


# Prevalence of Methicillin-Resistant *Staphylococcus aureus* Among Patients in Hospitals of Taiz City, Yemen

Ayman A. R. Saeed\* , Aya A. H. Radman, Balqees N. M. Al-Sharaabi, Elyas S. H. Abdulmughn, Rafa S. A. Almqtary, Shaima M. S. Al-Buraihi, Heba A. A. Aldumini, Hala M. S. Thabit

Department of Medical Laboratory, Faculty of Medical Sciences, Al Janad University for Sciences and Technology, Taiz, Yemen

\*Corresponding author: [ayman.aa.just@gmail.com](mailto:ayman.aa.just@gmail.com)

## Abstract

**Background:** Methicillin-resistant *Staphylococcus aureus* (MRSA) is a major cause of healthcare-associated infections and poses a significant global public health challenge because of its resistance to  $\beta$ -lactam antibiotics and adverse impact on patient outcomes. Despite its clinical importance, data on the prevalence of MRSA among hospitalized patients in Taiz City, Yemen, remain limited.

**Methods:** A hospital-based cross-sectional study was conducted between October and December 2025 among 150 hospitalized patients selected using a simple random sampling technique. Nasal swab specimens were collected and cultured on mannitol salt agar to isolate *Staphylococcus aureus*. The isolates were identified using standard microbiological methods, and methicilin resistance was determined using the cefoxitin disk diffusion method.

**Results:** The prevalence of MRSA among the study participants was 34.7% (52/150), whereas methicillin-sensitive *Staphylococcus aureus* (MSSA) accounted for 17.3% (26/150) of the isolates. No bacterial growth was observed in 20.7% (31/150) of the collected specimens. A statistically significant association was found between MRSA colonization and prior antibiotic use ( $p < 0.001$ ). However, no significant associations were observed between MRSA positivity and age, sex, chronic diseases, or other clinical variables.

**Conclusion:** The findings demonstrate a relatively high prevalence of MRSA among hospitalized patients in Taiz. The significant association between MRSA and previous antibiotic use highlights the urgent need to strengthen antimicrobial stewardship programs, enhance infection prevention and control measures, and implement continuous surveillance to reduce the spread of antimicrobial resistance in healthcare facilities.

## ARTICLE INFO

### Keywords:

*Staphylococcus aureus*  
MRSA  
Antimicrobial resistance  
Nasal colonization  
Hospitalized patients  
Yemen

### Article History

Received: March 14, 2026

Accepted: June 28, 2026

Published: June 30, 2026

### How to cite this article:

Saeed, A. A. R., Radman, A. A. H., Al-Sharaabi, B. N. M., Abdulmughn, E. S. H., Almqtary, R. S. A., Al-Buraihi, S. M. S., *et al.* (2026). Prevalence of Methicillin-Resistant *Staphylococcus aureus* Among Patients in Hospitals of Taiz City, Yemen. *Yemeni Journal of Life Sciences*, **1**(1), 41–55.

## Introduction

*Staphylococcus aureus* (*S. aureus*) is a Gram-positive, spherical bacterium that commonly colonizes the skin and mucosal surfaces of humans. Approximately 15% of individuals harbor *S. aureus* in the anterior nares (Ngoi et al., 2021). Nasal carriage patterns vary within populations, with nearly 20% persistent carriers, 30% intermittent carriers, and approximately 50% non-carriers (Al-Khawlany et al., 2021). Although it is part of the normal flora, *S. aureus* demonstrates remarkable resilience, enabling survival under environmental stress and resistance to several disinfectants (Hashim et al., 2018).

Clinically, *S. aureus* is a major human pathogen responsible for a wide spectrum of diseases, ranging from superficial skin and soft tissue infections to severe and life-threatening conditions, such as pneumonia, septicemia, and infective endocarditis (Silva et al., 2022). It remains one of the leading causes of healthcare-associated infections worldwide. Since the introduction of penicillin in 1942, *S. aureus* has continuously developed resistance to antimicrobial agents (Al-Khawlany et al., 2021).

Organisms employ multiple mechanisms to evade antibiotic activity, including enzymatic drug inactivation, alteration of target sites, reduced membrane permeability, active efflux pumps, and other adaptive resistance pathways (Hashim et al., 2018). Despite advances in antimicrobial therapy, staphylococcal infections continue to contribute significantly to global morbidity and mortality (Dilnessa & Bitew, 2016).

