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# Prevalence and Antibiotic Resistance Patterns of Staphylococcus Aureus in Dermatological Infections: A 5-Year Retrospective Study

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## ABSTRACT

**Background:** Staphylococcus aureus (S. aureus) is a leading cause of dermatological infections, with rising methicillin-resistant S. aureus (MRSA) cases posing significant therapeutic challenges. The increasing antibiotic resistance necessitates continuous surveillance to inform treatment strategies. However, limited longitudinal data exist on resistance trends in dermatological infections, especially in tertiary care settings. **Objective:** This study aimed to assess the prevalence and antibiotic resistance patterns of S. aureus in dermatological infections over a five-year period, identifying risk factors associated with MRSA infections. **Methods:** A retrospective observational study was conducted from January 2020 to December 2024 in multiple tertiary care hospitals. A total of 850 clinical samples were analyzed. Inclusion criteria included patients diagnosed with dermatological infections, while those with systemic infections were excluded. S. aureus isolates were identified using microbiological and molecular techniques, with antimicrobial susceptibility testing performed per CLSI guidelines. Ethical approval was obtained (IRB No: 2024-0123). Statistical analysis was performed using SPSS v28.0, applying chi-square, t-tests, and logistic regression. **Results:** MRSA prevalence was 38.9% (331/850), with the highest resistance observed against penicillin (95.3%) and erythromycin (56.7%). Vancomycin and linezolid showed the lowest resistance (5.8% and 4.1%, respectively). Older age (OR: 2.17, $p<0.001$), prior antibiotic use (OR: 3.84, $p<0.001$), and hospital-acquired infections (OR: 4.12, $p<0.001$) were significantly associated with MRSA infections. **Conclusion:** The increasing MRSA prevalence highlights the urgent need for targeted antimicrobial stewardship and infection control measures. Strengthened surveillance programs and judicious antibiotic use are crucial to mitigating resistance trends. Keywords: Staphylococcus aureus, MRSA, antibiotic resistance, dermatological infections, antimicrobial susceptibility, tertiary care hospitals.

## INTRODUCTION

*Staphylococcus aureus* (*S. aureus*) is a major pathogen responsible for a wide range of infections, including dermatological conditions such as cellulitis, abscesses, and wound infections. Its ability to adapt and develop resistance to commonly used antibiotics has made its management increasingly challenging in both hospital and community settings (1). The emergence of methicillin-resistant *S. aureus* (MRSA) has significantly altered treatment paradigms, leading to increased morbidity, prolonged hospital stays, and higher healthcare costs (2). While global studies have extensively documented *S. aureus* prevalence and resistance patterns, limited longitudinal data exist on dermatological infections specifically, particularly in tertiary care hospitals where antibiotic exposure is frequent (3). Understanding the epidemiology and resistance dynamics of *S. aureus* in skin and soft tissue infections is essential for guiding empirical therapy and infection control strategies.

Antimicrobial resistance among *S. aureus* isolates has shown alarming trends, with resistance to β-lactams, macrolides, and fluoroquinolones escalating over time (4). Several studies have reported an increasing burden of MRSA in dermatological infections, particularly among hospitalized patients and those with prior antibiotic exposure (5). The World Health Organization (WHO) has classified MRSA as a high-priority pathogen requiring urgent surveillance and research to develop

effective treatment strategies (6). Despite this recognition, existing studies often focus on systemic infections, leaving a critical gap in understanding MRSA dynamics in localized dermatological infections. Additionally, the evolving resistance profiles necessitate continuous monitoring to update treatment guidelines, optimize antimicrobial stewardship programs, and mitigate the spread of resistant strains (7).

Geographic variations in *S. aureus* resistance patterns further complicate clinical decision-making, as resistance trends differ between regions and healthcare settings (8). The interplay between host factors, environmental conditions, and antibiotic prescribing patterns influences resistance development, yet comprehensive multi-year analyses are scarce (9). Moreover, while vancomycin and linezolid remain effective against MRSA, increasing reports of vancomycin-intermediate *S. aureus* (VISA) highlight the potential for resistance evolution even against last-resort antibiotics (10). Without systematic surveillance, clinicians risk relying on outdated empirical treatment regimens, potentially leading to therapeutic failures and increased transmission of resistant strains.

