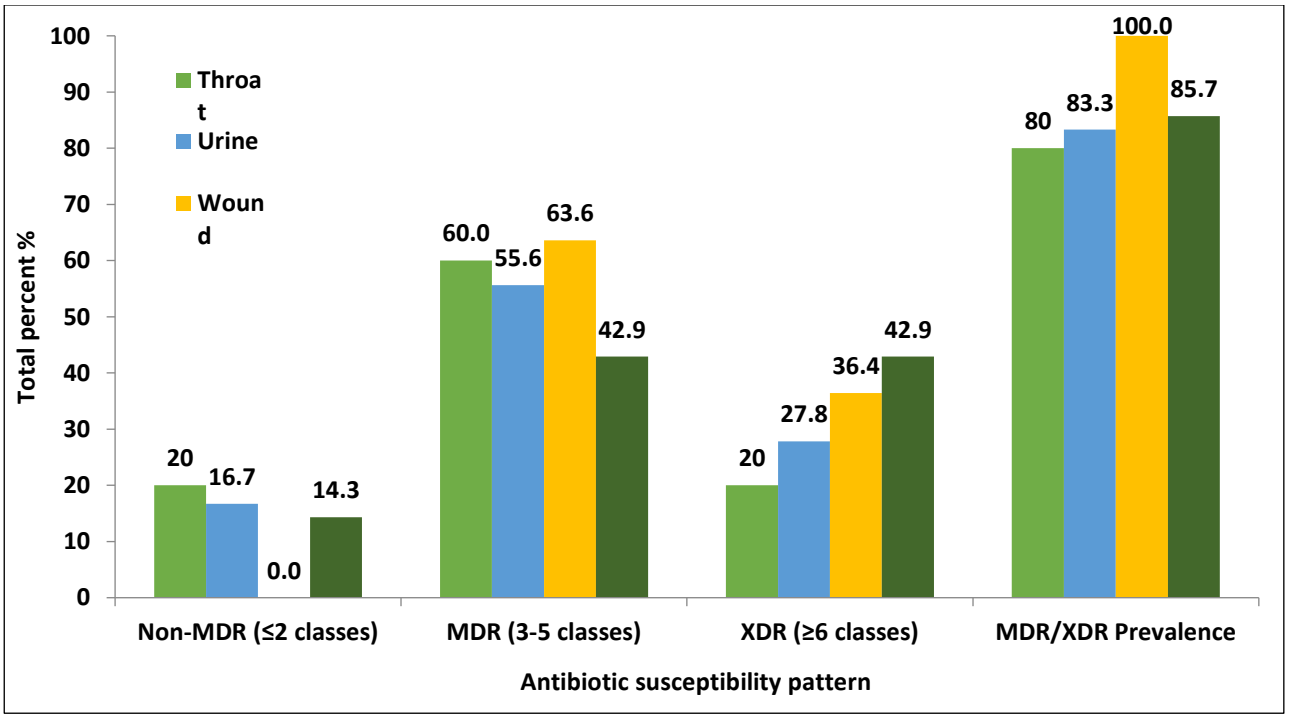

Figure (3): Histogram show the prevalence of Antibacterial Resistance pattern (*n*=56 Isolations).

DISCUSSION

The results of the present research serve as important light on the prevalence of methicillin-resistant Staphylococcus *aureus* (MRSA) and other Staphylococcus aureus among hospitalized patients in Diyala, Iraq. The study's total *Staphylococcus.Aureus* prevalence of 18.60% is in line with data from other areas, highlighting the pathogen's importance as a primary contributor to infections acquired in the community and clinical settings [**1**],[**2**],[**3**],[**4**]. Therapeutic choices for *S.aureus* infections are limited due to the elevated prevalence of antimicrobial resistance, especially against *β*-lactams, macrolides, also lincosamides. This study's universal resistance (100%) to β-lactams, such as cephems and penicillins, is consistent with the global trend of rising MRSA.A prevalent, which has been extensively documented in both wealthy as well as developing nations. [**4**],[**5**],[**12**],[**28**]. Methicillin resistance within *Staphylococcus aureus* is mostly conferred via the acquisition of the mecA-gene, which encodes a modified penicillin-binding protein (P.B.P.2a) with decreased affinity for *β*-lactam antimicrobial. [**4**],[**29**]. Worrying are the elevated incidences of susceptibility to lincosamides (clindamycin, 73.2%) as well as macrolides (erythromycin, 78.6%), especially in isolates from the neck as well as wounds, where resistance approached 100% [**6**],[**30**].

