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Evaluating antimicrobial resistance and clinical outcomes in surgical ICU using a machine learning perspective: a retrospective observational study

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Abstract

Background Antimicrobial resistance (AMR) poses a critical threat to patient outcomes in intensive care units (ICUs), complicating treatment regimens and elevating mortality. This study aimed to assess the prevalence and patterns of AMR, antibiotic utilization, and clinical outcomes among postoperative patients in a surgical ICU in southern Iran, and developed predictive models for clinically significant resistance (MDR/XDR).

Methods We conducted a retrospective study; 106 postoperative patients admitted to the surgical ICU between January 2022 and December 2023 were evaluated. Demographic and clinical data, antibiotic usage metrics (including Days of Therapy [DOT], Length of Therapy [LOT], and Antimicrobial-Free Days [AFD]), and microbial culture results were extracted from electronic health records. Resistance patterns were classified as minor, multidrug-resistant (MDR), extensively drug-resistant (XDR), or pan-drug-resistant (PDR). Predictive modeling was performed using an XGBoost classifier and a logistic regression (LR) baseline, with hyperparameter tuning, fivefold cross-validation, and SHAP (SHapley Additive exPlanations) analysis for feature importance. This exploratory, single-center study in a resource-limited setting highlights hypothesis-generating insights but is constrained by sample size and generalizability.

Results In this cohort of 106 postoperative surgical ICU patients (median age, 66 years; 63.2% male), hypertension (33.7%) and diabetes mellitus (26.9%) were the most common comorbidities. The median ICU stay was 14.5 days, with an all-cause in-hospital mortality rate of 91.5%. Extensive antibiotic exposure was observed, with median DOT and LOT of 29.5 and 14.5 days, respectively, and broad-spectrum antibiotics were administered in 96% of cases. Among 175 microbial entries, 145 (83.82%) were culture-positive, predominantly Gram-negative bacteria (71.72%), with *E. coli* (20%), *Acinetobacter* (17.24%), and *Klebsiella* (16.55%) as leading pathogens. Notably, 62.07% of isolates were MDR and 3.45% were XDR, while no pan-drug resistant strains were identified.

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The XGBoost model achieved a test ROC-AUC of 0.786 and mean cross-validation AUC of 0.896 ± 0.05, with 70% accuracy and a macro F1-score of 0.70. The LR baseline yielded a test AUC of 0.743 and 77% accuracy, showing higher sensitivity but lower specificity. SHAP analysis identified Gram-negative infection type, Gram-positive infection type, LOT, and age as the most influential predictors of resistance.

Conclusion Surgical ICU patients experienced high rates of MDR infections, prolonged antibiotic exposure, and elevated mortality. Machine learning, particularly XGBoost, showed promising potential in this exploratory context for early identification of high-risk patients, highlighting its role in guiding antimicrobial stewardship and empirical therapy in critical care settings, pending further validation.

Keywords Antibiotics Resistance, Antimicrobial Resistance, XGBoost, Multi-drug-resistant bacteria, Extensively-drug resistant bacteria, Surgical Intensive Care Unit

Introduction

The global rise of antimicrobial resistance (AMR) poses a critical threat to public health by limiting effective treatment options, increasing the severity of infections, prolonging hospital stays, and elevating mortality rates. In surgical intensive care units (ICUs), multidrug-resistant (MDR) pathogens are frequently implicated in serious healthcare-associated infections, including ventilator-associated pneumonia (VAP), bloodstream infections (BSIs), surgical site infections, and urinary tract infections (UTIs). The increasing prevalence of MDR organisms has significantly complicated the clinical management of such infections, placing both current and future medical practices at risk [1].

According to a 2019 report by the U.S. Centers for Disease Control and Prevention (CDC), antibiotic-resistant bacteria are responsible for approximately 2.8 million infections and 35,000 deaths annually in the United States alone [2]. The escalation of resistance has been largely attributed to the widespread and often inappropriate use of antibiotics in human medicine, veterinary practice, and agriculture, particularly in low- and middle-income countries where regulatory oversight is often limited. Resistance may develop either spontaneously through natural selection or be acquired via horizontal gene transfer. Prolonged antimicrobial exposure exerts selection pressure that favors the emergence and propagation of MDR organisms, which are associated with poor clinical outcomes and increased healthcare expenditures [3].

The misuse of antibiotics during the COVID-19 pandemic has further exacerbated resistance patterns worldwide, accelerating the spread of MDR bacteria and increasing the burden of secondary bacterial infections [4]. In response, the World Health Organization (WHO) has issued a global priority pathogen list, which categorizes antibiotic-resistant bacteria into three tiers—critical, high, and medium, based on the urgency of research and development for new antibiotics [5]. The critical tier includes carbapenem-resistant *Acinetobacter baumannii*, *Pseudomonas aeruginosa*, and *Enterobacteriaceae*, which are associated with life-threatening nosocomial infections. The high and medium priority groups encompass other major pathogens such as vancomycin-resistant *Enterococcus faecium* (VRE), methicillin-resistant *Staphylococcus aureus* (MRSA), and cephalosporin-resistant *Enterobacteriaceae* [5]. Although MRSA infections have declined in some regions and therapeutic options exist, the growing threat of MDR Gram-negative bacteria, including *Klebsiella pneumoniae*, *Escherichia coli*, and *Acinetobacter spp.*, remains a formidable challenge for global health systems [6].

Given the urgent need for updated surveillance and predictive models of AMR, this study aimed to evaluate the prevalence and distribution of antimicrobial resistance across various antibiotic classes among patients admitted to the surgical ICU of a tertiary care center in southern Iran following major surgical procedures. The primary objective was to evaluate the epidemiological aspects of AMR patterns and their impact on patient outcomes in the surgical ICU. Additionally, the study aimed to develop a machine learning model to predict resistance based on patient-level data, thereby informing clinical decision-making.

Furthermore, the research sought to identify key demographic and clinical risk factors associated with the development of AMR. To achieve this, we employed both conventional statistical methods, such as logistic regression, and advanced machine learning techniques, particularly eXtreme Gradient Boosting (XGBoost), to enhance prediction accuracy and support clinical decisions. This study uniquely integrates AMR surveillance with an XGBoost-based machine learning approach to predict resistance in a surgical ICU context in southern Iran, providing hypothesis-generating, region-specific insights in the post-COVID-19 era.

Methods

This retrospective, two-year cohort study was conducted in the surgical Intensive Care Unit (ICU) of Namazi Hospital, a tertiary care center, from January 2022 to December 2023. The objective was to assess antibiotic prescribing patterns, microbial resistance profiles, and

associated clinical outcomes among ICU patients, as well as to explore the development of a machine learning model to predict whether microbial isolates exhibit clinically significant antibiotic resistance. Ethical approval was granted by the Institutional Review Board (IR.SUMS.MED.REC.1403.267), adhering to the Declaration of Helsinki.

Inclusion and exclusion criteria

Adult patients (≥ 18 years) admitted to the surgical ICU post-surgery were included. Patients with incomplete microbiological culture or antibiogram data were excluded. Written informed consent for data use was obtained routinely.

Outcome measures

Primary outcomes included:

- Frequency and appropriateness of broad-spectrum antibiotic use
- Prevalence of multidrug-resistant (MDR), extensively drug-resistant (XDR), and pan-drug-resistant (PDR) pathogens
- All-cause in-hospital mortality
- Days of Therapy (DOT), Length of Therapy (LOT), Antimicrobial-Free Days (AFD), and ICU length of stay (LOS)

Data collection

Data were retrospectively retrieved from electronic health records. The following variables were collected: patient demographics (age, sex), comorbidities, types of surgical procedures, ICU and hospital stay durations, and in-hospital mortality. Additionally, laboratory results (cultures and antibiograms), infectious disease consultations, antibiotic prescriptions (drug name, dose, duration), and days with or without systemic antibiotic therapy were meticulously recorded using a researcher-developed data collection form. The cohort consisted of postoperative patients admitted to the surgical ICU, many of whom were critically ill with severe underlying conditions.

