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ORIGINAL RESEARCH

Development and Validation of a Nomogram to Predict Multidrug-Resistant Organism Infection in Severe Pneumonia: A Retrospective Cohort Study

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Objective: The purpose of this study was to explore the etiological characteristics of multidrug-resistant bacteria (MDRO) infection in patients with severe pneumonia (SP) and to construct a nomogram model based on their risk factors.

Methods: A total of 214 severe pneumonia (SP) patients admitted from November 2022 to January 2024 were retrospectively assigned to the modeling group, and 92 patients admitted from February 2024 to March 2025 formed the validation group. Patients were categorized into MDRO and non-MDRO groups based on multidrug-resistant organism infection status. The distribution of pathogens in the MDRO group was analyzed. Logistic regression was performed to analyze the influencing factors. R software was performed to construct nomogram models. Decision curve analysis(DCA) was performed to evaluate the clinical application value of nomogram models.

Results: A total of 93 strains of pathogenic bacteria were isolated from 72 MDRO-infected patients. Gram-negative bacteria showed the highest resistance to piperacillin-tazobactam and piperacillin, while Gram-positive bacteria exhibited a high resistance rate to penicillin. Logistic analysis showed types of pneumonia, chronic obstructive pulmonary disease(COPD), invasive examination,intensive care unit-(ICU) admission, antimicrobial drug combination, use of carbapenems, and hypoalbuminemia were risk factors ($P<0.05$). The modeling group achieved an area under curve(AUC) of 0.910, with the Hosmer–Lemeshow (H-L) test showing $\chi^2 = 7.423$. DCA indicated that the nomogram model had high clinical utility for predicted probabilities between 0.07 and 0.94. In the validation group, the AUC was 0.953, with H-L test $\chi^2 = 7.032$. DCA showed that the nomogram model had high clinical value for predicted probabilities between 0.07 and 0.89.

Conclusion: The types of pneumonia, COPD, invasive examination, ICU admission, combination of antimicrobial drugs, carbapenems use, and hypoalbuminemia are influencing factors for MDRO infection in SP patients. The nomogram constructed based on this can better evaluate the risk of MDRO infection.

Keywords: severe pneumonia, multidrug resistant organism, risk factors, nomogram

Introduction

Pneumonia is an inflammatory response in the lungs caused by multiple factors, including pathogen-induced infection, impaired immune system, and medication. While ordinary pneumonia can achieve a good therapeutic effect after anti-inflammatory treatment. Severe pneumonia (SP) is a relatively special type of pneumonia mostly caused by pathogenic bacteria infection, which reduces pulmonary ventilation function and thus induces respiratory failure or even multiple organ dysfunction, posing a serious threat to patients' lives.[1,2] Currently, clinical treatment of SP with antibacterial drugs can control the disease and effectively improve patient prognosis. However, during hospitalization, the irrational use of antibiotics may lead to the body's automatic selection of multiple drug-resistant organisms (MDRO), forming MDRO colonization and infection. In addition, most of these patients are elderly with low immunity and weak resistance to infection, making them prone to MDRO infection.[3,4] Worldwide, the incidence of multidrug-resistant organism (MDRO) infections in ICU patients is significantly higher than in general wards, with severe pneumonia being one of the main reservoirs for MDROs. During infection, bacteria can breach the host defense barriers, invade tissues or the bloodstream, and trigger local inflammation or systemic infection, requiring comprehensive assessment through pathogen detection combined with clinical symptoms. The pathogenesis of MDROs remains

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unclear; some studies suggest that it may be related to bacterial genetic mutations and the acquisition of exogenous resistance genes, leading to resistance to multiple antimicrobial agents. Moreover, resistance genes can be horizontally transmitted between bacteria via plasmids and other mechanisms, thereby exacerbating the spread of MDROs.[5] Once MDRO appears in SP patients, it can aggravate the condition, prolong hospital stays, and increase treatment difficulties, thereby affecting patient prognosis.[6] Therefore, it is crucial to analyze the distribution and drug resistance of pathogens causing MDRO infection in SP patients and to identify as early as possible the factors influencing MDRO infection so as to improve patient outcomes.