The co-occurrence of MRSA and macrolide/lincosamide resistance has been extensively described in other countries, as well as our susceptibility patterns are in line with other studies. [**18**],[**28**],[**31**]. The development of different resistant genes, such as erm well as msr, that may be carried on mobile genetic elements as well as speed up the spread of multidrug-resistant strains, is frequently the mechanism behind co-resistance to these antibiotic-classes [**4**],[**14**],[**29**],[**31**].

Glycopeptides (vancomycin), on the other hand, showed excellent effectiveness, exhibiting 100% resistance in isolates from the throat as well as urine. Vancomycin is regarded as a last-resort antibiotic for the treatment of MRSA infections; thus, the finding of concerning intermediate resistance (28.6%) in burn specimens as well as complete resistance (18.2%) in wound isolates is quite concerning [**4**],[**32**]. Vancomycin-intermediate and -resistant Staphylococcus aureus (VISA and VRSA) strains have been documented to have emerged worldwide, which presents a major problem for doctors as well as emphasizes the necessity of increased monitoring as well as the creation of alternate treatment approaches [**4**],[**18**]. Various healthcare facilities may have various selective strains and transmission dynamics, which could explain the variable resistance patterns seen for fluoroquinolones (ciprofloxacin, levofloxacin), with urine isolates showing higher susceptibility (61.1%) but wound isolates showing strong resistance (63.6%).

S. aureus fluoroquinolone resistance is frequently linked to mutations in the topoisomerase genes (gyrA, gyrB, parC, and parE), which can be obtained by horizontal gene transfer as well as clonal proliferation [**33**]. Interestingly, the antimicrobial agents used as a last option, including linezolid and tigecycline, were 100% effective against every isolate in our investigation. This research supports the use of these antibiotics in the treatment of extensively drug-resistant (XDR) and multidrug-resistant (MDR) Staphylococcus aureus infections, which are becoming more commonplace globally [**2**],[**16**],[**20**]. To stop the ongoing creation and expansion of resistance, it is imperative that these treatment choices be preserved and used sparingly within the framework of antimicrobial stewardship initiatives. This study's statistical analysis showed no significant correlation between the MDR/XDR prevalence and the sample source (burn, wound, urine, or throat), indicating that

resistance is general rather than source-dependent. This result is in line with the worldwide spread of MRSA strains, which can be explained by a number of things, such as the pathogens' capacity to colonize multiple body sites, the spread of resistant clones both inside and between healthcare facilities and the general public, and the selective pressure brought on by the overuse and abuse of antibiotics [**33**],[**34**]. Descriptive data did, however, draw attention to sharp differences: 100% of wound isolates were MDR/XDR, whereas 80–85.7% were from other sources. This finding highlights the serious public health risk that MRSA poses for wound infections, which are frequently linked to high rates of morbidity, extended hospital stays, as well as higher medical expenses [**11**]. The urgent need for focused treatments to slow the spread of these hard-to-treat illnesses is further highlighted by the high MDR/XDR burden (85.7% overall).

The results of this study highlight the serious public health threat that methicillin-resistant strains of Staphylococcus aureus represent to the hospitalized patient population in Diyala, Iraq. The growth of vancomycin-intermediate and -resistant strains, the high frequency of isolates resistant to antibiotics, and the extensive spread of multidrug-resistant clones underscore the necessity of tackling this problem from several angles[**34**]. To effectively treat S. aureus infections in the area, comprehensive antimicrobial stewardship programs, improved infection control measures, and the creation of innovative therapeutic approaches are essential. A deeper comprehension of the local epidemiology and the creation of focused treatments can also be facilitated by enhancing surveillance activities, developing diagnostic skills, and encouraging cooperative research. Additionally, the results of this study highlight the need of putting strict infection control procedures into place, especially in high-risk environments like burn and wound units where the prevalence of MDR/XDR S. aureus is higher. Healthcare institutions may assist stop the spread of these resistant strains by implementing measures including hand hygiene, environmental cleaning, and the prudent use of personal protective equipment. To sum up, this study offers important new information about the prevalence of MRSA and other Staphylococcus aureus among hospitalized patients in Diyala, Iraq. This disease poses a serious threat to public health, as evidenced by the high frequency of antibiotic-resistant strains, the appearance of vancomycin-intermediate as well as resistant isolates, and the extensive spread of multidrug-resistant clones. To effectively treat Staphylococcus aureus infections in the area, a thorough, multimodal strategy including improved infection control practices, antimicrobial stewardship, as well as the creation of innovative therapeutic approaches would be needed [**1**],[**36**],[**37**].