Definitions

1. Antibiotic Usage Metrics:
    - Days of Therapy (DOT): The number of days a patient received any antibiotic, calculated as one DOT for each antibiotic administered within a 24-h period.
    - Length of Therapy (LOT): The total number of days a patient received systemic antibiotics, regardless of the number of different antibiotics administered.
    - Antimicrobial-Free Days (AFD): The total hospital length of stay (LOS) minus the Length of Therapy (LOT), representing the days without antibiotic administration.
2. Microbial and Resistance Data:
    - Pathogens Isolated: Organisms identified from clinical specimens such as blood, sputum, wound swabs, and urine.
    - Antibiotic Susceptibility: Resistance profiles were classified based on susceptibility to specific antibiotics and classes (e.g., penicillins, carbapenems).
    - Resistance Classifications: Infections were categorized as non-Multidrug Resistant (non-MDR), Multidrug Resistant (MDR), Extensively Drug Resistant (XDR), or Pandrug Resistant (PDR) per Magiorakos et al. (2012) [7].
3. Resistance Pattern Definitions
    - Resistance definitions followed the internationally accepted framework proposed by Magiorakos et al. (2012) [7], adopted by the European Centre for Disease Prevention and Control (ECDC) and the Centers for Disease Control and Prevention (CDC):
        - ✓ MDR (Multidrug-resistant): Non-susceptibility to ≥ 1 agent in ≥ 3 antimicrobial categories.
        - ✓ XDR (Extensively drug-resistant): Non-susceptibility to all agents except ≤ 2 antimicrobial categories.
        - ✓ PDR (Pandrug-resistant): Non-susceptibility to all agents in all tested categories.

While these definitions were the primary reference, resistance categorization was adapted when complete susceptibility data were unavailable or when definitions did not apply to specific bacterial species. Custom resistance profiles were developed for such cases, guided by available data and reviewed by infectious disease specialists. Antibiotic availability limitations in our resource-constrained setting may have led to minor deviations from the standard definitions. Additional file 1outlines the custom classification criteria used. Final categorization of each isolate (MDR, XDR, or PDR) was based on its antimicrobial susceptibility pattern. Discrepancies were resolved through expert consensus.

This adaptive framework ensured clinically relevant classification of resistance across diverse pathogens while maintaining alignment with internationally recognized definitions.

Model development

A dataset of 106 patients was constructed to develop a predictive model for clinically significant antimicrobial resistance. The binary outcome variable was defined as:

- 1 = patient has at least one MDR/XDR isolate
- 0 = otherwise, including culture-negative patients

Due to insufficient cases of XDR and PDR infections, a multiclass classification model was not feasible. Instead, a binary classification approach was adopted. Input features included demographic, clinical, microbiological, and antibiotic usage variables.

To ensure the validity and generalizability of our machine learning model while minimizing the risk of data leakage, we implemented a deliberate feature selection strategy. We excluded variables that directly indicate the outcome, such as specific microbial isolates and antibiotic resistance classes, and instead focused on features routinely available in clinical settings. These features represent patient demographics, comorbidities, surgical history, infection sites, and antibiotic utilization metrics, allowing the model to predict resistance based on characteristics relevant to patient treatment rather than microbiological data. The final set of features included in an XGBoost (eXtreme Gradient Boosting) model comprised categorical variables such as sex, underlying diseases (hypertension, diabetes mellitus, chronic kidney disease, ischemic heart disease, hyperlipidemia, cerebrovascular accident, and gastrointestinal cancer), opium addiction, present illnesses (bowel obstruction, bowel perforation, gastrointestinal bleeding, sepsis, and surgical site infections), drug history (calcium channel blockers, angiotensin receptor blockers, and statins), surgical types (laparotomy, incision and drainage, ostomy insertion, adhesionolysis, and total colectomy), gram-negative and gram-positive indicators, and sites of cultures (blood, endotracheal tube, urine, wound, abdominal, and sputum). The numerical variables included age, total hospitalization period, total number of antibiotics used, DOT, LOT, and AFD.

An XGBoost classifier was employed and optimized using Optuna (100 trials), with performance metrics including area under the curve (AUC), accuracy, precision, recall, and F1-score. A logistic regression baseline was included for comparative purposes. The dataset (n = 106) was divided into an 80% training set and a 20% test set, stratified by outcome. Hyperparameter tuning was performed using Optuna (100 trials), and model performance was evaluated through ROC-AUC, accuracy, precision, recall, F1-score, and SHAP (SHapley Additive exPlanations) values, with fivefold cross-validation to assess robustness.

Features with zero SHAP values were removed for XGBoost, and variance inflation factor (VIF) analysis (threshold ≤ 10) was employed for logistic regression to mitigate multicollinearity, ensuring robust model performance. For a detailed overview of the XGBoost modeling stages and reproducibility assurance, please refer to Additional file 2, which may provide clarifications for statisticians. The dataset supporting the study is included within the article (see Additional file 3).

Statistical analysis

The statistical analysis involved descriptive statistics to summarize demographic and clinical characteristics, with continuous variables reported as means ± standard deviations or medians with interquartile ranges based on normality, and categorical variables expressed as frequencies and percentages. Antibiotic usage metrics were analyzed using appropriate central tendency measures, and resistance prevalence was stratified into categories (non-MDR, MDR, XDR, PDR). Group comparisons utilized parametric and non-parametric tests, while machine learning models were implemented in Python 3.8 using various libraries. An XGBoost classifier was optimized with Optuna, and performance metrics included AUC, accuracy, precision, recall, and F1-score, alongside a logistic regression baseline for comparison. Given the study's focus on predicting clinically significant resistance (MDR/XDR) to guide antibiotic therapy, and the presence of multiple isolates per patient, patient-level modeling was considered. The dataset was split into 80% training and 20% test sets, with hyperparameter tuning and model performance evaluated through ROC-AUC and fivefold cross-validation. Features with zero SHAP values were excluded, and VIF analysis was conducted to mitigate multicollinearity. A two-tailed p-value < 0.05 was considered statistically significant.

Results

Demographic and clinical characteristics

The study cohort comprised 106 postoperative patients admitted to the surgical ICU, predominantly male (63.2%), with a median age of 66 years (IQR 50.5–78.0). Table 1 summarizes the demographic and clinical characteristics of these patients. The most common comorbidities included hypertension (33.7%) and diabetes mellitus (26.9%), followed by gastrointestinal cancer (14.4%) and ischemic heart disease (13.2%). Additionally, 8.7% of patients had a history of opium addiction, and 5.7% had previously undergone coronary artery bypass grafting (CABG). This profile indicates a high-risk cohort susceptible to complex infections.

Primary clinical impressions included bowel obstruction (16%), gastrointestinal bleeding (16%), and sepsis (11.3%), with bowel perforation noted in 11.3% of cases. Laparotomy was the most frequently performed surgical procedure (65.05%), followed by ostomy insertion

Table 1 Demographic and clinical characteristics of surgical ICU patients post-operation

Variable	Values
Sex	
Male	67 (63.2%)
Female	39 (36.8%)
Age, years	63.66 (18.26) */66 (50.5—78)[$]
Underlying Diseases	
HTN	35 (33.7%)
DM	28 (26.9%)
CKD	10 (9.6%)
IHD	14 (13.2%)
HLP	11 (10.6%)
CVA	7 (6.7%)
GI Cancer	15 (14.4%)
Hypothyroidism	6 (5.8%)
BPH	10 (9.6%)
Asthma	5 (4.7%)
Other diseases	28 (26.4%)
Opium Addiction	9 (8.7%)
CABG History	6 (5.7%)
Drug History	
CCB	13 (12.3%)
ARB	14 (13.2%)
Statins	15 (14.1%)
Primary Impressions	
Bowel Obstruction	17 (16%)
Bowel Perforation	12 (11.3%)
GIB	17 (16%)
Sepsis	12 (11.3%)
SSI	9 (8.5%)
Mesenteric ischemia	8 (7.5%)
GI Cancer	9 (8.5%)
Other impressions	42 (39.6%)
Surgery Types	
Laparotomy	67 (65.05%)
I & D	14 (13.59%)
Ostomy Insertion	29 (28.16%)
JP Drain Insertion	20 (18.9%)
Nelaton Insertion	18 (17%)
Adhesionolysis	24 (22.6%)
Total Colectomy	7 (6.6%)
Thoracostomy Tube Insertion	13 (12.62%)

Other values are presented in frequency (percentages)

HTN Hypertension, *DM* Diabetes mellitus, *CKD* Chronic kidney disease, *IHD* Ischemic heart disease, *HLP* Hyperlipidemia, *CVA* Cerebrovascular accident, *GI* Gastrointestinal, *BPH* Benign prostatic hyperplasia, *CABG* Coronary artery bypass graft, *CCB* Calcium Channel blockers, *ARB* Angiotensin receptor blockers, *GIB* Gastrointestinal bleeding, *SSI* Surgical site infection, *I & D* Incision and drainage, *JP* Drain, Jackson-Pratt drain

[*]Indicates Mean (SD)

[$]indicates Median (Q1-Q3)

(28.16%) and adhesionolysis (22.6%). Other procedures, such as Jackson-Pratt (JP) drain insertion (18.9%) and thoracostomy tube placement (12.62%), are also detailed in Table 1.