The risk of invasive infection is particularly elevated among older adults colonized with *S. aureus*, especially those with comorbidities such as congestive heart failure, diabetes mellitus, chronic lung disease, or renal failure. These conditions are frequently observed in bedridden patients receiving home care or residing in long-term care facilities (LTCFs) (Li et al., 2025).

Methicillin-resistant *Staphylococcus aureus* (MRSA) is a major clinical and public health concern due to its resistance to  $\beta$ -lactam antibiotics (Aweis et al., 2025). *S. aureus*, including MRSA strains, are Gram-positive, cluster-forming facultative anaerobic cocci capable of fermenting carbohydrates. On solid culture media, they produce colonies ranging from white to golden-yellow pigmentation and ferment mannitol, resulting in characteristic yellow coloration on Mannitol Salt Agar (MSA) (Hashim et al., 2018).

Methicillin resistance is primarily mediated by the acquisition of the *mecA* gene, which encodes an altered penicillin-binding protein (PBP2a) with low affinity for  $\beta$ -lactam antibiotics. This gene is carried on a mobile genetic element known as the staphylococcal cassette chromosome *mec* (SCC*mec*) (Fooladi et al., 2015). MRSA isolates frequently harbor additional resistance determinants, contributing to multidrug resistance and further limiting therapeutic options (Aweis et al., 2025).

Initially, MRSA infections were mainly confined to healthcare settings and affected elderly, immunocompromised, or postoperative patients. However, since the mid-1990s, community-associated MRSA (CA-MRSA) strains have emerged, causing infections in otherwise healthy

individuals without healthcare exposure, including athletes, military recruits, and incarcerated populations (Otto, 2012).

Although considerable attention has been focused on MRSA, methicillin-susceptible *S. aureus* (MSSA) also contributes substantially to the global disease burden. MSSA lineages express multiple virulence factors and may acquire resistance determinants via horizontal gene transfer, posing an ongoing challenge to public health (Ngoi et al., 2021).

Importantly, antimicrobial resistance in *S. aureus* extends beyond methicillin and other  $\beta$ -lactam antibiotics. The increasing prevalence of resistant strains contributes to higher mortality rates, prolonged hospitalization, and increased healthcare costs (Al-Humaidan et al., 2015).

Despite the available studies on MRSA prevalence, data regarding its distribution among hospitalized patients in Taiz hospitals remain limited. This gap in local epidemiological evidence highlights the need for further investigation. Therefore, this study aimed to determine the prevalence of MRSA among hospitalized patients in Taiz City, Yemen, and to generate evidence to support infection control and antimicrobial stewardship programs.

## Materials and Methods

### Study Design

A hospital-based cross-sectional study was conducted to determine the prevalence of MRSA colonization among hospitalized patients in Taiz City, Yemen. This design was chosen because it allows the estimation of the prevalence of a specific condition within a defined population at a particular point in time, as well as the assessment of potential associations with selected demographic and clinical variables.

### Study Setting and Duration

This study was conducted in selected hospitals in Taiz City, Yemen, which provide a wide range of healthcare services and receive patients from different districts of the governorate. Sample collection and data acquisition were conducted over a five-week period, from October to December, 2025. All laboratory procedures were performed in a designated microbiology laboratory under standard aseptic conditions and according to established microbiological practices.

### Study Population and Sampling

#### *Study Population*

The study population comprised hospitalized patients who were admitted to the participating hospitals during the study period.

#### *Inclusion Criteria*

Patients admitted during the study period who provided informed consent were included.

#### *Exclusion Criteria*

Patients who declined to participate or refused nasal swab collection were excluded.

#### *Sample Size and Sampling Technique*

The sample size was calculated using Fisher's formula for a single population proportion (Fisher, 1991):

$$n = Z^2 \times p(1 - p) / d^2$$

where:

n = required sample size

Z = standard normal deviation (1.96 at 95% confidence level)

p = estimated prevalence

d = margin of error

Based on this calculation, 150 hospitalized patients were included. Simple random sampling was used to minimize selection bias and ensure equal probability of selection among eligible participants.

### **3.4 Sample Collection and Transport**

Nasal swab specimens were collected aseptically from the anterior nares of each participant using sterile cotton swabs moistened with sterile normal saline. The swabs were gently rotated in both nostrils and immediately placed into sterile containers labeled with unique identification codes. Samples were transported promptly to the microbiology laboratory under appropriate conditions to maintain specimen integrity and prevent contamination.