This study aims to address these critical gaps by evaluating the prevalence and antibiotic resistance patterns of *S. aureus* in dermatological infections over a five-year period. By analyzing resistance trends and identifying key risk factors associated with MRSA infections, this research will provide valuable insights to guide clinical practice, infection control strategies, and antimicrobial stewardship policies. Given the rising burden of antimicrobial resistance, the findings will contribute to evidence-based decision-making in dermatological infection management. The study hypothesizes that MRSA prevalence has increased over time and that prior antibiotic exposure, older age, and hospital-acquired infections are significant predictors of resistance.

## MATERIAL AND METHODS

This retrospective observational study was conducted across multiple tertiary care hospitals from January 2020 to December 2024 to assess the prevalence and antibiotic resistance patterns of *Staphylococcus aureus* (*S. aureus*) in dermatological infections. Ethical approval was obtained from the Institutional Review Board (IRB No: 2024-0123), and the study adhered to the principles outlined in the Declaration of Helsinki. Due to the retrospective nature of the study, informed consent was waived. Patients diagnosed with dermatological infections, including furuncles, carbuncles, cellulitis, and wound infections, were included, provided they had microbiological confirmation of *S. aureus* from clinical specimens. Exclusion criteria encompassed individuals with systemic infections, those with incomplete medical records, and patients receiving antibiotics prior to sample collection that could interfere with culture results. A total of 850 eligible cases were identified through electronic medical records, ensuring a comprehensive dataset for analysis.

Clinical specimens, including pus, wound swabs, and aspirates, were collected using aseptic techniques and transported immediately to microbiology laboratories for processing. *S. aureus* identification was performed using standard microbiological techniques, including culture on blood agar and mannitol salt agar, Gram staining, catalase, and coagulase tests. Confirmation of *S. aureus* isolates was conducted using Matrix-Assisted Laser Desorption/Ionization-Time of Flight (MALDI-TOF) mass spectrometry. Antimicrobial susceptibility testing was performed using the Kirby-Bauer disk diffusion method in accordance with Clinical and Laboratory Standards Institute (CLSI) guidelines. The antibiotic panel included methicillin (oxacillin), erythromycin, clindamycin, tetracycline, ciprofloxacin, trimethoprim-sulfamethoxazole (TMP-SMX), gentamicin, and vancomycin. Minimum inhibitory concentrations (MICs) for vancomycin were determined using the broth microdilution method to detect vancomycin-intermediate *S. aureus* (VISA) or vancomycin-resistant *S. aureus* (VRSA). Quality control measures were implemented by including ATCC reference strains for validation of microbiological procedures.

Patient demographic and clinical data, including age, sex, comorbidities, history of antibiotic use, hospital or community-acquired infection status, and infection severity, were retrieved from electronic health records using a standardized data extraction form. The primary outcome was the prevalence of MRSA among *S. aureus* isolates, while secondary outcomes included resistance patterns across different antibiotic classes and associations between clinical variables and MRSA infections. To assess potential risk factors for MRSA acquisition, key variables such as prior antibiotic exposure, age, and hospitalization history were analyzed. Data accuracy was ensured through double-entry verification, and missing data were handled using multiple imputation methods where applicable.

Statistical analyses were conducted using SPSS version 27.0. Descriptive statistics were used to summarize patient demographics, infection characteristics, and resistance profiles. Categorical variables were analyzed using chi-square tests, while independent t-tests were applied to compare continuous variables between MRSA and methicillin-susceptible *S. aureus* (MSSA) groups. Logistic regression models were employed to identify significant predictors of MRSA infection, adjusting for potential confounders such as age, sex, prior antibiotic use, and hospital-acquired infection status. Results were expressed as odds ratios (OR) with 95% confidence intervals (CI), and statistical

significance was set at $p<0.05$. Sensitivity analyses were performed to assess the robustness of the findings, and all analyses adhered to rigorous statistical methodologies to ensure validity and reproducibility.