Table 2 Clinical outcomes and antibiotic utilization metrics in post-operative surgical ICU patients

Variable	Mean (SD)	Median (Q1-Q3)	Frequency (%)
ICU Stay and Mortality			
ICU stay	16.40 (12.54)	14.5 (6.25- 22.25)	-
Mortality rate	-	-	97 (91.50%)
Antibiotic Usage			
Antibiotics Doses	108.83 (108.76)	76.0 (21.5- 146.25)	-
Days of Therapy (DOT)	38.30 (34.27)	29.5 (13.25- 54.0)	-
Length of Therapy (LOT)	16.62 (13.81)	14.5 (5.25- 23.0)	-
Antimicrobial-Free Days (AFD)	0.89 (1.97)	0.0 (0.0- 1.0)	-
Antibiotic Appropriateness			
Yes	-	-	61 (62.24%)
No	-	-	37 (37.75%)
Broad Spectrum for indication			
Yes	-	-	96 (96.0%)
No	-	-	4 (4.0%)

Clinical outcomes and antibiotic utilization metrics

Key clinical outcomes and antibiotic utilization data are presented in Table 2. The median ICU length of stay was 14.5 days (IQR: 6.25–22.25), and the all-cause in-hospital mortality rate was 91.5% (97 patients), indicative of a critically ill cohort. The antibiotic utilization analysis indicated a median cumulative antibiotic dose of 76.0 (IQR: 21.5–146.25) per patient, underscoring the critical nature of the patient population and the need for aggressive infection management. The median Days of Therapy (DOT) and Length of Therapy (LOT) were 29.5 days (IQR: 13.25–54.0) and 14.5 days (IQR: 5.25–23.0), respectively. Notably, antimicrobial-free days (AFD) had a median value of 0 (IQR: 0.0–1.0), reflecting continuous antibiotic exposure throughout the ICU stay. Antibiotic appropriateness was achieved in 62.24% of cases, while 37.75% were deemed inappropriate. Broad-spectrum antibiotics were prescribed in 96% of cases, indicating a predominant reliance on these agents in managing severe infections.

Antibiotic utilization patterns

A detailed summary of antibiotic utilization is provided in Additional file 4. Among the most frequently prescribed agents, Ceftriaxone was administered in 75.47% of patients, with a mean of 10.62 ± 9.77 doses and a median of 7.5 doses (IQR: 12.00). Metronidazole was given to 67.92% of patients, with a mean of 21.31 ± 21.61 doses and a median of 15.0 doses (IQR: 26.25). Meropenem was prescribed to 57.55% of patients, with a mean of 25.10 ± 31.07 doses and a median of 14.0 doses (IQR: 33.00). Other notable antibiotics include Vancomycin (administered in 51.89% of patients; mean: 20.71 ± 22.93 doses; median: 10.0 doses, IQR: 22.50) and Imipenem

(37.74% of patients; mean: 36.83 ± 53.68 doses; median: 12.0 doses, IQR: 55.50). Less frequently used agents included Clindamycin (30.19%), Linezolid (34.91%), and Ciprofloxacin (31.13%), each exhibiting variable dosing patterns. Antibiotics prescribed in fewer than 20% of patients, such as Ampicillin-Sulbactam (16.98%), Cefazolin (12.26%), Levofloxacin (11.32%), and Amikacin (9.43%), displayed wide dosing variations, with Ampicillin-Sulbactam showing a particularly high mean (76.94 ± 86.49 doses; median: 40.0 doses, IQR: 87.75). Rarely prescribed agents, including Cefepime, Cotrimoxazole, and Co-Amoxiclav, were used in less than 1% of cases; notably, Cefotaxime was not prescribed in this cohort.

Microbial isolate distribution and resistance patterns

A total of 175 entries (culture tests) were analyzed, which included both culture-negative results and multiple isolates from individual patients. Out of 175 microbial entries, 145 (83.8%) were culture-positive (see Additional file 5). Gram-negative bacteria accounted for 71.72% (104 isolates) of the culture-positive results, while Gram-positive bacteria comprised 28.27% (41 isolates). Sputum samples were the most common source of culture-positive specimens (48, 27.74%), followed by blood (27, 15.61%) and wound samples (25, 14.45%), with urine (18, 10.40%), abdominal specimens (10, 5.78%), and endotracheal tube (ETT) samples (8, 4.62%) being less frequent. Out of 145 culture-positive entries, the predominant pathogens identified included E. coli (20%), Acinetobacter (17.2%), and Klebsiella (16.6%).

Among Gram-negative isolates, *E. coli* was the most prevalent (29 isolates, 20%), followed by *Acinetobacter* (25 isolates, 17.24%) and *Klebsiella* (24 isolates, 16.55%). For Gram-positive organisms, *Enterococcus* was most frequently isolated (17 isolates, 11.72%), followed by *Staphylococcus epidermidis* (13 isolates, 8.96%) and *Staphylococcus aureus* (6 isolates, 4.13%). Methicillin-resistant *S. aureus* (MRSA) was identified in 2 isolates (1.38%). The microbial isolate distribution is depicted in Fig. 1.

Resistance patterns, as categorized into minor resistance, multidrug resistance (MDR), extensively drug-resistant (XDR), and pan-drug-resistant (PDR), are summarized in Table 3. Among the 145 culture-positive isolates, 90 (62.07%) exhibited MDR, 5 (3.45%) were classified as XDR, and none were PDR. Fifty isolates (34.48%) demonstrated minor or no resistance (Fig. 2). These patterns across the different isolates are further visualized in the figure included in Additional file 6.

- Minor Resistance: Observed in 34.48% ($n = 50$) of isolates, predominantly contributed by *Pseudomonas spp.* (8.28%), *Klebsiella spp.* (6.90%), and *E. coli* (6.21%).
- MDR: The most prevalent resistance type, accounting for 62.07% ($n = 90$) of isolates, with *E. coli* (13.79%) and *Acinetobacter spp.* (13.79%) as leading contributors, followed by *Enterococci spp.* (10.34%) and *Klebsiella spp.* (9.66%).
- XDR: Rare, identified in 3.45% (n = 5) of isolates, mainly associated with *Acinetobacter spp.* (1.38%) and *Pseudomonas spp.* (1.38%).

Resistance profiles among antibiotic families and individual agents

The analysis of *145 microbial isolates* revealed substantial variability in resistance rates across antibiotic classes (see Fig. 3 and the table included in Additional file 7). Resistance was highest for fluoroquinolones (68.27%) and third-generation cephalosporins (71.72%), with ciprofloxacin (66.89%) and cefotaxime (60%) showing particularly high resistance. Moderate resistance rates were observed for aminoglycosides (53.10%) and folate pathway inhibitors (62.76%), with gentamicin (46.21%) demonstrating higher resistance than amikacin (30.34%). Resistance to trimethoprim-sulfamethoxazole was also high at 62.76%. Resistance to β-lactamase inhibitor combinations was primarily driven by piperacillin/tazobactam (23.44%) compared to ampicillin-sulbactam (3.45%). Carbapenem resistance was variable, with imipenem (22.76%) exhibiting significantly higher resistance than meropenem (4.83%). Fourth-generation cephalosporins, such as cefepime, showed moderate resistance (23.44%), whereas no resistance to ceftazidime, a third-generation cephalosporin, was detected. Lower resistance rates were noted for glycopeptides (13.10%), polymyxins (6.89%), oxazolidinones (1.38%), and nitrofurans (3.45%), while macrolides, tetracyclines, and lincosamides demonstrated resistance rates around 20%.

Comparison of factors across antibiotic resistance patterns

Comparative analysis between patients with high resistance (MDR/XDR) and those with minor or no resistance is presented in Table 4. Patients in the high resistance group had significantly prolonged antibiotic therapy durations, with a median DOT of 41.5 days (IQR: 18–66) compared to 23 days (IQR: 7.75–38.5) in the low resistance group ($p = 0.002$). Similarly, LOT was significantly extended in the high resistance group (median: 18.5 days, IQR: 7–30.25) versus 11.5 days (IQR: 3.75–17) in the low resistance group ($p < 0.001$). No significant differences were observed for age, ICU length of stay, total antibiotic doses, or antimicrobial-free days (AFD) ($p > 0.05$). Although the median age was higher in the high resistance group (69 years) compared to the low resistance group (56.5 years), this difference did not reach statistical significance ($p = 0.061$).