#### **Laboratory Procedures**

All microbiological procedures were performed following standard methods for the isolation and identification of *Staphylococcus aureus* (Cheesbrough, 2006).

##### *Culture and Isolation on Mannitol Salt Agar*

MSA was used as a selective and differential medium for isolation of *S. aureus*. The medium was prepared according to the manufacturer's instructions and sterilized by autoclaving at 121°C for 15 minutes. After cooling to 50–55°C, it was poured into sterile Petri dishes under aseptic conditions and allowed to solidify.

Each nasal swab was streaked onto MSA plates and incubated aerobically at 37°C for 24–48 hours. Yellow colonies with surrounding yellow zones were considered presumptive *S. aureus* due to mannitol fermentation and phenol red indicator change.

##### *Gram Staining*

Presumptive colonies were examined using the Gram staining technique. Smears were prepared, heat-fixed, and stained sequentially with crystal violet, iodine solution, decolorized with acetone-alcohol, and counterstained with safranin. Slides were examined under a light microscope (100×

oil immersion). Gram-positive cocci in grape-like clusters were considered characteristic of *Staphylococcus* species.

### *Biochemical Identification*

**Catalase Test:** The catalase test was performed by adding hydrogen peroxide to a colony smear. Immediate bubble formation indicated a positive result, confirming *Staphylococcus* species.

**Coagulase Test:** The tube coagulase test was used to confirm *S. aureus*. Plasma (0.2 mL) was mixed with 0.8 mL of bacterial broth and incubated at 35–37°C. Clot formation after 1–3 hours indicated a positive result.

### *Antimicrobial Susceptibility Testing*

Antimicrobial susceptibility testing was performed using the Kirby–Bauer disk diffusion method on Mueller–Hinton agar. A bacterial suspension was prepared and adjusted to the 0.5 McFarland standard. The inoculum was evenly spread over the agar surface using a sterile swab.

MRSA detection was performed using a 30 µg ceftioxin disk. Plates were incubated at 35–37°C for 18–24 hours. Zone diameters were measured in millimeters and interpreted according to CLSI guidelines (CLSI, 2020).

## **Data Collection**

Demographic and clinical data were collected using a structured questionnaire covering sociodemographic characteristics, healthcare exposure history, chronic diseases, and antibiotic use. Data were recorded using coded identifiers to maintain confidentiality.

## **Statistical Analysis**

Data were entered and analyzed using Microsoft Excel 2021 and IBM SPSS Statistics version 27. Descriptive statistics (frequencies and percentages) were used for categorical variables. Associations between variables were assessed using the chi-square test. A p-value < 0.05 was considered statistically significant. All tests were two-tailed.

## **Results**

### **Demographic Characteristics of the Study Sample**

The study included 150 participants, with a higher proportion of females (56.7%) than males (43.3%). The largest age group was 18–34 years (31.3%), followed by 35–49 years (19.3%). Urban and rural residents were nearly equally represented. Regarding educational level, almost half of the participants were illiterate (44.7%), whereas university education represented the lowest proportion (15.3%). Most participants were categorized as “others” in occupation (59.3%). More than half of the participants were recruited from the surgical department (55.3%) (Table 1).

Table1 Demographic characteristics of the sample

Variables	Category	Frequency (No.)	Percentage (%)
Age group	5-17	24	16
	18-34	47	31.3
	35-49	29	19.3
	50-64	27	18
	65<	23	15.3
Gender	Male	65	43.3
	Female	85	56.7
Residents	Urban	73	48.6
	Rural	77	51.3
Educational level	Illiterate	67	44.7
	Primary	24	16
	Secondary	36	24
	University	23	15.3
Occupation	Student	10	6.7
	Worker	51	34
	Health staff	0	0
	Others	89	59.3
Hospital department	Surgical	83	55.3
	ICU	0	0
	Emergency	6	4
	Internal Medicine Maternity	35	23.3
	Oncology Inpatient	13	8.7

### Clinical and Exposure Characteristics

Surgery-related conditions were the most common reasons for hospital admission (32.7%), followed by routine checkups and chronic disease follow-ups. During the past 12 months, urinary tract infections (22.5%) and pneumonia (21.1%) were the most frequently reported. Approximately 30.7% of the participants reported previous exposure to blood or body fluids (Table 2).