CONCLUSION

This study provides a comprehensive evaluation of the prevalence and antimicrobial resistance patterns of Staphylococcus aureus, including methicillin-resistant strains (MRSA), among hospitalized patients in Diyala Province, Iraq. The overall prevalence rate of 18.60%, with the highest detection in throat and burn specimens, demonstrates the organism’s broad clinical distribution. Statistical analysis revealed no significant association between specimen type and isolation frequency ($\chi^2(3) = 1.03$, $p = .82$), suggesting a non-source-specific pattern of colonization or infection. Of greater concern is the substantial burden of antimicrobial resistance. Universal resistance (100%) to β-lactams was observed across all isolates, while high resistance to macrolides and lincosamides—particularly in wound and throat isolates—further limits treatment options. Although glycopeptides such as vancomycin

showed overall efficacy, the emergence of intermediate resistance (28.6%) in burn samples and full resistance (18.2%) in wound isolates raises serious therapeutic challenges. Notably, all isolates remained fully susceptible to last-resort agents, linezolid and tigecycline. Multidrug resistance was prevalent in 85.7% of isolates, with no statistically significant association between resistance classification (non-MDR, MDR, or XDR) and specimen source ($\chi^2(3) = 5.82$, $p = .12$). This widespread resistance pattern—regardless of clinical source—underscores the need for robust, cross-cutting strategies that include strengthened antimicrobial stewardship programs, enhanced infection control practices, and active surveillance systems. The findings highlight an urgent call for coordinated clinical and public health interventions to mitigate the spread of highly resistant S. aureus strains and preserve the efficacy of remaining therapeutic options.

REFERENCES

1. Tong, S. Y., Davis, J. S., Eichenberger, E., Holland, T. L., & Fowler, V. G. (2015). Staphylococcus aureus infections: epidemiology, pathophysiology, clinical manifestations, and management. Clinical Microbiology Reviews, 28(3), 603-661. https://doi.org/10.1128/cmr.0013414
2. Gu J, Xiong M, Zhang J, Li Y. Prevalence and characterization of community-associated Staphylococcus aureus isolates from human mastitis in Beijing, China. International Journal of Medical Microbiology. 2024 Jun 1;315:151623.https://doi.org/10.1016/j.ijmm.2024.151623
3. Abbas AA. Staphylococcus aureus in Oral Infections: Epidemiology, Virulence Factors, and Treatment Strategies. Cuestiones de Fisioterapia. 2025 Jan 2;54(2):306-18. https://doi.org/10.48047/CU
4. Lakhundi, S., & Zhang, K. (2018). Methicillin-resistant Staphylococcus aureus: molecular characterization, evolution, and epidemiology. Clinical Microbiology Reviews, 31(4), e00020-18. DOI: 10.1128/CMR.00020-18
5. Sansom SE, Benedict E, Thiede SN, Hota B, Aroutcheva A, Payne D, Zawitz C, Snitkin ES, Green SJ, Weinstein RA, Popovich KJ. Genomic update of phenotypic prediction rule for methicillin-resistant Staphylococcus aureus (MRSA) USA300 discloses jail transmission networks with increased resistance. Microbiology Spectrum. 2021 Aug 31;9(1):10-128.DOI: 10.1128/Spectrum.00376-21
6. Akkou M, Titouche Y, Bentayeb L, Bes M, Laurent F, Ramdani-Bouguessa N. Risk factors for dairy cows mastitis in Algeria, antibiotic resistance and molecular typing of the causative Staphylococcus aureus. Veterinary Research Communications. 2024 Oct;48(5):3007-18. https://doi.org/10.1007/s11259-024-10457
7. Donkor ES, Codjoe FS. Methicillin resistant Staphylococcus aureus and extended spectrum beta-lactamase producing enterobacteriaceae: a therapeutic challenge in the 21st century. The Open Microbiology Journal. 2019 Apr 30;13(1).DOI: 10.2174/1874285801913010094
8. Kaushik A, Kest H, Sood M, Thieman C, Steussy BW, Padomek M, Gupta S. Infective Endocarditis by Biofilm-Producing Methicillin-Resistant Staphylococcus aureus—Pathogenesis, Diagnosis, and Management. Antibiotics. 2024 Nov 25;13(12):1132.https://doi.org/10.3390/antibiotics13121132
9. Esteves MA, Carvalho MF, Viana AS, Martini CL, Longo LG, Silva DN,

Ferreira AL, Ferreira-Carvalho BT, Planet PJ, Figueiredo AM. Decoding the evolutionary history of ST30 Staphylococcus aureus: insights into a potentially silent MSSA bloodstream pathogen. Frontiers in Microbiology. 2025 Apr 9;16:1522747. https://doi.org/10.3389/fmicb.2025.1522747