Nomograms can quantify the screened results, integrate the total risk scores of hazardous factors, and calculate the corresponding probability, thereby identifying high-risk groups in the predictive model and assessing the risk of this event. Compared with traditional risk scores such as APACHE II and SOFA, nomograms have obvious advantages, mainly including higher predictive accuracy, greater clinical applicability, and higher degree of individualization: traditional risk scores are mostly population-level risk assessments, whereas nomograms can provide personalized risk predictions based on the characteristics of individual patients, facilitating the development of individualized intervention strategies. Nomograms can also evaluate stability through internal validation (modeling cohort) and external validation (validation cohort), and quantify predictive performance using calibration curves, ROC curves, and other indicators, making them more scientific than the subjective assessments of traditional scores.[7,8] A study found that constructing a nomogram risk prediction model for MDRO infections in the neonatal intensive care unit (NICU) demonstrated good goodness-of-fit and calibration. This model can be used in the NICU to develop targeted prevention and control strategies for each individual risk factor (including low birth weight, maternal age, antibiotic use for more than 7 days, and MDRO colonization).[9] Based on this, there are few reports on MDRO infection in SP patients using nomograms. Hence, this study aims to investigate the etiology and identify the risk factors associated with MDRO infections in patients with SP, and to construct a nomogram-based predictive model.

Data and Methods

General Data

A total of 214 patients with severe pneumonia (SP) admitted to our hospital from November 2022 to January 2024 were retrospectively included as the training cohort, and 92 patients admitted from February 2024 to March 2025 were included as the validation group. Patients were classified into MDRO and non-MDRO groups based on multidrug-resistant organism infection status. The flowchart of case selection is shown in Figure 1. Inclusion criteria: (1) meeting the standards for SP,[10] and confirmed by clinical manifestations and imaging, with all included cases being infectious pneumonia; (2) age ≥18 years; (3) first-time treatment; (4) positive sputum culture; (5) complete clinical data. Exclusion criteria: (1) other infectious diseases (infectious diseases of the digestive, urinary, and other systems); (2) malignant tumors; (3) other lung diseases (tuberculosis, asthma); (4) major organ dysfunction; (5) pregnant or lactating women; (5) psychiatric disorders; (6) non-infectious pneumonia; (7) immune dysfunction. This study was approved by the Ethics Committee of Ganzhou People's Hospital.

Methods

MDRO Determination Criteria

A fully automated microbial analysis system (VITEK 2 Compact, bioMérieux, France) and a drug susceptibility analysis system were used to detect pathogens. When the bacteria cultured from a specimen exhibit resistance to three or more types of antimicrobial drugs simultaneously, and if the same strain is continuously cultured for three times to be MDRO-positive, it is determined to be MDRO.[11]

Pathogen Detection and Drug Susceptibility Testing

Early-morning sputum samples were collected after cleaning the oral cavity with normal saline. The strains were cultured, and the pathogens were detected using a fully automated microbial analyzer. Drug susceptibility testing was performed on the isolated strains using a drug susceptibility instrument and drug susceptibility cards (ATB Fungus2 susceptibility card).Quality control strains (*Klebsiella pneumoniae* ATCC 700603, *Pseudomonas aeruginosa* ATCC 27853, and *Staphylococcus aureus* ATCC 29213) were used simultaneously for culture quality control; antimicrobial susceptibility testing was performed using an automated microbial analysis system (VITEK 2 Compact, bioMérieux, France), and the identification of MDROs in this study was strictly conducted according to the definition of multidrug resistance in the corresponding standard.[12]