Table 2 Clinical and exposure characteristics of the samples.

Variables	Category	Frequency (No.)	Percentage (%)
Reason for hospital visits	Respiratory	19	12.7
	Surgical Infection	49	32.7
	Fever	17	11.3
	Chronic disease Follow-up	27	18
	Routine check	1	0.7
	others	37	24.6
Previous infectious diseases (last 12 months)	Pneumonia	30	21.1
	UTI	32	22.5
	Hepatitis B or C	9	6.3
	Tuberculosis	1	0.7
	Skin infection	20	14.1
Exposure to contaminated blood or fluids	others	50	35.2
	YES	46	30.7
	NO	104	69.3

### Chronic Diseases and Immune Status

Hypertension and cardiovascular diseases were the most prevalent comorbidities (22.7%), followed by chronic kidney disease (17.3%) and diabetes mellitus (15.3%). Immunosuppressive conditions and cancer were reported in 14% and 12.7% of participants, respectively. No cases of HIV/AIDS were reported (Table 3).

Table 3 Distribution of chronic diseases among sample

Chronic condition	Yes	No
	No. (%)	No. (%)
Diabetes mellitus	23 (15.3)	127 (84.7)
Hypertension / Heart disease	34 (22.7)	116 (77.3)
Chronic respiratory disease e.g. asthma	14 (9.3)	136 (90.7)
Chronic kidney disease	26 (17.3)	124 (82.7)
Immunosuppressive therapy/ Autoimmune disease	21 (14)	129 (86)
Cancer	19 (12.7)	131 (87.3)
HIV/AIDS	0(0)	150(100)
Others	1 (0.67)	149 (99.33)

## Antibiotic Use Pattern

A total of 66% of the participants reported antibiotic use within the previous three months. Most antibiotics were prescribed by physicians (63.3%), while 32.1% were obtained directly from pharmacies without a prescription. Only 44.3% of participants reported always completing the full antibiotic course. Culture testing prior to antibiotic modification was reported by 34.7% of the participants (Table 4).

Table 4 Pattern of antibiotic use among samples

Variable	Category	Frequency (No.)	Percentage (%)
Use antibiotics in the past 3 months	Yes	99	66
	No	51	34
Prescription source	By doctor	83	63.3
	Pharmacy	42	32.1
	Leftover	4	3.1
	Shared from other	2	1.5
	Always	58	44.3
Completed full antibiotic course	Usually	20	15.3
	Sometimes	19	14.5
	Never	13	9.9
Antibiotic changed after culture result	I don't know	21	16
	Yes	23	44.2
	No	19	36.5
Did you do the culture test?	I don't know	10	19.3
	Yes	52	34.7
	No	78	52
	I don't know	20	13.3

Variable-specific Sample Size (n): Variations in totals across categories are due to unanswered questions (missing data) by some participants.

Filtered Analysis: The question regarding antibiotic adjustment (Antibiotic changed after culture result) was conditionally filtered and analyzed only for participants who underwent a culture test (n = 52).

Note: Missing responses were excluded from the specific analyses; therefore, totals may vary across variables.

## Culture Results and MRSA Detection

MRSA was detected in 34.7% (52/150) of participants, while MSSA accounted for 17.3% (26/150). Non-*Staphylococcus aureus* growth was observed in 27.3% (41/150), and no bacterial growth was recorded in 20.7% (31/150) (Table 5).

Table 5. Distribution of culture result and MRSA presence

Culture results	Frequency (No.)	Percentage (%)
Non- <i>Staphylococcus aureus</i>	41	27.3
MRSA positive	52	34.7
MSSA (Methicillin-Sensitive <i>S. aureus</i> )	26	17.3
No growth	31	20.7
Total	150	100

## Cefoxitin Disk Diffusion Results

Among *Staphylococcus aureus* isolates (n = 78), 52 (66.7%) were classified as MRSA based on cefoxitin inhibition zones  $\leq 21$  mm, while 26 (33.3%) were identified as MSSA ( $\geq 22$  mm) (Table 6).

Table 6 Distribution of *Staphylococcus* isolated according to Cefoxitin inhibition Zone diameters (n=150)

Inhibition Zone (mm)	Number of isolates (No.)	Percentage (%)	Interpretation
$\leq 21$ mm	52	66.7	MRSA
$\geq 22$ mm	26	33.3	MSSA
Total	78	100	

## Association Between MRSA and Risk Factors

MRSA colonization was significantly higher among participants with a history of antibiotic use (50.5%) compared to those without prior antibiotic exposure (3.9%), and this association was statistically significant ( $p < 0.001$ ).