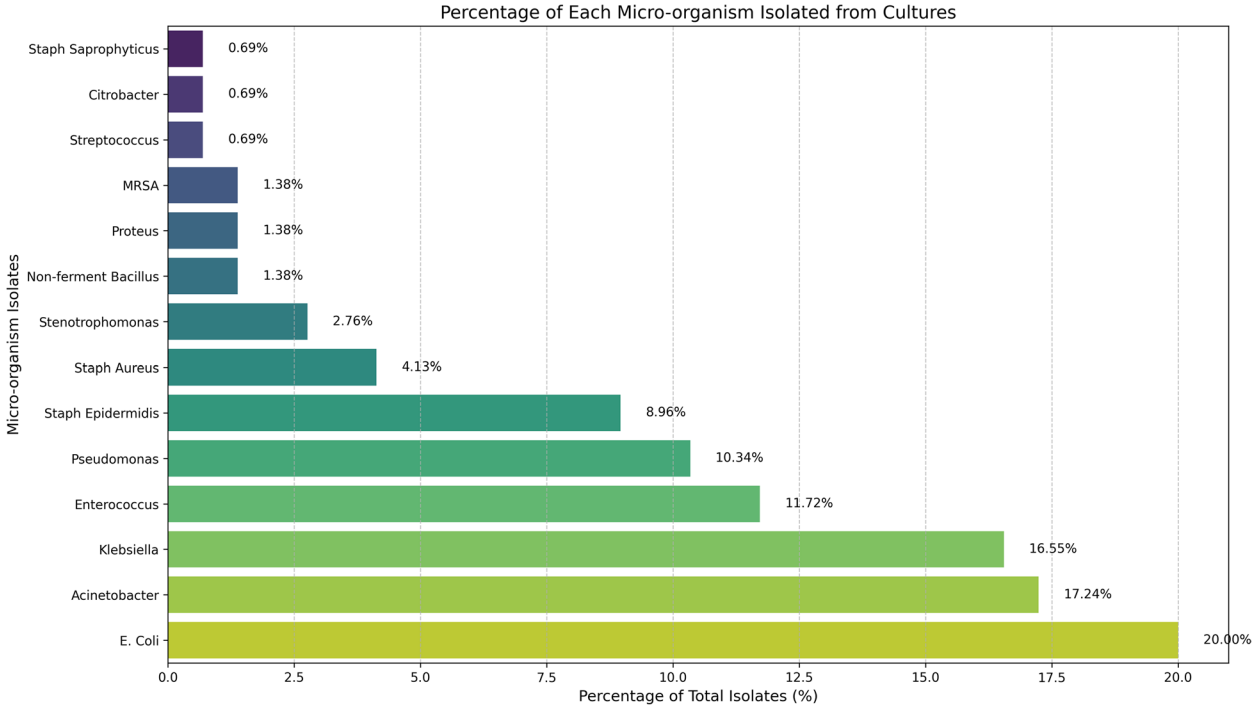

Fig. 1 Micro-organism isolates from cultures in surgical ICU patients. This bar chart displays the frequency and percentage of various micro-organism isolates ($n=145$) identified in cultures ($n=175$) from post-operative ICU patients. The chart highlights the most common isolates, including E. coli, Acinetobacter, and Klebsiella

Analysis of resistance patterns by antibiotic class, using an isolate-based dataset (Table 5), revealed that Gram-negative isolates were more common in the low resistance group (38.46%) than in the high resistance group (61.54%), while Gram-positive isolates predominated in the high resistance group (75.61% vs. 24.39%); however, this difference was not statistically significant ($p=0.158$). Notably, resistance to aminoglycosides, β-lactamase inhibitor combinations, carbapenems, first- and third-generation cephalosporins, fluoroquinolones, and macrolides was significantly higher in the high resistance group ($p<0.001$ for most comparisons). In contrast, resistance to nitrofurans, oxazolidinones, penicillins, tetracyclines, polymyxin E, and phenicols showed no significant differences.

Table 3 Incidence and contributions of antibiotic resistance patterns among microbial isolates

Resistance Type	Incidence (n, %)	Common Isolated Pathogens	Key Microbial Contributions (Scaled by Overall Frequencies)
Minor Resistance	50 (34.48%)	*E. coli, Pseudomonas, Klebsiella*	- *E. coli* (6.21%) - *Pseudomonas* (8.28%) - *Klebsiella* (6.90%) - *Staph Epidermidis* (3.45%) - *Stenotrophomonas* (2.76%)
MDR	90 (62.07%)	*Acinetobacter, E. coli, Enterococci*	- *E. coli* (13.79%) - *Acinetobacter* (13.79%) - *Enterococci* (10.34%) - *Klebsiella* (9.66%) - *Staph Epidermidis* (5.52%)
XDR	5 (3.45%)	*Acinetobacter, Pseudomonas, Enterococci*	- *Acinetobacter* (1.38%) - *Pseudomonas* (1.38%) - *Enterococci* (0.69%)
PDR	0.0 (0.0%)	No isolates	No significant microbial contributions identified

Among the antibiotic classes, aminoglycosides showed significant resistance, with 92.21% of isolates in the high resistance group compared to 7.79% in the low resistance group ($p<0.001$). Similarly, β-lactamase inhibitor combinations revealed 84.62% resistance in the high resistance group versus 15.38% in the low resistance group ($p=0.006$). Carbapenem resistance was markedly higher in the high resistance group (90% vs. 10%, $p<0.001$), as well as in 1 st and 3rd generation cephalosporins (86.79% vs. 13.21%, $p<0.001$; 71.15% vs. 28.85%, $p=0.037$). Resistance to fluoroquinolones was also significant, with 88.89% in the high resistance group compared to 11.11% in the low resistance group ($p<0.001$). In macrolides, 85.71% of isolates in the high resistance group were resistant, versus 14.29% in the low resistance group ($p=0.022$). Lincosamide resistance also differed significantly between the groups ($p=0.049$). In contrast, nitrofurans and oxazolidinones exhibited minimal resistance with no significant differences ($p=0.340$ and $p=0.545$, respectively). Notably, 100% of isolates in the high resistance group were resistant to glycopeptides, while none in the low resistance group were ($p=0.002$). Resistance to folate pathway inhibitors was significantly higher in the

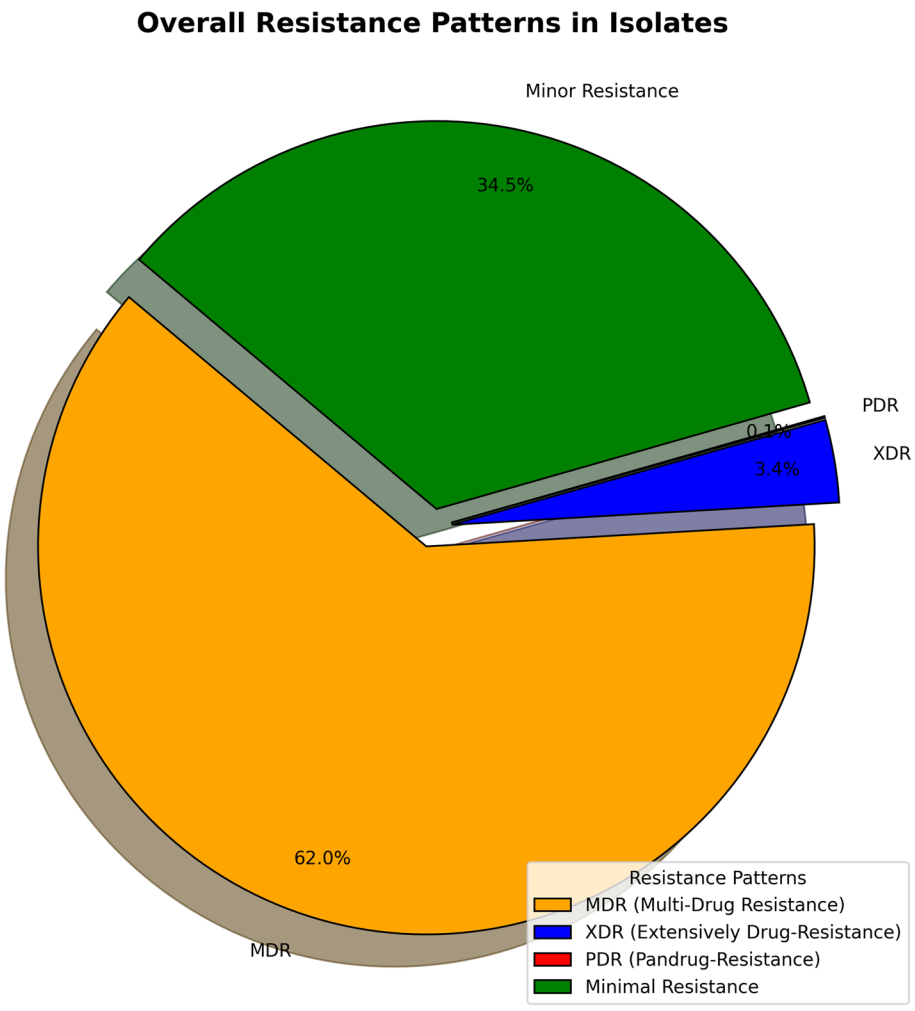

Fig. 2 Distribution of antibiotic resistance patterns in micro-organisms isolated from post-operative ICU patients. This pie chart illustrates the distribution of antibiotic resistance patterns among all microbial isolates (n = 145) in patients admitted to the surgical ICU after operation. The chart categorizes the micro-organisms into no-or-minimal antibiotic resistant, multidrug-resistant (MDR), extensively drug-resistant (XDR), and pan-drug-resistant (PDR) infections