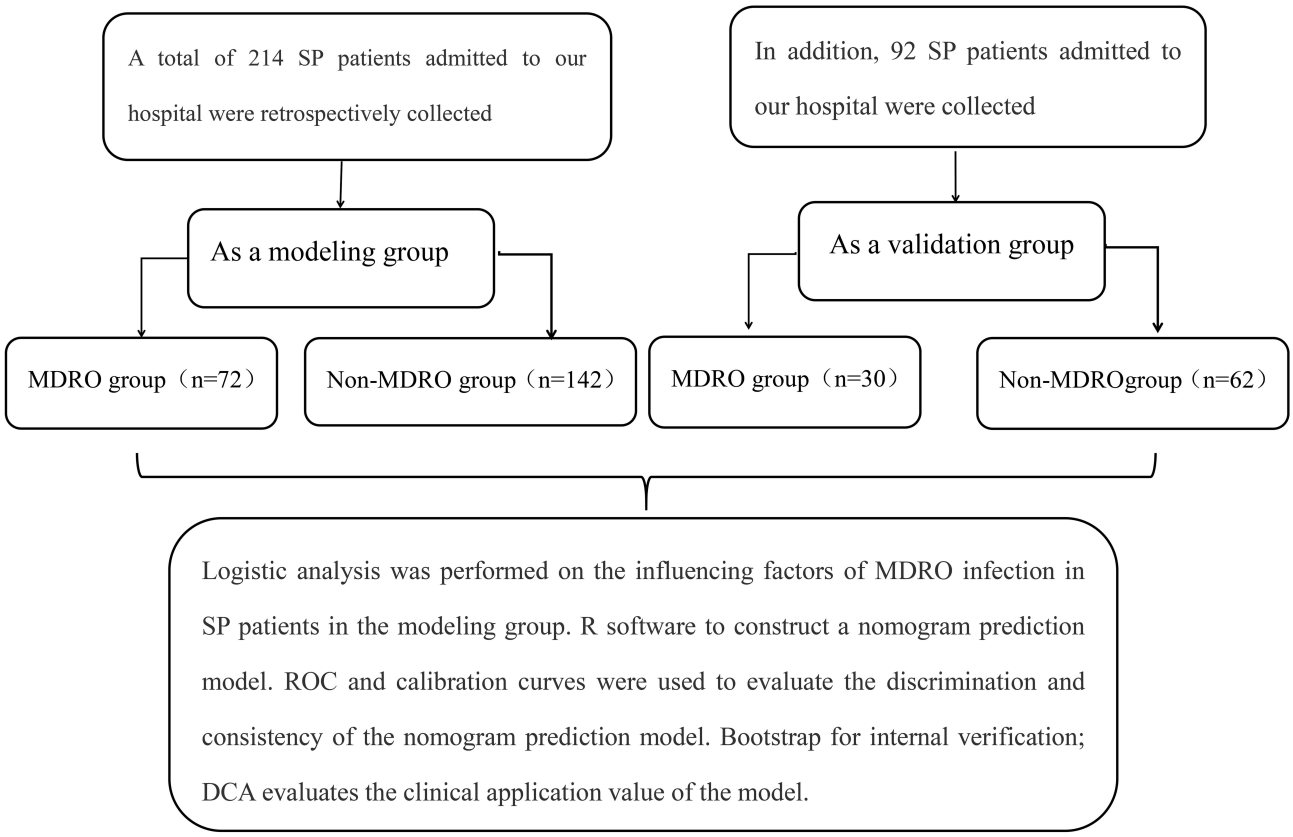

Figure 1 Case flow collection diagram.

Clinical Data Collection

Clinical data were collected from the electronic medical record system (all personnel responsible for data collection had undergone professional training; the study data were entered independently by two individuals into the database, and cross-checked after entry to correct any errors and ensure accuracy). Main variables included age, sex, BMI, length of hospital stay, duration of fever, duration of antibiotic use, diabetes, hypertension, hyperlipidemia,coronary heart disease (CHD),smoking history, alcohol use, pneumonia type (community-acquired pneumonia [CAP]:It is an infectious parenchymal inflammation of the lungs acquired outside the hospital, hospital-acquired pneumonia [HAP]:It refers to pneumonia that was neither present nor incubating at the time of hospital admission but developed 48 hours or more after hospitalization), chronic obstructive pulmonary disease (COPD), invasive procedures, indwelling urinary catheter, admission to ICU, combination antibiotic therapy, use of carbapenems antibiotics, disturbance of consciousness, hypoproteinemia,deep venous catheterization,GCS score, coma, body temperature, endotracheal intubation, central venous catheter, mechanical ventilation time, white blood cell count (WBC), platelet count (PLT), fasting blood glucose (FBG), triglycerides (TG), total cholesterol (TC), hemoglobin (Hb), and APACHE II score. Variables with a missing rate exceeding 5% were excluded to ensure the reliability and rigor of the results.