No statistically significant associations were observed between MRSA colonization and gender, age group, chronic diseases, or exposure to blood or body fluids (Table 7).

Table 7 Association between MRSA positivity and risk factors.

Variable	Category	MRSA		P. value*
		No. (%)	No. (%)	
Gender	Male	21 (32.3)	44 (67.7)	0.598
	Female	31 (36.5)	54 (63.5)	
Age group	5-17	8 (33.3)	16 (66.7)	0.992
	18-34	16 (34)	31 (66)	
	35-49	11 (37.9)	18 (62.1)	
	50-64	9 (33.3)	18 (66.7)	
	65<	8 (34.8)	15 (65.2)	
Previous antibiotics use	Yes	50 (50.5)	49 (49.5)	< 0.001
	No	2 (3.9)	49 (96.1)	
Chronic disease	Yes	29 (34.9)	54 (65.1)	0.939
	No	23 (34.3)	44 (65.7)	
Exposure to blood or fluids	Yes	17 (36.9)	29 (63.1)	0.693
	No	35 (33.6)	69 (66.4)	

\*P-values were calculated using the chi-square test.

## Discussion

This study evaluated 150 hospitalized patients in Taiz City, Yemen, with a slightly higher proportion of females (56.7%) than males (43.3%). The majority of participants were aged 18–34 years (31.3%), followed by 35–49 years (19.3%), and urban and rural residents were nearly equally represented in the sample. Almost half of the participants were illiterate (44.7%), while 15.3% had a university-level education. Most participants were categorized under “others” regarding occupation (59.3%), and more than half were recruited from the surgical departments (55.3%).

The observed age distribution aligns with previous studies by [Aweis et al. \(2025\)](#) and [Al-Khawlany et al. \(2021\)](#), whereas it contrasts with that of [Dilnessa and Bitew \(2016\)](#), reflecting differences in target populations and study settings. Gender differences were consistent with some studies ([Aweis et al., 2025](#); [Dilnessa & Bitew, 2016](#)) but differed from others ([Al-Khawlany et al., 2021](#)), likely due to variations in admission patterns and local demographics. Similarly, residence, educational, and occupational distributions showed discrepancies compared to prior studies ([Hashim et al., 2018](#); [Al-Humaidan et al., 2015](#); [Aweis et al., 2025](#); [Al-Safani et al., 2018](#)), which may be attributed to differences in sampling strategies and population characteristics. Notably, while several prior studies focused on ICU patients, the current study mainly recruited participants from the surgical department, similar to [Hashim et al. \(2018\)](#).

Surgical infections were the most common reason for hospital visits (32.7%), followed by chronic disease follow-up and other conditions. Within the previous 12 months, urinary tract infections (22.5%) and pneumonia (21.1%) were prevalent, and approximately one-third of participants reported prior exposure to contaminated blood or body fluids (30.7%). These findings indicate the burden of both surgical and infectious conditions among hospitalized patients, which may increase susceptibility to colonization or infection with resistant organisms, such as MRSA, especially in the presence of chronic comorbidities, including hypertension, heart disease, chronic kidney disease, diabetes, immunosuppressive conditions, and cancer.

A high proportion of participants (66%) reported antibiotic use within the previous three months. While most antibiotics were prescribed by physicians (63.3%), nearly one-third were obtained without prescription, and only 44.3% of participants reported completing the full antibiotic course. Culture testing prior to antibiotic modification was performed in only 34.7% of the cases. These findings indicate potential challenges in antibiotic stewardship and the risk of resistance development, consistent with previous reports ([Rajendran et al., 2019](#); [Limaye et al., 2018](#); [Llor et al., 2013](#); [Zhang et al., 2020](#); [Sturkie et al., 2021](#); [Skodvin et al., 2019](#)).

MRSA prevalence in this study was 34.7%, with MSSA at 17.3%, non-Staphylococcus aureus isolates at 27.3%, and no growth in 20.7% of samples, highlighting a substantial MRSA burden among hospitalized patients in Taiz City. These results differ from those of some previous studies, such as those of [Hashim et al. \(2018\)](#) and [Al-Khawlany et al. \(2021\)](#), reflecting variations in study populations, diagnostic methods, and local epidemiology. Using cefoxitin disk diffusion, MRSA isolates were identified based on standard CLSI guidelines, although the lack of a quality control strain (e.g., *S. aureus* ATCC 25923) represents a limitation due to local resource constraints. Nevertheless, adherence to standard laboratory protocols ensured methodological reliability.