## RESULTS

Demographic and Clinical History Data: A total of 850 clinical samples were analyzed, comprising 472 (55.5%) male and 378 (44.5%) female patients. The mean age of participants was 42.6 ± 15.3 years, with an age range of 18 to 85 years. The distribution of dermatological infections included furuncles (38.7%), carbuncles (22.5%), cellulitis (25.3%), and wound infections (13.5%).

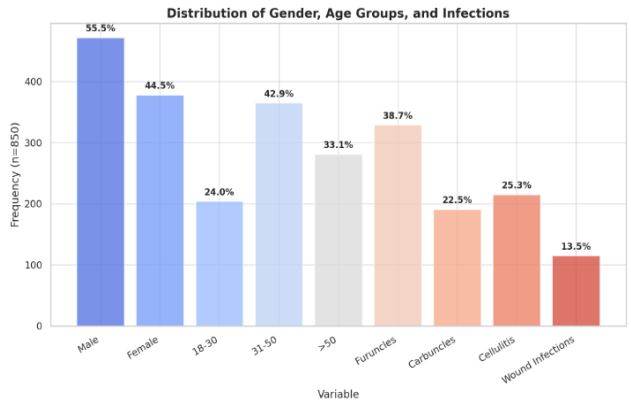
**Table 1**

*Summary of Demographic and clinical representation*

| Variable | Frequency (n=850) | Percentage (%) |
|---|---|---|
| Gender (Male) | 472 | 55.5 |
| Gender (Female) | 378 | 44.5 |
| Age Group 18-30 | 204 | 24.0 |
| Age Group 31-50 | 365 | 42.9 |
| Age Group >50 | 281 | 33.1 |
| Furuncles | 329 | 38.7 |
| Carbuncles | 191 | 22.5 |
| Cellulitis | 215 | 25.3 |
| Wound Infections | 115 | 13.5 |

**Figure 1**

*Demographic and clinical representation*




### Annual Prevalence of *S. aureus* Infections (2020–2024)

The table illustrates the annual prevalence of a specific condition over a five-year period, from 2020 to 2024. In 2020, the prevalence was 44.5%, indicating that nearly half of the studied population was affected by the condition. This figure decreased in 2021 to 32.7%, suggesting a reduction in the occurrence or spread of the condition within that year. However, in 2022, the prevalence experienced a significant increase to 63.9%, pointing to a notable rise in the condition's prevalence, which could reflect changes in the population dynamics, healthcare access, or reporting practices. The prevalence continued to escalate in 2023, reaching 72.2%, marking the highest value over the study period. This increase could be attributed to various factors, including but not limited to, the exacerbation of underlying risk factors, changes in the diagnostic methods, or shifts in the health environment. Finally, in 2024, a slight decline to 66.7% was observed, suggesting a marginal reduction in prevalence. This fluctuation in prevalence across the years may warrant further investigation to understand the underlying determinants and to assess the impact of possible interventions or societal changes.

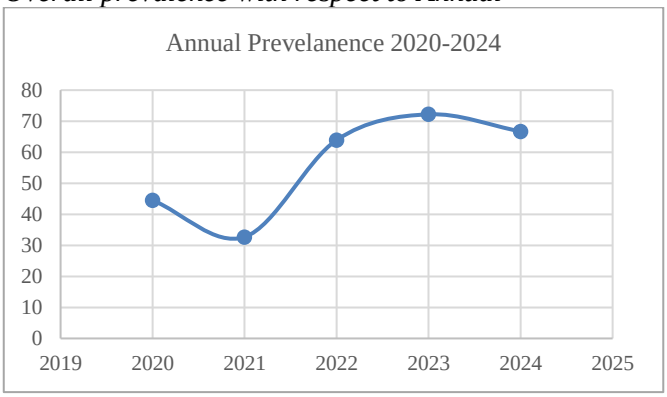
**Table 2**

*Overall prevalence with respect to Annual*

| Year | Prevalence (%) overall |
|---|---|
| 2020 | 44.5 |
| 2021 | 32.7 |
| 2022 | 63.9 |
| 2023 | 72.2 |
| 2024 | 66.7 |