high resistance group (79.12%) compared to 20.88% in the low resistance group ($p < 0.001$). No significant differences were observed between the two groups for penicillins, tetracyclines, polymyxin E, or phenicols, although resistance rates were slightly higher in the high resistance group for some of these antibiotics.

Analysis of machine learning model performance

An XGBoost classifier was developed to predict patients with clinically significant antimicrobial resistance (MDR/XDR/PDR) versus those with non-significant resistance infections. Hyperparameter tuning using the Optuna framework (100 trials) yielded optimal parameters, achieving a test ROC-AUC of 0.786 on the test set ($n = 22$) and a mean fivefold cross-validation ROC-AUC of 0.896 ± 0.05 (range: 0.817–0.940). On the held-out test set, the model achieved an accuracy of 70%. For predicting patients developing infections with resistant isolates (class 1), it attained a precision of 0.75, recall of 0.71, and F1-score of 0.72; for non-resistant cases (class 0), precision was 0.60, recall 0.67, and F1-score 0.63. The macro-average F1-score was 0.70, and the weighted-average F1-score was also 0.70, indicating balanced performance across classes. Additional file 8 contains more detailed metrics.

A logistic regression (LR) baseline model was developed using a subset of features selected via Variance Inflation Factor (VIF) analysis to mitigate multicollinearity. The LR model achieved a test ROC-AUC of 0.743, with a mean cross-validation ROC-AUC of 0.789 ± 0.07 (range: 0.648–0.897), and a test accuracy of 77%. For cases with resistant isolates, it achieved a precision of 0.72, recall of 1.00, and F1-score of 0.84; for non-resistant cases, precision was 1.00, recall 0.44, and F1-score 0.62. The LR confusion matrix showed 4 true negatives, 5 false positives, 0 false negatives, and 13 true positives, indicating high sensitivity but lower specificity.

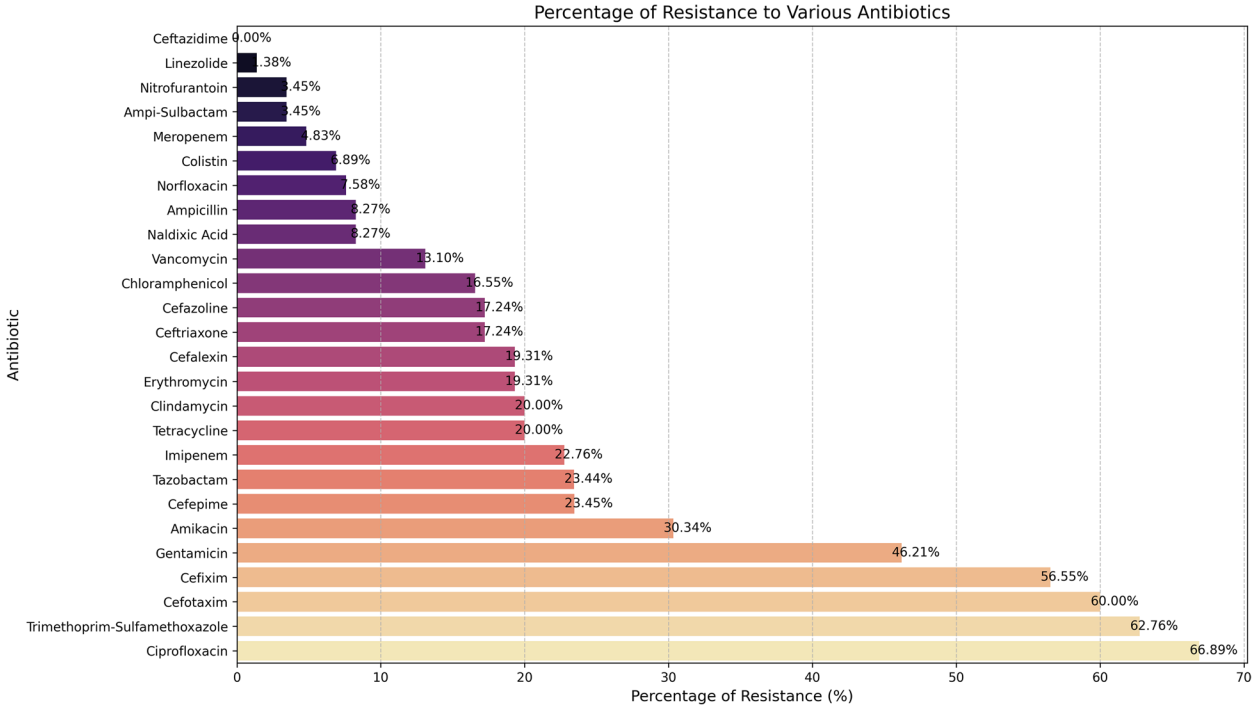

Fig. 3 Bar chart of antibiotic resistance patterns in bacteria isolated from surgical ICU patients. The bar chart in Fig. 3 illustrates the prevalence of resistance to various antibiotics isolates in patients admitted to the surgical ICU post-operation. Resistance rates are shown as frequencies and percentages for each antibiotic tested. The chart highlights significant resistance trends and identifies antibiotics with the highest and lowest resistance rates in isolated microbial agents

Five-fold cross-validation yielded a mean AUC of 0.896 ± 0.05 for XGBoost and 0.789 ± 0.07 for logistic regression, supporting the robustness of the models. The logistic regression baseline achieved a test AUC of 0.743 and accuracy of 77%, compared to XGBoost's test AUC of 0.786 and accuracy of 70%, justifying the use of a more complex model due to its superior discriminative ability (Fig. 4).

Figure 5 presents the feature importance derived from SHAP (SHapley Additive exPlanations) analysis for the XGBoost model, highlighting the predictors most influential in identifying MDR/XDR infections. Gram-negative (1.76) and Gram-positive (1.36) infections, followed by length of therapy (LOT) (1.31) and age (1.14), exhibited the highest mean absolute SHAP values, underscoring their critical roles in driving model predictions. Total hospitalization period (0.87) and total number of antibiotics used (0.48) also contributed significantly, while features such as bowel perforation had negligible impact (0.00). This visualization underscores the clinical relevance of infection type and treatment duration in predicting resistance, guiding targeted stewardship interventions.

Table 4 Comparison of different factors and outcomes across antibiotic resistance patterns in surgical ICU patients

Variable	High Resistance Group	Low Resistance Group	p-value
Age, years	69 (62, 78)	56.5 (44, 76.25)	0.061
ICU Stay-days	14.5 (7, 26.5)	14.5 (5, 18.25)	0.274
Sum Number of Antibiotic Doses	98.5 (28.5, 140.5)	59.5 (19.5, 150.75)	0.459
Days of Therapy (DOT)	41.5 (18, 66)	23 (7.75, 38.5)	0.002
Length of Therapy (LOT)	18.5 (7, 30.25)	11.5 (3.75, 17)	< 0.001
Antimicrobial-Free Days (AFD)	1.02 ± 2.12 [0 (0, 1)]	0.73 ± 1.77 [0 (0, 1)]	0.457

The values are presented in median (25th percentile, 75th percentile). Mann–Whitney U-test was used to measure the differences. High resistance group included patients with MDR and XDR infections, and low resistance group included those with culture negative and minimal resistant infections

Discussion

Antimicrobial resistance (AMR) is defined as the ability of microorganisms to withstand antimicrobial agents that were once effective against them. The World Health Organization (WHO) has recognized AMR as a critical global public health threat, particularly due to the growing ineffectiveness of key antimicrobial agents [8]. The WHO report highlights seven multidrug-resistant (MDR) bacterial strains of major global concern, with Iran situated in a region exhibiting elevated resistance to over five of these pathogens [8]. This retrospective cohort study aimed to evaluate AMR patterns, demographic associations, and clinical outcomes, especially surgical outcomes, among ICU patients in a tertiary care hospital over a two-year period.

