

Keywords:

Surgical site infection, antimicrobial resistance, bacterial pathogens, antimicrobial stewardship, public health

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Received:19-06-2026

Revised:21-07-2026

Accepted:28-07-2026

Doi:10.1922/ejpr.v34i7s.1689

Biotechnological and Microbiological Approaches to Reducing Surgical Site Infections in Oral and Maxillofacial Procedures: A Public Health Perspective

Abstract

Surgical site infections (SSIs) remain a significant cause of healthcare-associated infections and are increasingly complicated by antimicrobial resistance (AMR), resulting in prolonged hospitalization, increased healthcare costs, and adverse patient outcomes. Continuous microbiological surveillance and antimicrobial stewardship are therefore essential for effective infection prevention and control. This study aimed to identify the predominant bacterial pathogens associated with surgical site infections, evaluate antimicrobial resistance patterns, and examine factors associated with antimicrobial resistance using integrated secondary datasets. A quantitative retrospective secondary data analysis was conducted using two publicly available datasets comprising 2,648 records, including an Antibiotic Resistance Tracking Dataset (n = 2,200) and an Orthopaedic Surgical Site Infection Dataset (n = 448). Descriptive statistics were used to summarize pathogen distribution and antimicrobial susceptibility profiles, while Chi-square tests assessed associations between antimicrobial resistance and selected demographic and microbiological variables. *Staphylococcus aureus* was the predominant bacterial pathogen (48.2%), followed by *Pseudomonas aeruginosa* (15.4%) and *Escherichia coli* (12.1%). The highest resistance rates were observed for Cefexime (46.7%), Ceftriaxone (37.3%), Meropenem (34.3%), Ciprofloxacin (31.5%), and Vancomycin (29.3%). No statistically significant associations were identified between antimicrobial resistance and gender, age group, specimen type, or resistance gene category ($p > 0.05$), although resistance prevalence remained consistently high across all subgroups. Overall, the findings demonstrate the persistent burden of antimicrobial resistance among pathogens associated with surgical site infections and emphasize the importance of strengthening microbiological surveillance, antimicrobial stewardship programmes, and evidence-based infection prevention strategies to support sustainable public health and improve clinical outcomes.

Introduction

Surgical site infections (SSIs) are one of the most common healthcare-associated infections (HAIs) today, and a significant threat to patient safety and the quality of healthcare around the world. Despite advances in surgical techniques, surgical standards of cleanliness and perioperative management, SSI continues to be a significant contributor to post-operative morbidity, longer hospital stay, increased healthcare costs and mortality [1]. These infections world-wide contribute significant portion of preventable adverse surgical events and cost a lot of the healthcare systems due to the additional cost of treatment, re-admission and heavy utilization of resources [2]. Consequently, prevention of SSIs is a key public health problem with the goal of improving the quality of health care and patient outcomes.

The microbiology of SSIs is complex and can include a variety of bacterial pathogens such as *Staphylococcus aureus*, *Escherichia coli*, *Pseudomonas aeruginosa*, *Klebsiella pneumoniae*, and *Enterococcus* species [3]. These microorganisms have various virulence factors, among them the ability to form biofilms, which contributes to microbial persistence and decreases the efficacy of host immune system and antimicrobial treatment. Further, healthcare settings are a source of hospital-acquired pathogens, which raises the potential for postoperative infections and treatment failures [4]. Thus, knowledge of the distribution and resistance of pathogens is crucial to enhance infection control measures and to optimize clinical management.

Management of surgical site infections has become more challenging due to antimicrobial resistance (AMR), which limits the use of empirical antibiotic therapy [5]. The rise of multidrug-resistant organism (MDR) – such as methicillin resistant *Staphylococcus aureus* (MRSA) and carbapenem-resistant Gram-negative (CR-GN) bacteria – has led to extended hospital stays, greater health care expenses and mortality rates [6]. As one of the most critical health threats in the world, the World Health Organization has called for constant surveillance, rational antibiotic usage and good antimicrobial stewardship programmes to ensure the efficacy of available antimicrobial drugs [7].