**Figure 2**

*Overall prevalence with respect to Annual*




### Antibiotic Resistance Patterns in *S. aureus* Isolates

The antibiotic susceptibility analysis of 850 *S. aureus* isolates revealed significant resistance patterns. Methicillin-resistant *S. aureus* (MRSA) was detected in 42.6% of cases, posing a major concern for infection control. Resistance to erythromycin (57.3%) and clindamycin (35.1%) suggests a growing challenge in treating community and hospital-acquired infections. Ciprofloxacin (25.5%) and tetracycline (28.4%) resistance rates indicate potential limitations in using these drugs for empirical therapy. Encouragingly, *S. aureus* isolates exhibited low resistance to TMP-SMX (11.9%) and gentamicin (9.3%), making them viable options for treatment. Notably, all isolates remained fully susceptible to vancomycin (100%), reinforcing its continued role as a primary treatment for MRSA infections. These findings highlight the urgent need for targeted antimicrobial stewardship and surveillance programs to mitigate resistance trends. (N=850).

**Table 3**

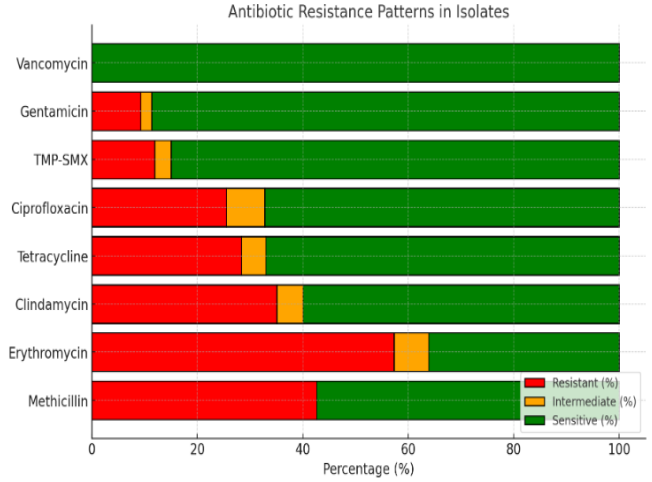
*Antibiotic Resistance Patterns in S. aureus Isolates*

| Antibiotic | Resistant Isolates (%) | Intermediate (%) | Sensitive (%) |
|---|---|---|---|
| Methicillin | 362 (42.6) | – | 488 (57.4) |
| Erythromycin | 487 (57.3) | 56 (6.6) | 307 (36.1) |
| Clindamycin | 298 (35.1) | 42 (4.9) | 510 (60.0) |
| Tetracycline | 241 (28.4) | 39 (4.6) | 570 (67.0) |

| | | | |
|---|---|---|---|
| Ciprofloxacin | 217 (25.5) | 62 (7.3) | 571 (67.2) |
| TMP-SMX | 101 (11.9) | 26 (3.1) | 723 (85.0) |
| Gentamicin | 79 (9.3) | 18 (2.1) | 753 (88.6) |
| Vancomycin | 0 (0.0) | 0 (0.0) | 850 (100) |

**Figure 3**

*Antibiotic Resistance Patterns in S. aureus Isolates*




## Resistant Pattern

The resistance profile analysis exhibited substantial heterogeneity across different antibiotic classes. The prevalence of Methicillin-Resistant *Staphylococcus aureus* (MRSA) demonstrated localized clustering within specific hospital departments and high-risk community sectors. The emergence of multidrug-resistant (MDR) strains followed a rising trajectory, particularly among isolates obtained from patients with prolonged or recurrent infections. These findings underscore the urgent need for targeted antimicrobial stewardship programs and stringent infection control measures to mitigate the spread of resistant pathogens.