Table 5 Antimicrobial resistance patterns and comparison between high and low resistance groups in surgical ICU patients

Variable	Categories	High Resistance Group	Low Resistance Group	*p*-value
Gram Stain	Negative	64 (61.54%)	40 (38.46%)	0.158
	Positive	31 (75.61%)	10 (24.39%)	
Aminoglycosides	Nonresistant	24 (35.29%)	44 (64.71%)	< 0.001
	Resistant	71 (92.21%)	6 (7.79%)	
Penicillins	Nonresistant	84 (63.16%)	49 (36.84%)	0.058
	Resistant	11 (91.67%)	1 (8.33%)	
β-lactamase Inhibitor Combinations	Nonresistant	62 (58.49%)	44 (41.51%)	0.006
	Resistant	33 (84.62%)	6 (15.38%)	
Carbapenems	Nonresistant	59 (56.19%)	46 (43.81%)	< 0.001
	Resistant	36 (90.0%)	4 (10.0%)	
1 st Generation Cephalosporins	Nonresistant	49 (53.26%)	43 (46.74%)	< 0.001
	Resistant	46 (86.79%)	7 (13.21%)	
3rd Generation Cephalosporins	Nonresistant	21 (51.22%)	20 (48.78%)	0.037
	Resistant	74 (71.15%)	30 (28.85%)	
4th Generation Cephalosporins	Nonresistant	70 (63.06%)	41 (36.94%)	0.359
	Resistant	25 (73.53%)	9 (26.47%)	
Fluoroquinolones	Nonresistant	7 (15.22%)	39 (84.78%)	< 0.001
	Resistant	88 (88.89%)	11 (11.11%)	
Macrolides	Nonresistant	71 (60.68%)	46 (39.32%)	0.022
	Resistant	24 (85.71%)	4 (14.29%)	
Tetracyclines	Nonresistant	74 (63.79%)	42 (36.21%)	0.512
	Resistant	21 (72.41%)	8 (27.59%)	
Lincosamides	Nonresistant	71 (61.21%)	45 (38.79%)	0.049
	Resistant	24 (82.76%)	5 (17.24%)	
Nitrofurans	Nonresistant	93 (66.43%)	47 (33.57%)	0.340
	Resistant	2 (40.0%)	3 (60.0%)	
Oxazolidinones	Nonresistant	93 (65.03%)	50 (34.97%)	0.545
	Resistant	2 (100.0%)	0 (0.0%)	
Phenicols	Nonresistant	75 (61.98%)	46 (38.02%)	0.076
	Resistant	20 (83.33%)	4 (16.67%)	
Folate Pathway Inhibitors	Nonresistant	23 (42.59%)	31 (57.41%)	< 0.001
	Resistant	72 (79.12%)	19 (20.88%)	
Glycopeptides	Nonresistant	76 (60.32%)	50 (39.68%)	0.002
	Resistant	19 (100.0%)	0 (0.0%)	
Polymyxin E	Nonresistant	90 (66.67%)	45 (33.33%)	0.313
	Resistant	5 (50.0%)	5 (50.0%)	

High resistance group included patients with MDR and XDR infections, and low resistance group included those with culture negative and minimal resistant infections

Our cohort predominantly comprised male patients with a mean age of 63.66 years, in line with findings by Uzman et al. [9], who also reported male predominance among AMR-affected patients. However, neither our study nor that of Uzman et al. identified sex or age as statistically significant contributors to AMR development [9]. In contrast, a large-scale surveillance study by Waterlow et al. [10] in Europe found both age and sex to be conditionally significant risk factors for AMR. These inconsistencies suggest the influence of complex interrelated factors such as public awareness, socioeconomic status, healthcare policy, and local antimicrobial prescribing patterns. Our findings emphasize the need for future research to clarify the demographic determinants of AMR across diverse populations and healthcare settings.

Diabetes mellitus (DM), particularly type 2, has been variably associated with AMR risk. Although previous literature suggests DM may act as an independent risk factor for recurrent infections and subsequent antimicrobial exposure [11], our study did not find a significant association between type 2 DM and AMR development. This discrepancy may be attributable to our relatively small sample size or differences in the spectrum of infections analyzed. Carrillo-Larco et al. [11] similarly observed insufficient evidence to firmly establish type 2 DM as a direct risk factor for AMR, although indirect associations through increased infection burden remain plausible.

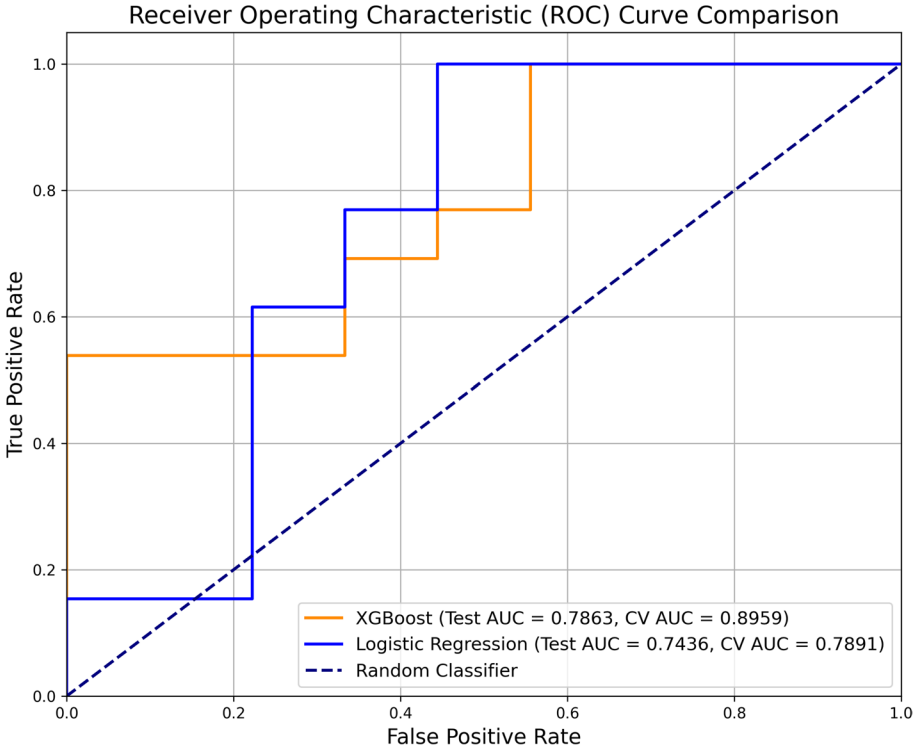

Fig. 4 Receiver operating characteristic (ROC) curve for the XGBoost and logistic regression predicting antibiotic resistance in surgical ICU patients. The ROC curves demonstrate the performance of each model in predicting antibiotic resistance (MDR or XDR) on test set. The mean area under the curve (AUC) cross-validation values of the models' ability to discriminate between patients with high resistant and low resistant infections, and clearly noted in plot guide box

In terms of clinical outcomes, our cohort exhibited an alarmingly high in-hospital mortality rate of 91.5%, significantly exceeding the 30% reported in a similar ICU population by Atramont et al. [12]. Additionally, the median Days of Therapy (DOT) and Length of Therapy (LOT) in our study were 29.5 and 14.5 days, respectively. These figures surpass the average reported in earlier studies, which typically observed antimicrobial therapy durations of 7–14 days in critically ill patients [13, 14]. This observation is consistent with other research that highlights the inherent trade-off between sensitivity and specificity in machine learning models applied to clinical data. The analysis of feature importance revealed that the type of infection, specifically Gram-negative and Gram-positive bacteria, is one of the most significant predictors. This finding is consistent with previous research that underscores the critical role of microbial characteristics in outcomes associated with antimicrobial resistance (AMR). Additionally, variables such as patient age and duration of therapy were identified as crucial factors, aligning with established correlations between these elements and adverse clinical outcomes.