Measures related to comprehensive infection prevention and control (IPC) programmes, antimicrobial stewardship initiatives, and hospital surveillance systems are essential to sustainable healthcare from a public health perspective. These strategies enable early detection of resistant pathogens, aid in evidence-based clinical decision making and enhance the resilience of the healthcare system from healthcare-associated infections (HAI) [8]. Historically, however, there has been a lack of studies that have examined both surgical site infections and antimicrobial resistance in a single cohort and with a collection of microbiological surveillance and resistance data. Moreover, this type of secondary analyses of publicly available datasets is relatively scarce, even though it can provide useful epidemiological evidence. Hence, the goal of this study is to explore the microbiological causes and antimicrobial resistance of surgical site infections by secondary data analysis to get evidence for infection prevention measures and public health policy.

Research Objectives

- 1.To identify the predominant bacterial pathogens associated with surgical site infections.
- 2.To evaluate antimicrobial resistance patterns among pathogens isolated from surgical site infections.
- 3.To examine factors associated with antimicrobial resistance to support infection prevention and public health strategies.

2. Methodology

2.1 Study Design

This study used a quantitative, retrospective secondary data analysis approach to determine the microbiological determinants and antimicrobial resistance patterns of surgical site infections (SSIs). The secondary data analysis can be considered a suitable method for using existing data to derive epidemiological evidence for the assessment of infection trends and the emergence of antimicrobial resistance from a public health point of view, since it can be used without recruiting new patients or performing clinical interventions.

2.2 Data Sources

The study was based on two public datasets that were obtained from trusted open data repositories. The first dataset comprised clinical and microbiological data regarding surgical site infections (SSIs) such as patient demographics, bacterial species isolated from the wound and other infection-related parameters [9]. The second dataset was made up of antimicrobial resistance (AMR) surveillance data collected, with antibiotic susceptibility data made available for clinically important bacterial pathogens [10]. Both were combined into a single analytical database to carry out a comprehensive study of pathogen distribution and resistance patterns.

2.3 Data Integration and Pre-processing
Data cleaning and harmonization were performed on both data sets before analysis. Records were duplicated; categorical variables were recorded and standardized to make them consistent across the data sets; and variable names were standardized. All fields were checked for missing data, and where required, records with missing microbiological or antimicrobial susceptibility data were excluded. For each observation, a source identifier was left to keep the data provenance throughout the analysis.

2.4 Study Variables

The main outcome variables were identification of the bacterial pathogens and the presence of antibiotic resistance. Independent variables included demographic variables, specimen type, bacterial species, antibiotic tested, susceptibility, and other clinical variables in the data sets. AMS data from the reported multidrug-resistant organism (MDRO) were used to define/multidrug-resistant organisms.

2.5 Statistical Analysis

Python was used to analyze data. Descriptive statistics including frequencies, percentages, means and standard deviations were used to summarize the demographic characteristics, the distribution and patterns of antimicrobial resistance. To assess the associations of

categorical variables, Chi-square test or Fisher's exact test was used as appropriate. Factors associated with antimicrobial resistance were determined by binary logistic regression analysis; and adjusted odds ratios (AORs) with 95% confidence interval (CI) were reported. Statistically significance was determined as p value < 0.05 .

3. Results

3.1 Descriptive Characteristics of the Study Population

The descriptive features of the study population are shown in Table 1. Of the 2,648 records, 2,200 (83.1%) were from

the Antibiotic Resistance Tracking Dataset and 448 (16.9%) from the Orthopaedic Surgical Site Infection Dataset. After harmonisation of the demographic variables, 1,217 (46.0%) females and 1,431 (54.0%) males were included in the study.

Information about the age of the participants was available for 2,200 participants with a mean age of 45.65 ± 26.27 years (range 1–90 years). The >65 years age group ($n = 633$) and the <18 age group ($n = 451$) were the next largest groups, followed by the 18–35 age group ($n = 412$). The most common clinical specimens collected were blood ($n = 449$), sputum ($n = 448$), wound swab ($n = 448$), urine ($n = 433$), and stool ($n = 422$) (Table 1).