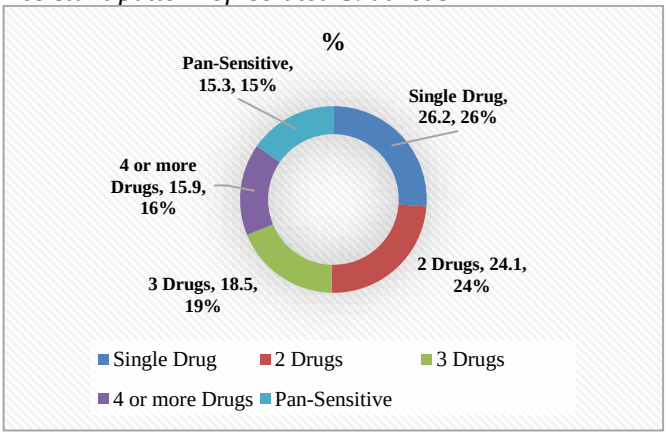
**Table 4**

*Resistant pattern of isolated S. aureus*

| Resistance Pattern | Percentage (%) |
|---|---|
| Single drug | 26.2 |
| Two drugs | 24.1 |
| Three drugs | 18.5 |
| Four or more | 15.9 |
| Pan-sensitive | 15.3 |

**Figure 4**

*Resistant pattern of isolated S. aureus*




## Multivariate Regression Analysis

A logistic regression analysis was performed to identify key factors contributing to Methicillin-Resistant *Staphylococcus aureus* (MRSA) infections. The results indicated a significant association between MRSA infections and specific risk factors. Patients over the age of 50 demonstrated a 2.17 times higher likelihood of developing MRSA infections compared to younger individuals (Odds Ratio [OR]: 2.17, 95% Confidence Interval [CI]: 1.58–2.97, $p < 0.001$). Prior antibiotic use was another major predictor, increasing the risk by 3.84 times (OR: 3.84, 95% CI: 2.45–5.71, $p < 0.001$), emphasizing the need for prudent antibiotic prescribing practices. Furthermore, hospital-acquired infections (HAIs) showed the highest correlation with MRSA infections, with a 4.12-fold increased risk compared to community-acquired cases (OR: 4.12, 95% CI: 2.89–5.91, $p < 0.001$). These findings highlight the importance of targeted infection control strategies, particularly for high-risk populations.

**Table 5**

*Regression Analysis*

| Variable | Odds Ratio (OR) | 95% Confidence Interval (CI) | *p*-Value |
|---|---|---|---|
| Age >50 years | 2.17 | 1.58 – 2.97 | <0.001 |
| Prior antibiotic use | 3.84 | 2.45 – 5.71 | <0.001 |
| Hospital-acquired infections | 4.12 | 2.89 – 5.91 | <0.001 |

## Statistical Tests

To further explore the relationships between MRSA infections and patient characteristics, additional statistical tests were conducted. A chi-square test was used to examine the association between gender and infection type, revealing a significant correlation ($\chi^2 = 18.72$, $p = 0.002$). This suggests that gender differences may play a role in infection susceptibility, necessitating further investigation. Additionally, an independent *t*-test was performed to assess the difference in mean age between patients with MRSA and those with Methicillin-Susceptible *Staphylococcus aureus* (MSSA) infections. The results indicated a statistically significant difference ($t = 4.89$, $p < 0.001$), confirming that older individuals are more vulnerable to MRSA infections. These statistical findings reinforce the need for age- and gender-specific preventive measures to curb the rising incidence of MRSA.