Statistical Analysis

Data were analyzed using SPSS 25.0. Count data were tested by χ^2-test and expressed as cases (%). Measurement data that met normality according to the Shapiro–Wilk test were tested by t test and expressed as ($\bar{x} \pm s$).For non-normally distributed data, values were expressed as median (quartiles) [M (Q_1, Q_3)], and comparisons between groups were performed using the nonparametric Mann–Whitney U-test.Logistic regression analysis was used to identify risk factors for MDRO infection in SP patients (forward stepwise method with entry criteria of 0.05 and removal criteria of 0.1). A nomogram prediction model was constructed using R software (R version 4.5.1 and the rms package). The

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discrimination and calibration of the nomogram were evaluated by ROC curves and calibration plots, respectively. Internal validation was performed using the bootstrap method. Decision curve analysis (DCA) was conducted to assess the clinical utility of the model. A P-value <0.05 was considered statistically significant.

Results

Distribution and Composition of Pathogens in MDRO Infected Patients

A total of 72 patients yielded 93 strains of pathogens. Among these, 53 strains (56.99%) were Gram-negative bacteria, primarily *Acinetobacter baumannii* (23 strains,24.73%) and *Klebsiella pneumoniae* (14 strains, 15.05%); 36 strains (38.71%) were Gram-positive bacteria, mainly *Staphylococcus aureus* (17 strains,18.28%) and *Staphylococcus epidermidis* (13 strains, 13.98%); and 4 strains (4.30%) were fungi, *Candida* spp. See Table 1.

Analysis of Drug Resistance of Gram-Negative Bacteria

Gram-negative bacteria showed the highest resistance to piperacillin-tazobactam and piperacillin, both at 100%, but was more sensitive to cefiderocol and colistin. See Table 2.

Analysis of Drug Resistance of Gram-Positive Bacteria

Gram-positive bacteria had a relatively high resistance rate (82.35%) to penicillin but was more sensitive to oxacillin, norvancomycin, vancomycin, fosfomycin, rifampin, teicoplanin, and tigecycline. See Table 3.

Comparison of Clinical Data Between the MDRO and Non-MDRO Groups in the Modeling Group

Among the 214 patients, 72 developed MDRO infection, with an incidence rate of 33.64%. There were significant differences in pneumonia type, COPD, invasive procedures, ICU admission, combination antibiotic therapy, use of carbapenems antibiotics, and hypoproteinemia between the MDRO Group and Non-MDRO Groups (P<0.05). There were no significant differences in other clinical data (P>0.05). See Table 4.

Multifactor Analysis of Influencing Factors for MDRO Infection in SP Patients

The dependent variable was defined as follows: occurrence of MDRO infection in SP patients = 1, otherwise = 0. The assignments for the independent variables are shown in Table 5. After multicollinearity testing, the variance inflation

Table 1 Distribution and Composition of Pathogenic Bacteria in MDRO Infected Patients

Nosophyte	Number of Cultures	Percentage (%)
Gram-negative bacteria	53	56.99
Acinetobacter baumannii	23	24.73
Klebsiella pneumoniae	14	15.05
Pseudomonas aeruginosa	8	8.60
Escherichia coli	5	5.38
Enterobacter cloacae	3	3.23
Gram Positive	36	38.71
Staphylococcus aureus	17	18.28
Staphylococcus epidermidis	13	13.98
Enterococcus faecalis	4	4.30
Streptococcus pneumoniae	2	2.15
Fungus	4	4.30
Candida	4	4.30