Table 1. Descriptive characteristics of the study population

Variable	Category	Frequency
Dataset	Antibiotic Resistance Tracking Dataset	2,200
	Orthopaedic Surgical Site Infection Dataset	448
Gender	Female	1,217
	Male	1,431
Age (years)	Mean $\pm$ SD	45.65 ± 26.27
	Range	1–90
Age Group	<18	451
	18–35	412
	36–50	370
	51–65	334
	>65	633
Specimen Type	Blood	449
	Sputum	448
	Wound swab	448
	Urine	433
	Stool	422

3.2 Distribution of Bacterial Pathogens

The frequency distribution of the bacterial pathogens are summarized in Table 2 and their relative distribution is shown in Figure 1. 13 types of bacteria were identified. *S. aureus* was the most common pathogen (216 isolates, 48.2%), followed by *P. aeruginosa* (69 isolates, 15.4%), *E. coli* (54 isolates, 12.1%), *K. pneumoniae* (33 isolates, 7.4%) and *Proteus vulgaris* (25 isolates, 5.6%). All other pathogens accounted for less than 4% of the total number of isolates.

Table 2. Distribution of bacterial pathogens

Bacterial pathogen	Frequency	Percentage (%)
<i>Staphylococcus aureus</i>	216	48.2
<i>Pseudomonas aeruginosa</i>	69	15.4
<i>Escherichia coli</i>	54	12.1
<i>Klebsiella pneumoniae</i>	33	7.4

<i>Proteus vulgaris</i>	25	5.6
ACB complex	16	3.6
<i>Citrobacter freundii</i>	11	2.5
<i>Streptococcus</i> spp.	8	1.8
CoNS	7	1.6
<i>Enterobacter</i> spp.	4	0.9
<i>Serratia marcescens</i>	3	0.7
<i>Morganella morganii</i>	1	0.2
<i>Providencia rettgeri</i>	1	0.2

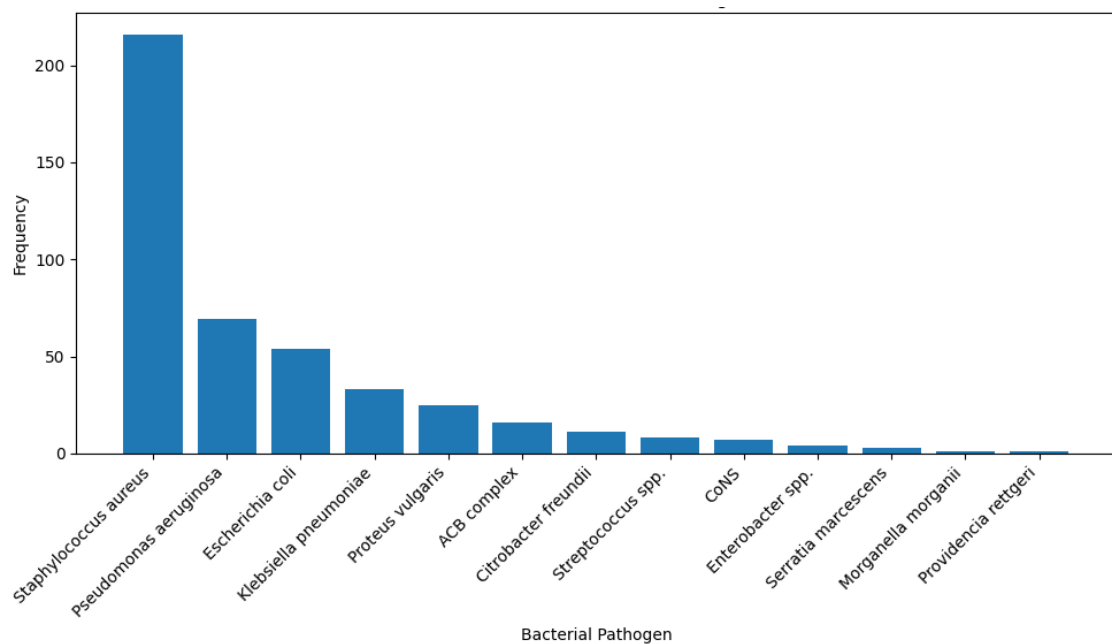


Figure 1. Distribution of bacterial pathogens

3.3 Antimicrobial Resistance Profile

The findings of antimicrobial susceptibility are summarized in Table 3 and the overall antimicrobial resistance pattern is shown in Figure 2. The highest resistance rates were observed for Cefexime (46.7%), Ceftriaxone (37.3%), Meropenem (34.3%), Ciprofloxacin (31.5%), Cloxacillin (30.1%), Vancomycin (29.3%), Amoxicillin (28.7%), and Colistin (26.9%). Differences in resistance were observed, with moderate levels of resistance (> 10%) for Gentamicin (14.3%), Imipenem (12.9%), Ampicillin (12.9%), Cotrimoxazole (12.7%), Cefazolin (11.8%) and Amikacin (10.9%), while the resistance level of other antibiotics was not exceeding 10%.