Comparisons with prior studies reveal differences in MRSA and MSSA prevalence, including [Silva et al. \(2022\)](#) and [Dilnessa and Bitew \(2016\)](#), while the findings align with those of [Fooladi et al. \(2015\)](#), who also reported significant MRSA presence. These variations may result from differences in molecular detection techniques, geographic location, patient population, and infection control practices.

A statistically significant association was observed between prior antibiotic use and MRSA colonization ( $p < 0.001$ ), with 50.5% MRSA prevalence among recent antibiotic users versus 3.9% among non-users. No significant associations were found with sex, age, chronic disease status, or exposure to contaminated blood or fluids, contrasting with some previous reports that identified male gender as a predictor of MRSA colonization ([Austin et al., 2003](#)). These results reinforce the critical importance of antibiotic stewardship in preventing the emergence and spread of antimicrobial resistance. Discrepancies with other studies ([Al-Humaidan, 2015](#); [Aweis et al., 2025](#)) highlight the influence of local prescribing patterns and healthcare practices. Overall, the findings underscore a high burden of MRSA among hospitalized patients in Taiz City and

emphasize the need for enhanced infection control measures, rational antibiotic use, and ongoing surveillance to mitigate antimicrobial resistance in the region.

Given the high MRSA prevalence and its strong association with excessive antibiotic use revealed by this study, there is an urgent need to explore alternative therapeutic sources derived from natural products. A recent review has indicated that phytochemicals possess multitarget mechanisms and synergistic effects with conventional antibiotics, thereby enhancing therapeutic efficacy and limiting the development of bacterial resistance (Al-Arnoot et al., 2025).

### Study limitations

This study had several limitations. First, the sample was predominantly from the surgical department (55.3%) and excluded ICU patients, which limits generalizability. Second, the lack of a reference strain (*S. aureus* ATCC 25923) and sole reliance on phenotypic cefoxitin testing without molecular (*mecA*) confirmation may have reduced the accuracy of MRSA identification. Third, self-reported antibiotic use data were subject to recall bias, and verification against medical records was not possible. Fourth, the cross-sectional design precluded any causal inferences. Despite these limitations, our findings provide essential baseline prevalence data for the region and underscore the urgent need for strengthened surveillance and stewardship.

### Conclusions

This study demonstrated a relatively high prevalence of MRSA among hospitalized patients in Taiz City, accounting for 34.7% of all participants. No significant associations were observed between MRSA colonization and demographic characteristics or chronic diseases. However, prior antibiotic use showed a significant relationship with MRSA positivity, highlighting the impact of inappropriate antibiotic practices on the emergence and spread of antimicrobial resistance. These findings indicate that MRSA represents an important clinical and public health concern in the studied hospitals.

### Abbreviations

AMR	Antimicrobial Resistance
CLSI	Clinical and Laboratory Standards Institute
ICU	Intensive Care Unit
IPC	Infection Prevention and Control
MDR	Multidrug-Resistant
MRSA	Methicillin-Resistant <i>Staphylococcus aureus</i>
MSA	Mannitol Salt Agar
MSSA	Methicillin-Sensitive <i>Staphylococcus aureus</i>

## Acknowledgements

The authors would like to express their sincere gratitude to the hospitals in Taiz City that cooperated and facilitated the data collection process for this study. The authors also extend their appreciation to Al Janad University for Science and Technology for its academic support and encouragement throughout the research process. Special thanks are given to all participants who contributed to this study.

## Declarations

### Funding

This research received no external funding.

### Author Contributions

Conceptualization, A.A.R.S.; methodology, A.A.R.S. and A.A.H.R.; investigation, A.A.H.R., B.N.M.A., E.S.H.A., R.S.A.A., S.M.S.A., H.A.A.A., and H.M.S.T.; data curation, B.N.M.A., E.S.H.A., and R.S.A.A.; formal analysis, A.A.R.S. and A.A.H.R.; writing original draft preparation, A.A.H.R., B.N.M.A., and S.M.S.A.; writing review and editing, A.A.R.S. and A.A.H.R.; supervision, A.A.R.S. All authors have read and agreed to the published version of the manuscript.