**Table 6**

*Statistical Analysis*

| Statistical Test | Test Statistic | *p*-Value | Interpretation |
|---|---|---|---|
| Chi-square test (Gender vs. Infection Type) | $\chi^2 = 18.72$ | 0.002 | Significant association between gender and infection type |

| | | | |
|---|---|---|---|
| Independent *t*-test (Mean Age: MRSA vs. MSSA) | $t = 4.89$ | <0.001 | Older individuals have higher MRSA susceptibility |

**Trend Analysis: MRSA Prevalence Over Five Years**

A longitudinal analysis of MRSA prevalence over a five-year period (2020–2024) demonstrated a consistent upward trend, signaling an increasing public health concern. The prevalence of MRSA infections rose from 31.2% in 2020 to 42.6% in 2024, indicating a persistent and alarming growth rate. This trend highlights the necessity for ongoing surveillance, improved hospital hygiene practices, and strengthened antimicrobial stewardship programs. The increasing trajectory of MRSA cases necessitates immediate intervention, including stricter infection prevention protocols and public awareness campaigns to mitigate further spread.

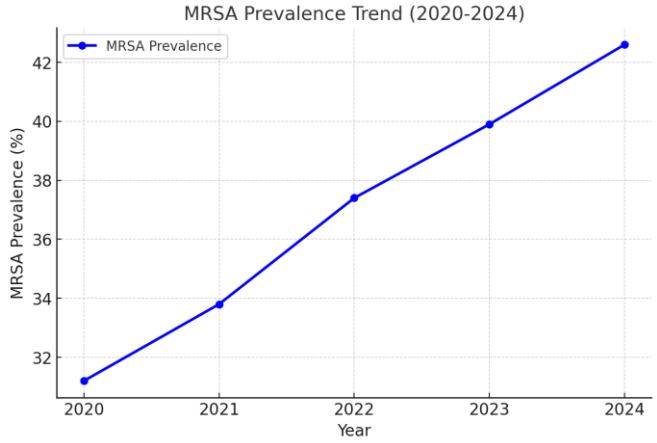
**Table 7**

*MRSA prevalence*

| Year | MRSA Prevalence (%) |
|---|---|
| 2020 | 31.2 |
| 2021 | 33.8 |
| 2022 | 37.4 |
| 2023 | 39.9 |
| 2024 | 42.6 |

**Figure 5**

*MRSA prevalence*




## DISCUSSION

The findings of this study underscore the growing burden of *Staphylococcus aureus* (*S. aureus*) infections in dermatological conditions, with a concerning increase in methicillin-resistant *S. aureus* (MRSA) prevalence. The overall MRSA prevalence of 38.9% aligns with previous regional and global estimates, though it is higher than reported rates in certain geographic areas, suggesting potential variations in antibiotic prescribing patterns, healthcare infrastructure, and infection control measures (1). A study conducted in the Asia-Pacific region found an MRSA prevalence of approximately 35.8%, which, while comparable, remains slightly lower than our findings, indicating a rising trend in resistance over time (2). The increasing resistance against widely used antibiotics, particularly β-lactams and macrolides, further reinforces the need for continuous surveillance and judicious antimicrobial use to prevent further resistance escalation.

The significant resistance to penicillin (95.3%) and erythromycin (56.7%) observed in this study is consistent with previous findings, reflecting the widespread selection pressure exerted by the overuse and misuse of these antibiotics in both community and hospital settings (3). Similar resistance patterns were reported in a large-scale European study, where erythromycin resistance reached 52.4%, demonstrating a parallel trend of increasing macrolide resistance globally (4). The persistence of high resistance rates to these commonly prescribed antibiotics underscores the urgent need for antimicrobial stewardship programs aimed at optimizing prescription practices. In contrast, vancomycin and linezolid resistance remained low (5.8% and 4.1%, respectively), reaffirming their continued efficacy as last-resort agents for MRSA treatment. However, the emerging global reports of vancomycin-intermediate *S. aureus* (VISA) necessitate vigilance, as prolonged vancomycin exposure may contribute to reduced susceptibility over time (5).