Table 3. Antimicrobial resistance profile

Antibiotic	Resistance (%)
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Cefexime	46.7
Ceftriaxone	37.3
Meropenem	34.3
Ciprofloxacin	31.5
Cloxacillin	30.1
Vancomycin	29.3
Amoxicillin	28.7
Colistin	26.9
Gentamicin	14.3
Imipenem	12.9
Ampicillin	12.9
Cotrimoxazole	12.7
Cefazolin	11.8
Amikacin	10.9
Doxycycline	10.0

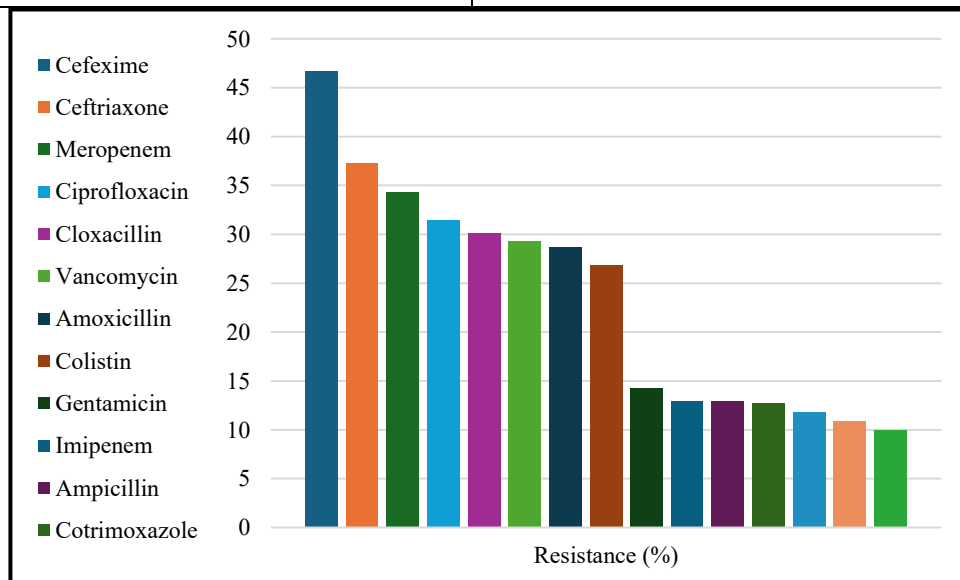


Figure 2. Antimicrobial Resistance Rates Among Frequently Tested Antibiotics

Figure 2 illustrates the percentage of antimicrobial resistance observed among the most frequently tested antibiotics. Cefexime exhibited the highest resistance rate (46.7%), followed by Ceftriaxone and Meropenem, whereas Gentamicin, Imipenem, and Ampicillin demonstrated comparatively lower resistance rates, highlighting substantial variability in antibiotic effectiveness.

3.4 Factors Associated with Antimicrobial Resistance

The correlations between selected variables and antimicrobial resistance shown in Tables 4–6.

No difference in antimicrobial resistance could be concluded between the different specimen types ($\chi^2 = 1.554$, $df = 4$, $p = 0.817$) as revealed in Table 4. The resistance was found to be high in all specimen categories from 84.6% to 87.1%.

Likewise, Table 5 shows that there was no significant association between resistance gene category and antimicrobial resistance ($\chi^2 = 3.400$, $df = 3$, $p = 0.334$). 88.9% of the KPC isolates, 85.9% of the NDM-1 isolates,

86.0% of the OXA-48 isolates and 84.9% of the VIM-positive isolates were resistant.

Demographic also showed that there was no significant association between antimicrobial resistance and gender ($\chi^2 = 0.138$, $p = 0.711$) or age group ($\chi^2 = 0.631$, $p = 0.960$) (Table 6). There was, however, a statistically significant difference between the two source data sets ($\chi^2 = 5.529$, $df = 1$, $p = 0.019$) rather than biological variation, which was due to differences in the composition of data from the two sources.