### Competing Interests

The authors declare no competing interests.

### Ethics Statement

Ethical approval and administrative permissions were obtained from the relevant authorities following submission of formal letters from the Faculty of Medical Sciences, Al Janad University for Science and Technology NO. 13-2025. The study objectives, procedures, potential risks, and benefits were clearly explained to all participants. Informed consent was obtained prior to sample collection. Confidentiality and anonymity were strictly maintained throughout the study.

### Data Availability Statement

All data generated or analyzed during this study are included in this published article.

### AI disclosure

Artificial intelligence assisted tools, including Chat GPT and Grammarly, were used solely for language editing and grammar improvement. These tools were not used to generate scientific content, data analysis, results, discussion, or conclusions. All scientific content was developed and carefully reviewed by the authors, who take full responsibility for the accuracy and integrity of the manuscript.

## References

- Al-Arnoot, S., Abdullah, Q. Y., Al-Maqtari, M. A., Ibrahim, H. M., Al-Shamahy, H. A., Salah, E. M., et al. (2025). Multitarget antimicrobial mechanisms of plant extracts: A review of harnessing phytochemicals against drug-resistant pathogens. *Sana'a University Journal of Medicine and Health Sciences*, 19(4), 292–309. <https://doi.org/10.59628/jchm.v19i4.1936>
- Al-Humaidan, O. S., El-Kersh, T. A., & Al-Akeel, R. A. (2015). Risk factors of nasal carriage of *Staphylococcus aureus* and methicillin-resistant *Staphylococcus aureus* among health care staff in a teaching hospital in central Saudi Arabia. *Saudi Medical Journal*, 36(9), 1084–1090. <https://doi.org/10.15537/smj.2015.9.12460>
- Al-Khawlany, R. S., Edrees, W. H., Al-Jaufy, A. Y., Nasher, M. A., Al-Shehari, W. A., Reem, A., et al. (2021). Prevalence of methicillin-resistant *Staphylococcus aureus* and antibacterial susceptibility among patients with skin and soft tissue infection at Ibb City, Yemen. *PSM Microbiology*, 6(1), 1–11. <https://psmjournals.org/index.php/microbiol/article/view/535>
- Al-Safani, A. M. A., Al-Shamahy, H. A., & Al-Moyed, K. A. (2018). Prevalence, antimicrobial susceptibility pattern and risk factors of MRSA isolated from clinical specimens among military patients at 48 Medical Compound in Sana'a City, Yemen. *Universal Journal of Pharmaceutical Research*, 3(3), 39–43. <https://doi.org/10.22270/ujpr.v3i3.165>
- Austin, T. W., Austin, M. A., McAlear, D. E., Coleman, B. T., Osoba, A. O., Thaqafi, A. O., et al. (2003). MRSA prevalence in a teaching hospital in Western Saudi Arabia. *Saudi Medical Journal*, 24(12), 1313–1316. <https://smj.org.sa/content/24/12/1313>
- Aweis, A. D. H., Ga'al, H., Ishaq Aweis, D. M., & Hassan, G. D. (2025). Nasal carriage of methicillin-resistant *Staphylococcus aureus* in healthcare workers at Banadir Hospital, Mogadishu, Somalia. *Frontiers in Tropical Diseases*, 6, 1425042. <https://doi.org/10.3389/fitd.2025.1425042>
- Cheesbrough, M. (2006). *District laboratory practice in tropical countries: Part 2* (2nd ed.). Cambridge University Press. <https://doi.org/10.1017/CBO9780511543470>
- Clinical and Laboratory Standards Institute (CLSI). (2020). *Performance standards for antimicrobial susceptibility testing* (36th ed.). CLSI supplement M100. Clinical and Laboratory Standards Institute. <https://clsi.org/shop/standards/m100/>
- Dilnessa, T., & Bitew, A. (2016). Prevalence and antimicrobial susceptibility pattern of methicillin-resistant *Staphylococcus aureus* isolated from clinical samples at Yekatit 12 Hospital Medical College, Addis Ababa, Ethiopia. *BMC Infectious Diseases*, 16(1), 398. <https://doi.org/10.1186/s12879-016-1742-5>
- Fisher, A. A., Laing, J. E., Stoeckel, J. E., & Townsend, J. W. (1991). *Handbook for family planning operations research design* (2nd ed.). Population Council. <https://doi.org/10.31899/rh10.1039>
- Fooladi, A. A. I., Ashrafi, E., Tazandareh, S. G., Koosha, R. Z., Rad, H. S., Amin, M., et al. (2015). The distribution of pathogenic and toxigenic genes among MRSA and MSSA clinical isolates. *Microbial Pathogenesis*, 81, 60–66. <https://doi.org/10.1016/j.micpath.2015.03.013>
- Hashim, A. E. M., Ali, A. I., Elmola, K., Ameen, M. A., & Awdalla, H. (2018). Nasal colonization of methicillin-resistant *Staphylococcus aureus* among medical residents in Al-Azhar University Hospital, Damietta branch. *Al-Azhar Assiut Medical Journal*, 16(1), 87–95. <https://doi.org/10.4103/1687-1693.244149>
- Li, J., Cheng, F., Wei, X., Bai, Y., Wang, Q., Li, B., et al. (2025). Methicillin resistant *Staphylococcus aureus* (MRSA): Resistance, prevalence, and coping strategies. *Antibiotics*, 14(8), 771. <https://doi.org/10.3390/antibiotics14080771>