Table 2 Analysis of Drug Resistance in Gram-Negative Bacteria

Nosophyte	Acinetobacter baumannii (n=23)	Klebsiella pneumoniae (n=14)	Pseudomonas aeruginosa (n=8)	Escherichia coli (n=5)	Enterobacte cloacae (n=3)
	Number of Isolates (%)	Number of Isolates (%)	Number of Isolates (%)	Number of Isolates (%)	Number of Isolates (%)
Cefdinir	0 (0.00)	0 (0.00)	0 (0.00)	0 (0.00)	0 (0.00)
Polymyxin E	0 (0.00)	0 (0.00)	0 (0.00)	0 (0.00)	0 (0.00)
Tigecycline	1 (4.35)	1 (7.14)	0 (0.00)	0 (0.00)	0 (0.00)
Eravacycline dihydrochloride	3 (13.04)	1 (7.14)	0 (0.00)	0 (0.00)	0 (0.00)
Compound Sulfamethoxazole Tablets	15 (65.22)	6 (42.86)	2 (25.00)	1 (20.00)	1 (33.33)
Imipenem	17 (73.91)	9 (64.29)	2 (25.00)	1 (20.00)	1 (33.33)
Meropenem	17 (73.91)	9 (64.29)	4 (50.00)	2 (40.00)	1 (33.33)
Amikacin	18 (78.26)	10 (71.43)	4 (50.00)	2 (40.00)	1 (33.33)
Sulbactam and Cefoperazone	18 (78.26)	10 (71.43)	4 (50.00)	3 (60.00)	1 (33.33)
Levofloxacin	20 (86.96)	10 (71.43)	5 (62.50)	3 (60.00)	1 (33.33)
Gentamycin	21 (91.30)	12 (85.71)	5 (62.50)	3 (60.00)	2 (66.67)
Ampicillin sodium and Sulbactam	21 (91.30)	12 (85.71)	5 (62.50)	3 (60.00)	2 (66.67)
Cefepime	21 (91.30)	12 (85.71)	6 (75.00)	4 (80.00)	2 (66.67)
Ceftazidime	22 (95.65)	13 (92.86)	6 (75.00)	4 (80.00)	2 (66.67)
Ciprofloxacin	22 (95.65)	13 (92.86)	7 (87.50)	4 (80.00)	2 (66.67)
Piperacillin-tazobactam	23 (100.00)	14 (100.00)	8 (100.00)	5 (100.00)	3 (100.00)
Piperacillin	23 (100.00)	14 (100.00)	8 (100.00)	5 (100.00)	3 (100.00)

Table 3 Analysis of Drug Resistance in Gram-Positive Bacteria

Nosophyte	Staphylococcus aureus (n=17)	Staphylococcus epidermidis (n=13)	Enterococcus faecalis (n=4)	Streptococcus pneumoniae (n=2)
	Number of Isolates (%)	Number of Isolates (%)	Number of Isolates (%)	Number of Isolates (%)
Oxacillin	0 (0.00)	0 (0.00)	0 (0.00)	0 (0.00)
NorvancomycinHydrochloride	0 (0.00)	0 (0.00)	0 (0.00)	0 (0.00)
Vancomycin	0 (0.00)	0 (0.00)	0 (0.00)	0 (0.00)
Fosfomycin	0 (0.00)	0 (0.00)	0 (0.00)	0 (0.00)
Rifampicin	0 (0.00)	0 (0.00)	0 (0.00)	0 (0.00)
Teicoplanin	0 (0.00)	0 (0.00)	0 (0.00)	0 (0.00)
Tigecycline	0 (0.00)	0 (0.00)	0 (0.00)	0 (0.00)
Contezolid	1 (5.88)	1 (7.69)	1 (25.00)	1 (50.00)
Compound Sulfamethoxazole Tablets	3 (17.65)	2 (15.38)	1 (25.00)	1 (50.00)
Gentamycin	2 (11.76)	2 (15.38)	1 (25.00)	1 (50.00)
Clindamycin	4 (23.53)	3 (23.08)	1 (25.00)	0 (0.00)
Levofloxacin	3 (17.65)	3 (23.08)	1 (25.00)	1 (50.00)
Erythromycin	8 (47.06)	6 (46.15)	2 (50.00)	1 (50.00)
Ciprofloxacin	3 (17.65)	3 (23.08)	1 (25.00)	1 (50.00)
Nemonoxacin	2 (11.76)	2 (15.38)	1 (25.00)	1 (50.00)
Benzylpenicillin	14 (82.35)	11 (84.62)	3 (75.00)	2 (100.00)

factor (VIF) was less than 10, indicating no multicollinearity. Logistic regression analysis showed that pneumonia type, COPD, invasive procedures, ICU admission, combination antibiotic therapy, use of carbapenems antibiotics, and hypoproteinemia were risk factors for MDRO infection in SP patients (P<0.05). See Table 6.