Table 4. Association between specimen type and antimicrobial resistance

Variable	χ^2	df	p-value
Specimen type	1.554	4	0.817

Table 5. Association between resistance genes and antimicrobial resistance

Variable	χ^2	df	p-value
Resistance genes	3.400	3	0.334

Table 6. Association of demographic variables with antimicrobial resistance

Variable	χ^2	df	p-value
Gender	0.138	1	0.711
Age group	0.631	4	0.960
Source dataset	5.529	1	0.019

4. Discussion

The aim of this study was to explore the microbiological profile and antimicrobial resistance (AMR) experienced with surgical site infections (SSI) through integrated secondary data. The results showed that the main bacterial pathogen was *Staphylococcus aureus*, *Pseudomonas aeruginosa*, *Escherichia coli*, and *Klebsiella pneumoniae* [11]. The findings are in line with previous studies that reported the predominance of *S. aureus* as the most common causative pathogen of SSI due to its virulence factors, the ability to form biofilms and survival in the health care environment [12]. The majority of pathogens associated with HAIs are Gram-negative, further reinforcing the microbiological spectrum of HAIs.

Antimicrobial susceptibility test showed a high level of resistance to some of the regularly prescribed antibiotics including Cefexime, Ceftriaxone, Meropenem, Ciprofloxacin, Vancomycin, Amoxicillin and Colistin [13]. The results are consistent with other surveillance reports of the resistance rates of clinically important bacterial pathogens [14] and highlight the importance of regular susceptibility testing to ensure the effectiveness of empirical antibiotic therapy. The identified resistances confirm the worldwide worry about emergence and spread of multi-drug-resistant organisms.

There were no statistically significant associations seen between gender, age group, specimen type, or category of

antimicrobial resistance gene and antimicrobial resistance [15]. Based on these results, antimicrobial resistance might be more affected by antimicrobial exposure, healthcare practices, and microbial evolution than demographic or specimen-related variables [16]. Therefore, there is a need to focus on the implementation of broad-based surveillance and evidence-based antibiotic policies, instead of demographic risk stratification, as part of efforts to prevent infection.

The conclusions reinforce the call to enhance antimicrobial stewardship programmes to ensure proper antibiotic prescribing and minimize unnecessary use of antimicrobials. Stewardship interventions have been shown to have beneficial effects on the use of antimicrobials and have been found to help lower resistance rates [5,7]. In addition, new technologies like biomaterial-based antimicrobial treatments and molecular rapid diagnostic tests are promising avenues to improve infection prevention and to optimize individualized antimicrobial therapy in the future [17,18,19].

5. Conclusion

In this study, the microbiological features of SSIs and their antimicrobial resistance patterns are analyzed in a secondary manner, and the significance of these findings in terms of infection prevention and public health are

discussed. The results reveal that the predominant bacteria isolated were *Staphylococcus aureus* (SA), *Pseudomonas aeruginosa* (PA), *Escherichia coli* (EC) and *Klebsiella pneumoniae* (KP) which are still the main bacteria detected in healthcare-associated bacteria. The high level of resistance of the antibiotics which are often prescribed like Cefexime, Ceftriaxone, Meropenem, Ciprofloxacin, Vancomycin, Amoxicillin shows the issue of antimicrobial resistance and the need for evidence-based antimicrobial prescribing. The high proportion of resistant isolates for each of the antimicrobial resistance categories studied highlight the need for continued microbiological monitoring and consistency in susceptibility testing. Demographic characteristics, specimen type and resistance gene type were not associated with antimicrobial resistance, but the high prevalence of resistant isolates suggests that there is a need for continued microbiological surveillance and consistency of testing susceptibility. This study's findings corroborate the need for the implementation of a full antimicrobial stewardship programmes, improved infection prevention and control, and regular monitoring programmes for their ability to reduce the effect of surgical site infections. Furthermore, novel technologies such as new biomaterials with antimicrobial property and rapid molecular diagnosis will help to improve pathogen identification and more precise targeted drug treatment in the clinical setting. Further multi-center studies with comprehensive clinical, microbiological and molecular information are needed to better understand the factors associated with antimicrobial resistance and provide effective, sustainable, public health strategies to prevent HAIs.

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