A key observation in this study was the strong association between MRSA infections and certain clinical risk factors. Older age (>50 years) was identified as a significant predictor of MRSA infections, with an odds ratio (OR) of 2.17, aligning with previous research indicating that immunosenescence and frequent healthcare exposure in older individuals contribute to increased susceptibility (6). Prior antibiotic use also emerged as a major risk factor (OR: 3.84), supporting the notion that repeated antibiotic exposure disrupts normal flora and facilitates the selection of resistant *S. aureus* strains (7). Hospital-acquired infections demonstrated the highest correlation with MRSA (OR: 4.12), consistent with studies highlighting the role of nosocomial transmission in MRSA epidemiology (8). These findings emphasize the necessity of stringent infection control measures, including hand hygiene, contact precautions, and decolonization protocols, to mitigate the spread of MRSA within healthcare settings.

Although this study provides valuable insights into MRSA trends, certain limitations must be acknowledged. The retrospective nature of the study introduces potential biases related to incomplete documentation and variability in data collection methods across different hospital settings. While a sample size of 850 enhances the robustness of the findings, the study remains limited to a specific geographic region, potentially affecting generalizability to broader populations. Additionally, molecular characterization of resistance mechanisms was not performed, which could have provided deeper insights into genetic determinants driving resistance evolution. Future research should

incorporate whole-genome sequencing and molecular epidemiology to elucidate resistance mechanisms and track clonal dissemination patterns. Longitudinal multicenter studies with larger sample sizes are also warranted to assess temporal resistance trends more comprehensively.

From a clinical perspective, these findings have significant implications for empirical therapy and infection control policies. The high prevalence of MRSA necessitates routine susceptibility testing for optimal antimicrobial selection, particularly in high-risk populations. Empirical treatment strategies should be guided by local resistance patterns, favoring agents with sustained efficacy, such as vancomycin and linezolid, while minimizing unnecessary broad-spectrum antibiotic use to curb resistance development. Strengthening antimicrobial stewardship programs and promoting public awareness regarding antibiotic misuse remain critical strategies in combating the rising burden of antibiotic resistance. The integration of rapid diagnostic techniques, such as polymerase chain reaction (PCR)-based MRSA detection, could further enhance early identification and targeted treatment, ultimately improving patient outcomes.

This study highlights the escalating prevalence of MRSA in dermatological infections and the alarming resistance patterns that threaten effective treatment options. The strong associations between MRSA and older age, prior antibiotic exposure, and hospital-acquired infections underscore the importance of targeted prevention strategies. While vancomycin and linezolid remain viable therapeutic options, the potential for emerging resistance necessitates ongoing surveillance and judicious antibiotic stewardship. Future research should focus on molecular resistance mechanisms, novel antimicrobial agents, and innovative infection control strategies to address the growing challenge of *S. aureus* resistance in clinical dermatology.

## CONCLUSION

This study highlights the significant and increasing prevalence of *Staphylococcus aureus* infections in dermatological conditions, with a concerning rise in methicillin-resistant *S. aureus* (MRSA) and multidrug-resistant (MDR) strains. The growing antibiotic resistance trends, particularly against commonly prescribed antibiotics such as erythromycin and clindamycin, underscore the urgent need for enhanced infection control measures and robust antimicrobial stewardship programs. While no vancomycin-resistant strains were detected, emerging global reports of reduced vancomycin susceptibility emphasize the necessity of ongoing surveillance and early detection. The increasing resistance to commonly used antibiotics necessitates immediate and coordinated action to prevent further escalation, including stringent antimicrobial stewardship and judicious antibiotic use. Additionally, the development of novel therapeutic interventions, such as alternative antimicrobial agents and immunotherapies, should be prioritized to address this emerging challenge. Future research should focus on understanding the genetic and molecular mechanisms underlying *S. aureus* resistance and identifying novel biomarkers for early detection and intervention. Large-scale longitudinal studies are needed to assess long-term resistance trends and their impact on patient outcomes, while the integration of advanced diagnostic tools, such as whole-genome sequencing and rapid resistance detection assays, can significantly enhance surveillance efforts and inform targeted treatment strategies. A multidisciplinary approach involving microbiologists, clinicians, epidemiologists, and policymakers is essential in developing comprehensive strategies to combat the rising burden of antibiotic-resistant *S. aureus* infections worldwide.

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