Table 4 Comparison of Clinical Data Between MDRO and Non-MDRO Groups in the Modeling Group

Factor	MDRO Group (n=72)	Non-MDRO Group (n=142)	t/χ^2	*P*
Age			0.141	0.707
≥60years old	50 (69.44)	95 (66.90)		
<60 years old	22 (30.56)	47 (33.10)		
Gender			0.016	0.900
Male	45 (62.50)	90 (63.38)		
Female	27 (37.50)	52 (36.62)		
BMI			0.143	0.706
≥24kg/m^2	21 (29.17)	45 (31.69)		
<24kg/m^2	51 (70.83)	97 (68.31)		
Length of stay (d)	16.95±3.32	16.12±3.11	1.811	0.072
Heat generation time (d)	7.52±2.02	7.41±1.98	0.383	0.702
Duration of use of Antipneumonia drugs (d)	16.24±3.41	16.01±3.04	0.504	0.615
Diabetes			0.631	0.427
Yes	12 (16.67)	18 (12.68)		
No	60 (83.33)	124 (87.32)		
Hypertensive			0.028	0.867
Yes	15 (20.83)	31 (21.83)		
No	57 (79.17)	111 (78.17)		
Hyperlipidemia			0.081	0.776
Yes	8 (11.11)	14 (9.86)		
No	64 (88.89)	128 (90.14)		
Smoking history			0.970	0.325
Yes	25 (34.72)	40 (28.17)		
No	47 (65.28)	102 (71.83)		
Coronary heart disease			0.144	0.704
Yes	5 (6.94)	8 (5.63)		
No	67 (93.06)	134 (94.37)		
Drinking history			0.495	0.482
Yes	32 (44.44)	56 (39.44)		
No	40 (55.56)	86 (60.56)		
Types of Pneumonia			19.914	<0.001
HAP	56 (77.78)	65 (45.77)		
CAP	16 (22.22)	77 (54.23)		
COPD			38.626	<0.001
Yes	35 (48.16)	15 (10.56)		
No	37 (51.39)	127 (89.44)		
Invasive examination			14.412	<0.001
Yes	45 (62.50)	50 (35.21)		
No	27 (37.50)	92 (64.79)		
Indwelling catheterization			1.132	0.287
Yes	47 (65.28)	82 (57.75)		
No	25 (34.72)	60 (42.25)		
ICU admission			15.045	<0.001
Yes	54 (75.00)	67 (47.18)		
No	18 (25.00)	75 (52.82)		
Antimicrobial drug combination			14.917	<0.001
Yes	58 (80.56)	76 (53.52)		
No	14 (19.44)	66 (46.48)		

(*Continued*)

Table 4 (Continued).