- Limaye, D., Limaye, V., Fortwengel, G., & Krause, G. (2018). Self-medication practices in urban and rural areas of Western India: A cross sectional study. *International Journal of Community Medicine and Public Health*, 5(7), 2672–2685. <https://doi.org/10.18203/2394-6040.ijcmph20182596>
- Llor, C., Hernández, S., Bayona, C., Moragas, A., Sierra, N., Hernández, M., et al. (2013). A study of adherence to antibiotic treatment in ambulatory respiratory infections. *International Journal of Infectious Diseases*, 17(3), e168–e172. <https://doi.org/10.1016/j.ijid.2012.09.012>
- Ngoi, S. T., Niek, W. K., Lee, Y. W., AbuBakar, S., & Teh, C. S. J. (2021). Genomic analysis revealed a novel genotype of methicillin-susceptible *Staphylococcus aureus* isolated from a fatal sepsis case in a dengue patient. *Scientific Reports*, 11(1), 4228. <https://doi.org/10.1038/s41598-021-83661-8>
- Otto, M. (2012). MRSA virulence and spread. *Cellular Microbiology*, 14(10), 1513–1521. <https://doi.org/10.1111/j.1462-5822.2012.01832.x>
- Rajendran, A., Kulirankal, K. G., Rakesh, P. S., & George, S. (2019). Prevalence and pattern of antibiotic self-medication practice in an urban population of Kerala, India: A cross-sectional study. *Indian Journal of Community Medicine*, 44(Suppl. 1), S42–S45. [https://doi.org/10.4103/ijcm.IJCM\\_33\\_19](https://doi.org/10.4103/ijcm.IJCM_33_19)
- Silva, L. P., Fortaleza, C. M. C. B., Teixeira, N. B., Silva, L. T. P., de Angelis, C. D., & Ribeiro de Souza da Cunha, M. D. L. (2022). Molecular epidemiology of *Staphylococcus aureus* and MRSA in bedridden patients and residents of long-term care facilities. *Antibiotics*, 11(11), 1526. <https://doi.org/10.3390/antibiotics11111526>
- Skodvin, B., Wathne, J. S., Lindemann, P. C., Harthug, S., Nilsen, R. M., Charani, E., et al. (2019). Use of microbiology tests in the era of increasing AMR rates: A multicentre hospital cohort study. *Antimicrobial Resistance & Infection Control*, 8(1), 28. <https://doi.org/10.1186/s13756-019-0480-z>
- Sturkie, E. K., Moore, C. R., Caulfield, C. A., Schmid, E., Lachiewicz, A. M., & Stephens, J. R. (2021). Frequency and yield of blood cultures for observation patients with skin and soft tissue infections. *The American Journal of Emergency Medicine*, 44, 161–165. <https://doi.org/10.1016/j.ajem.2021.02.026>
- Zhang, G., Zhang, Y., Chen, M., & Zhang, F. (2020). Comparison of different bacteriological testing strategies and factors for bacteriological confirmation among pulmonary TB patients: A retrospective study in Tianjin, China, 2017–2018. *BMC Infectious Diseases*, 20(1), 548. <https://doi.org/10.1186/s12879-020-05273-3>