10. Alfeky AA, Tawfick MM, Ashour MS, El-Moghazy AN. High prevalence of multi-drug resistant methicillin-resistant Staphylococcus aureus in tertiary Egyptian Hospitals. The Journal of Infection in Developing Countries. 2022 May 30;16(05):795-806. https://orcid.org/0000-0002-9825-2198
11. Aubaid, Adnan H. Al-Shawi, Haider A. Al-Dujaili, Nawfal H. A novel antibiotic-like substance isolation from a dermatophyte, Trichophyton rubrum. REV RES MED. 2018, 29(2), pp. 89–100.
12. Lade H, Kim JS. Molecular determinants of β-lactam resistance in methicillin-resistant Staphylococcus aureus (MRSA): an updated review. Antibiotics. 2023 Aug 24;12(9):1362. https://doi.org/10.3390/antibiotics12091362
13. M Shoaib · 2023 MRSA compendium of epidemiology, transmission, pathophysiology, treatment, and prevention within one health framework https://doi.org/10.3389/fmicb.2022.1067284
14. Chambers, H. F., & DeLeo, F. R. (2023). Waves of resistance: Staphylococcus aureus in the antibiotic era. Nature Reviews Microbiology, 21(4), 236-251. https://doi.org/10.1038/s41579-022-00838-2
15. Kieffer, N., Saviola, B., Foster, D., Koller, P., & Adhikari, R. P. (2021). Staphylococcus aureus Toxins: Their Role in Pathogenesis and Their Potential for Therapeutic Applications. Toxins, 13(9), 624. https://doi.org/10.3390/toxins13090624
16. Kourtis, A. P., Hatfield, K., Baggs, J., Mu, Y., See, I., Epson, E., Nadle, J., Kainer, M. A., Dumyati, G., Petit, S., Ray, S. M., Schaffner, W., Townes, J., Jernigan, J., & Cardo, D. (2019). Vital Signs: Epidemiology and Recent Trends in Methicillin-Resistant and in Methicillin-Susceptible Staphylococcus aureus Bloodstream Infections - United States. MMWR. Morbidity and Mortality Weekly Report, 68(9), 214-219. https://doi.org/10.15585/mmwr.mm6809e1
17. Price, J. R., Baker, G., Heath, I., Walker, A. S., Robotham, J. V., Crook, D. W., & Peto, T. E. (2022). Clinical impact of MRSA in hospitals: An evaluation of excess length of stay and mortality in an English NHS trust. BMC Medicine, 10, 33. https://doi.org/10.1186/1741-7015-10-33202
18. Köck, R., Becker, K., & Cookson, B. (2023). Methicillin-resistant Staphylococcus aureus in hospitals. Clinical Microbiology and Infection, 29(1), 33-41. https://doi.org/10.1016/j.cmi.2022.08.022
19. JY Lin · 2025 — Methicillin-resistant Staphylococcus aureus (MRSA) bloodstream infections (BSIs) are a major public health challenge worldwideGlobal insights into MRSA bacteremia: a bibliometric analysis and future outlook. https://doi.org/10.3389/fmicb.2024.1516584
20. Ammar Mehfooz, Maryam Almas, Maria Mukhtar, Afsar Ali, Iqra Arooj, Maryam Khalid, Shahzeera Begum, Rehmatullah Zadran, Mohsan Aslam, & Mehak Khalid. (2024). VIRULENCE FACTORS AND

ANTIBIOTIC RESISTANCE IN STAPHYLOCOCCUS AUREUS: A COMPREHENSIVE STUDY. *Journal of Population Therapeutics and Clinical Pharmacology*, *31*(7), 1485-1493. https://doi.org/10.53555/jptcp.v31i7.7293

21. Beshiru A, Igbinosa IH, Akinnibosun O, Ogofure AG, Dunkwu-Okafor A, Uwhuba KE, Igbinosa EO. Characterization of resistance and virulence factors in livestock-associated methicillin-resistant Staphylococcus aureus. Scientific Reports. 2024 Jun 9;14(1):13235.https://doi.org/10.1038/s41598-024-63963-3

22. Vittorakis, E.; Vica, M.L.; Zervaki, C.O.; Vittorakis, E.; Maraki, S.; Mavromanolaki, V.E.; Schürger, M.E.; Neculicioiu, V.S.; Papadomanolaki, E.; Junie, L.M. A Comparative Analysis of MRSA: Epidemiology and Antibiotic Resistance in Greece and Romania. *Int. J. Mol. Sci.* 2024, *25*, 7535. https://doi.org/10.3390/ijms25147535