The model's reliance on these features underscores the importance of incorporating clinical context into predictive analytics. However, the confusion matrix indicates that there is room for improvement, especially in reducing misclassifications. As evidenced by previous studies, optimizing model parameters through techniques such as hyperparameter tuning and cross-validation could enhance predictive accuracy further [15, 16]. It can be concluded that although our XGBoost model shows promise, ongoing optimization and validation against more extensive datasets will be essential for improving its applicability and reliability in clinical settings. Findings should be interpreted within the specific patient population and setting.

The elevated DOT compared to LOT indicates the frequent use of combination therapy or serial antibiotic changes [17], which are common in ICU settings but often lead to prolonged exposure, increased resistance, adverse effects, and higher healthcare costs [18]. Our median DOT of 295/100 patient-days is nearly double that reported by a previous study in a tertiary care setting (153.3 DOT/100 patient-days) [19], reflecting institutional differences and potentially overuse. Moreover, the median Antimicrobial-Free Days (AFD) of zero in our cohort underscores a heavy dependence on continuous antibiotic administration, an outcome contrary to the goals of antimicrobial stewardship programs [20, 21].

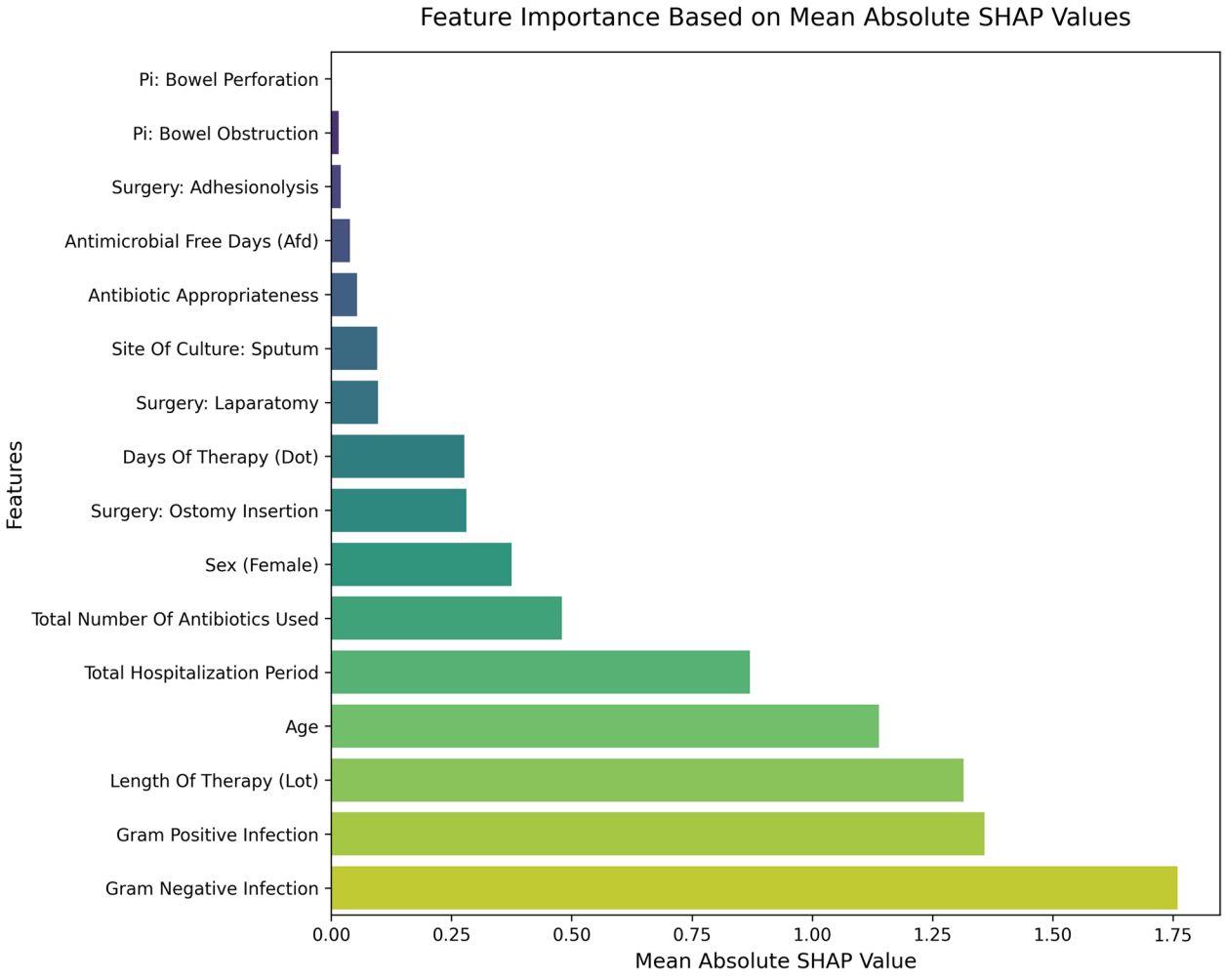

Fig. 5 SHAP plots visualizing global feature importance and interactions. SHAP (SHapley Additive exPlanations) values were used to quantify each feature's contribution to model predictions. Features were ranked by mean absolute SHAP values to identify the most influential predictors

Among the patients who underwent surgery, open laparotomy was the most frequently performed and most commonly associated with mortality, being observed in over 65% of cases. This invasive procedure typically requires broad-spectrum prophylactic antibiotics [22]. Ceftriaxone and metronidazole were the most commonly prescribed agents (75.5% and 67.9%, respectively), a regimen consistent with empirical strategies recommended by Tan et al. [23] for intra-abdominal infections such as appendicitis and cholecystitis. However, our resistance data raise serious concerns: 17.24% of isolates were resistant to ceftriaxone, and overall, 71.72% exhibited resistance to third-generation cephalosporins. This reflects a potentially inappropriate continuation of empirical therapies despite microbiological evidence to the contrary. Similar high resistance levels have been documented by Gelaw et al. [24] and Hamadalneel et al. [25], who reported ceftriaxone resistance rates of 57.2% and 70.7%, respectively, with Klebsiella and E. coli among the most resistant strains. In our study, 71.15% of patients received antibiotics to which their isolates were resistant ($p = 0.037$), signaling an urgent need for timely therapy adjustment.

The dominant culture-positive pathogens in our cohort were *Escherichia coli* (20%), *Acinetobacter baumannii* (17.24%), *Klebsiella pneumoniae* (16.55%), and *Enterococcus* spp. (11.72%). This distribution is consistent with previous studies from Iran and Ethiopia [24, 25]. Notably, *E. coli*, *Acinetobacter*, and *Klebsiella* demonstrated high rates of resistance, particularly to third-generation cephalosporins and fluoroquinolones. Mousavi et al. (2024) [26] also reported a similar pathogen distribution in Iran, with *E. coli* (27.5%), *A. baumannii* (18.5%), and *K. pneumoniae* (15.2%) being the most frequently isolated organisms from hospital-acquired infections. Another study from southwest Iran showed 53% of infections were caused by MDR bacteria, and 33.5% by bacteria resistant to all tested antimicrobials [27].

Multidrug resistance, often driven by resistance gene accumulation and efflux pump mechanisms [28], is of particular concern in ICU settings due to selective antibiotic pressure [29]. Our findings revealed a significant MDR prevalence, especially among gram-negative bacteria such as *E. coli*, *A. baumannii*, and *K. pneumoniae*, in line with Salarvan et al. [30], who reported a 96.3% MDR rate in an Iranian ICU. Extensively drug-resistant (XDR) strains, defined by resistance to all but one or two antimicrobial categories [7], were also observed in our cohort. These findings highlight the urgent need for nationwide infection control policies and antimicrobial stewardship strategies tailored to high-risk ICU populations.

Resistance to fluoroquinolones, including ciprofloxacin (66.89%) and nalidixic acid (8.27%), was particularly notable in our study, with a total fluoroquinolone resistance rate of 68.27%. This echoes national findings where resistance to ciprofloxacin among ICU isolates was reported at 51.3% [30]. Our high resistance rates to both fluoroquinolones and third-generation cephalosporins are especially concerning given their widespread use in empirical treatment. European surveillance reports have similarly advised against fluoroquinolone use as empirical therapy, with countries like Poland showing continued overuse despite EU-wide reductions [31].