23. Co EM, Keen III EF, Aldous WK. Prevalence of methicillin-resistant Staphylococcus aureus in a combat support hospital in Iraq. Military medicine. 2011 Jan 1;176(1):89-93. https://doi.org/10.7205/MILMED-D-09-00126

24. S M'Aiber · 2022 · Cited by 16 — This study describes a high prevalence of antibiotic resistance in patients with trauma-related wounds in Mosul, Iraq. https://doi.org/10.1016/j.jgar.2022.06.022

25. Khudhair MK, AlAubydi MA. Determination the prevalence and antimicrobial susceptibility of bacteria isolated from burns and wounds. Iraqi Journal of Agricultural Sciences. 2023 Feb 22;54(1):93-9.DOI: https://doi.org/10.36103/ijas.v54i1.1679

26. Vinshia JJ, Padmavathy K, Sathyapriya B. Comparison of the VITEK® 2 system with conventional methods for species identification and antimicrobial susceptibility pattern of staphylococcal carrier isolates. International Research Journal of Multidisciplinary Scope (IRJMS). 2024;5(2):940-8.DOI: 10.47857/irjms.2024.v05i02.0689

27. Clinical and Laboratory Standards Institute (CLSI). (2023). Performance standards for antimicrobial susceptibility testing (33rd ed.). CLSI. marketing@clsi.org

28. Anwar**,** K. A., Saadalla, S. M., Muhammad Amin, A. J., Ahmed, S. M., & Qadir, M. K. (2024). Antibiotic susceptibility and phenotypic profile of Staphylococcus species isolated from different clinical samples from health facilities: A cross-sectional study. *SAGE Open Medicine*, *12*, 20503121241306968. https://doi.org/10.1177/20503121241306968

29. chambers, H. F., & Deleo, F. R. (2009). Waves of resistance: Staphylococcus aureus in the antibiotic era. Nature Reviews Microbiology, 7(9), 629-641. https://doi.org/10.1038/nrmicro2200

30. Tluanpuii V, Mahajan R. Detection of the mecA gene and its association with antimicrobial resistance among coagulase-negative staphylococci isolated from clinical samples in a tertiary care hospital: A cross-sectional study. Cureus. 2025 Apr 3;17(4):e81643.DOI: 10.7759/cureus.81643

31. Andrea T.. Feßler, Yang Wang, Congming Wu, Stefan Schwarz,Mobile macrolide resistance genes in staphylococci**,**https://doi.org/10.1016/j.plasmid.2018.05.001

32. Kumar BB, Selvam KP. CARRIER AND CLINICAL-DERIVED REGIONAL VANCOMYCIN RESISTANT STAPHYLOCOCCUS AUREUS (VRSA): PHENOTYPIC SCREENING OF VIRULENCE FACTORS AMONG SELECTIVE ISOLATES. Biochemical & Cellular Archives. 2025 Apr 1;25(1). DOI10.51470/bca.2025.25.1.999

33. Tamara Lopes Rocha de Oliveira, Fernanda Sampaio Cavalcante, Raiane Cardoso Chamon, Rosana Barreto Rocha Ferreira, Kátia Regina Netto dos Santos,Genetic mutations in the quinolone resistance-determining region are related to changes in the epidemiological profile of methicillin-resistant Staphylococcus aureus isolates,Journal of Global Antimicrobial Resistance. https://doi.org/10.1016/j.jgar.2019.05.026

34. Elghanam M, Emara M, Abdelhalim M, Moustafa W. Prevalence and Antibiotic Resistance Patterns of Multidrug-Resistant (MDR) Bacteria Isolated from Pediatric Intensive Care Units. Egyptian Journal of Medical Microbiology. 2024 Jan 1;33(1):119-28.DOI: 10.21608/ejmm.2024.332173

35. Milkias Abebe [a], Getachew Alemkere [b], G izachew Ayele [c]Methicillin and vancomycin-resistant *Staphylococcus aureus* and associated risk factors among patients with wound infection in East Wallaga Zone, Western Ethiopia. https://doi.org/10.1016/j.infpip.2024.100409

36. Keugtae Kim, Environmental occurrence of antibiotic resistance, control measures and challenges in finding therapeutic management https://doi.org/10.1016/j.emcon.2024.100440

Aubaid, Adnan H., Mahdi, Ziadoon H.; Abd-Alraoof, Tabarek S.; Jabbar, Noor M.Detection of mec a, van a and van b genes of staphylococcus aureus isolated from patients in al muthanna province hospitals. *Indian J. Forensic Med. Toxicol.* 2020, 14(2), pp. 1002–1008.