Comparative analysis between high-resistance (MDR or XDR) and low-resistance groups in our study revealed significantly elevated resistance rates across multiple antibiotic classes in the high-resistance group—including aminoglycosides, carbapenems, cephalosporins, fluoroquinolones, and folate pathway inhibitors ($p < 0.001$). This trend mirrors WHO global data, which attribute over 929,000 deaths annually to six leading AMR pathogens, including *E. coli*, *S. aureus*, *K. pneumoniae*, *S. pneumoniae*, *A. baumannii*, and *P. aeruginosa* [32]. Moreover, certain pathogen-drug combinations, such as third-generation cephalosporin-resistant *E. coli* and carbapenem-resistant *K. pneumoniae*, accounted for over 100,000 deaths in 2019 alone [32].

Additionally, our exploratory application of an XGBoost machine learning model demonstrated commendable performance. The model's recall for MDR/XDR cases (0.71) emphasizes the identification of high-risk patients, but the precision for non-resistant cases (0.60) indicates a higher rate of false positives. This trade-off, common in clinical prediction models, may lead to unnecessary interventions, underscoring the need for future refinements to balance precision and recall.

On other hand, the logistic regression model demonstrated higher recall for resistant cases (1.00) but lower precision (0.72) and recall for non-resistant cases (0.44), highlighting complementary strengths (Fig. 5). This observation reflects the well-documented trade-off between sensitivity and specificity in machine learning models applied to clinical datasets [33, 34]. Importantly, our XGBoost model was designed with an emphasis on preventing data leakage through careful feature selection. To preserve model generalizability and avoid circular reasoning, we excluded variables directly related to microbial species and their resistance profiles, focusing instead on demographic, clinical, surgical, and antibiotic utilization data (e.g., DOT, LOT, AFD), as well as infection type (Gram-positive vs. Gram-negative).

In contrast, Vihta et al. [34] included prior antibiotic exposure and pathogen-specific resistance histories for each pathogen–antibiotic combination across UK hospital Trusts. Their model leveraged more granular microbiological features and historical resistance patterns, which, while improving predictive performance, may introduce bias or limit applicability in settings lacking comprehensive longitudinal data. Similarly, Yang and Wu [35] utilized genomic data and pan-genome-based feature selection to predict resistance at the gene level, offering a highly granular, molecular approach that differs fundamentally from our clinical-variable-based strategy. By integrating clinical and antibiotic utilization data with machine learning, this study offers a promising framework for predicting MDR/XDR infections in resource-limited settings, contributing to both AMR surveillance and ICU management.

The superior cross-validation AUC of XGBoost (0.896) compared to logistic regression (0.789) underscores the potential of advanced machine learning to enhance predictive accuracy (Fig. 5). The XGBoost model leverages clinical data to identify high-risk MDR/XDR patients, serving as a scalable tool for ICU decision-making. This demonstrates the additive benefit of machine learning in capturing complex patterns in clinical data, potentially optimizing antibiotic therapy and stewardship, pending further validation. Our analysis of feature importance revealed that certain variables, particularly the presence of infections caused by Gram-negative organisms, patient age, and length of therapy (LOT), were among the strongest predictors of resistance. These findings align with previous studies that underscore the influence of microbial characteristics and patient-level factors on AMR outcomes.

This aligns with prior evidence [36, 37], highlighting the central role of microbial characteristics in AMR-related prognosis, especially in ICU settings with intense selective antibiotic pressure. Our model also identified patient age and therapy duration (DOT and LOT) as key factors, consistent with established associations between prolonged antimicrobial exposure, advanced age, and worse outcomes. Notably, these findings resonate with recent clinical studies: extended colistin therapy (≥14 days) improved survival and microbiologic clearance in critically ill patients with carbapenem-resistant *A. baumannii*, whereas colistin–fosfomycin combination therapy for CRE offered no mortality benefit [36, 37]. Together, these

insights underscore that readily accessible clinical variables—rather than pathogen-specific genomic data—can meaningfully predict outcomes and inform antimicrobial strategies, particularly in resource-limited environments. While the model shows promising potential, the confusion matrix highlights opportunities for further refinement, particularly in minimizing misclassification of non-resistant cases. While our XGBoost model shows promise in this exploratory, hypothesis-generating study, the small sample size (n = 106, test set n = 22) raises concerns for overfitting and model instability. The single-center design in southern Iran, coupled with the unusually high mortality (91.5%), limits generalizability to other ICUs. Lack of external validation further restricts applicability. Enhancing model performance through hyperparameter tuning, external validation on large cohorts, and the inclusion of additional clinical variables, without compromising data integrity, could further boost accuracy and robustness [15, 16].

In summary, our findings illustrate the formidable challenge posed by AMR in the surgical ICU setting, where extensive antibiotic use and high rates of MDR pathogens coalesce to adversely impact patient outcomes. These results underscore the imperative for implementing robust antimicrobial stewardship programs and revising empirical treatment protocols to better align with local resistance patterns. Given the high mortality rate observed, prompt and effective interventions are essential to improve clinical outcomes in this vulnerable population. Although our XGBoost model demonstrates promising predictive capability using readily available clinical data, future work involving larger and more diverse datasets, coupled with external validation, will be essential to enhance its utility and reliability in real-world clinical decision-making.

Limitations

This study has several limitations. First, it was conducted at a single tertiary care center in southern Iran, which may limit the generalizability of our findings to other institutions, particularly those in developed countries with different patient demographics, AMR patterns, and healthcare practices. The unusually high mortality rate (91.5%) further restricts applicability. Second, although a wide range of clinical variables was included, microbiological features such as specific pathogen identification and antibiotic susceptibility profiles were intentionally excluded to avoid data leakage, potentially reducing the model's predictive precision. Third, the retrospective design and reliance on electronic medical records may have introduced information bias or incomplete data capture, potentially affecting model performance. In addition, the small sample size and limited test set ($n = 22$) increase the risk of overfitting and reduce model stability. The absence of external validation restricts the applicability of our findings to other settings. Larger, multicenter datasets incorporating molecular data (e.g., ESBL or carbapenemase genes) are needed to confirm and extend these results.

Conclusion

In this exploratory, single-center study, the high prevalence of multidrug-resistant (MDR) pathogens and the elevated in-hospital mortality observed in this cohort highlight the substantial challenges of managing postoperative surgical ICU patients in a resource-limited setting. Gram-negative organisms predominated, and the frequency of MDR isolates underscores the complexity of infection control and the need for optimized empiric therapy. These hypothesis-generating findings reinforce the importance of robust antimicrobial stewardship programs and the adaptation of treatment protocols to local resistance trends. Our XGBoost model demonstrates the promising potential of machine learning for resistance prediction and clinical decision support in high-risk ICU populations, but findings should be interpreted within this specific context. However, further research is required to refine predictive performance, integrate molecular resistance data, and evaluate generalizability in larger, multicenter cohorts. Future studies should also clarify the relationship between AMR and patient outcomes in broader, less selective populations to inform both clinical management and stewardship strategies.

Abbreviations

AMR	Antimicrobial Resistance
MDR	Multidrug-resistant
XDR	Extensively drug-resistant
PDR	Pan-drug-resistant
ICU	Intensive Care Unit
DOT	Days of Therapy
LOT	Length of Therapy
AFD	Antimicrobial-Free Days
XGBoost	Extreme Gradient Boosting
ROC-AUC	Receiver Operating Characteristic—Area Under the Curve
SHAP	SHapley Additive exPlanations
EHR	Electronic Health Record

Supplementary Information

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Additional file 1.

Additional file 2.

Additional file 3.

Additional file 4.

Additional file 5.

Additional file 6.

Additional file 7.

Additional file 8.

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Declaration of Generative AI Use
AI tools for paraphrasing, proofreading, and grammar refinement. These tools were employed to improve linguistic accuracy without altering the scientific content. All authors take full responsibility for the final manuscript and have thoroughly reviewed and approved its contents.

Authors' contributions
BZ and AT contributed to the conception of the work. HH contributed to the design and methodology of the work, interpretation of data, data visualization, manuscript writing, revisions, and performed the statistical analysis. ShY led the investigators team, managed administrative tasks, and drafted the initial manuscript. MK, AE, SGH, AS, SDN, HRSH, RAZ, SM, AR, BZq, SSh, and AY contributed to the investigation and data collection. All authors read and approved the final manuscript.

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Data availability
The dataset supporting the conclusions of this article is included within the article (see Additional file 3).

Declarations

Ethics approval and consent to participate
This study was conducted in accordance with the ethical standards of the Research Ethics Committee of Shiraz University of Medical Sciences (Approval ID: IR.SUMS.MED.REC.1403.267) and the principles of the Declaration of Helsinki. Written informed consent was obtained from all participants before enrollment in the study.

Consent for publication
Not applicable.

Competing Interests
The authors declare no competing interests.

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