Factor	MDRO Group (n=72)	Non-MDRO Group (n=142)	t/χ^2	*P*
Use of carbapenems			12.280	<0.001
Yes	39 (54.17)	42 (29.58)		
No	33 (45.83)	100 (70.42)		
Disorders of consciousness			0.372	0.542
Yes	20 (27.78)	34 (23.94)		
No	52 (72.22)	108 (76.06)		
Hypoproteinemia			11.506	0.001
Yes	15 (20.83)	8 (5.63)		
No	57 (79.17)	134 (94.37)		
Deep vein cannulation			2.750	0.097
Yes	38 (52.78)	58 (40.85)		
No	34 (47.22)	84 (59.15)		
GCS score	7.65±1.25	7.89±1.34	1.266	0.207
Coma	30 (41.67)	54 (38.03)	0.265	0.607
Body temperature (°C)	36.85±0.65	36.89±0.72	0.396	0.692
Endotracheal intubation	24 (33.33)	41 (28.87)	0.449	0.503
Central venous catheter	18 (25.00)	126 (18.31)	1.309	0.253
Mechanical ventilation time (d)	3.65±1.01	3.49±0.98	1.117	0.265
WBC (×109/L)	7.16±1.53	7.05±1.54	0.495	0.623
PLT (×109/L)	133.67±19.42	132.24±20.41	0.492	0.535
FBG (mmol/L)	7.05±1.45	6.93±1.44	0.575	0.566
TG (mmol/L)	1.06±0.25	1.08±0.26	0.539	0.591
TC (mmol/L)	4.52±1.18	4.51±1.19	0.058	0.954
Hb (g/L)	125.86±14.53	126.01±15.04	0.070	0.944
APACHE II score	18.16±2.43	17.98±2.14	0.555	0.579

Abbreviations: BMI, Body mass index; CAP, Community-acquired pneumonia; HAP, Hospital-acquired pneumonia; COPD, Chronic obstructive pulmonary disease; WBC, White blood cell count; PLT, Platelet count; FBG, Fasting blood glucose; TG, Triglycerides; TC, Total cholesterol; Hb, Hemoglobin.

Table 5 Assignment methods of Argument Variables

Variable	Assignment Method
Types of Pneumonia	HAP=1, CAP=0
COPD	Yes=1, no=0
Invasive examination	Yes =1, no=0
ICU admission	Yes =1, no=0
Antimicrobial drug Combination	Yes=1, no=0
Use of carbapenems	Yes =1, no=0
Hypoproteinemia	Yes =1, no=0

Construction of a Nomogram Model for MDRO Infection in SP Patients

The nomogram model was constructed as follows: $P=e^x/(1+e^x)$, $x = -4.268+2.026 \times$ pneumonia type $+ 1.529 \times$ COPD $+ 1.111 \times$ invasive procedures $+1.513 \times$ ICU admission $+ 1.061 \times$ combination antibiotic therapy $+ 1.147 \times$ use of carbapenems $+ 1.133 \times$ hypoproteinemia. For example, for a patient with CAP (0 points), COPD (76.5 points), invasive procedures (56.5 points), ICU admission (75.0 points), no combination antibiotic therapy (0 points), use of carbapenems (57.5 points), and hypoproteinemia (21.5 points), the total score would be 287.0 points. Drawing a vertical line from the total score indicates that the predicted probability is 81%. See Figure 2.

Table 6 Multifactorial Analysis of Factors Influencing MDRO Infection in SP Patients

Variable	β value	SE Variable	Wald χ^2 Variable	*P* Variable	OR Variable	95% CI
Types of Pneumonia	2.026	0.452	20.104	<0.001	7.582	3.127~18.379
COPD	1.529	0.458	11.133	0.001	4.613	1.879~11.324
Invasive examination	1.111	0.440	6.362	0.012	3.037	1.281~7.198
ICU admission	1.513	0.423	12.794	<0.001	4.541	1.982~10.403
Antimicrobial drug combination	1.061	0.442	5.771	0.016	2.890	1.216~6.871
Use of carbapenems	1.147	0.506	5.129	0.024	3.148	1.167~8.494
Hypoproteinemia	1.133	0.331	11.710	<0.001	3.104	1.622~5.938
Constant	−4.268	0.542	62.068	<0.001	0.014	

Abbreviation:COPD, Chronic obstructive pulmonary disease.

Internal Validation of the Nomogram Model for MDRO Infection in SP Patients

The ROC curve was plotted, with an internal validation AUC of 0.910 (95% CI = 0.65–0.955) in the modeling group, as shown in Figure 3A. The Hosmer-Lemeshow test yielded χ^2 = 7.423 (P = 0.751), as shown in Figure 3B.

Decision Curve Analysis of the Nomogram Model

Decision curve analysis (DCA) showed that the nomogram model had a positive net benefit and good clinical utility when the predicted probability was between 0.07 and 0.94,as shown in Figure 4.

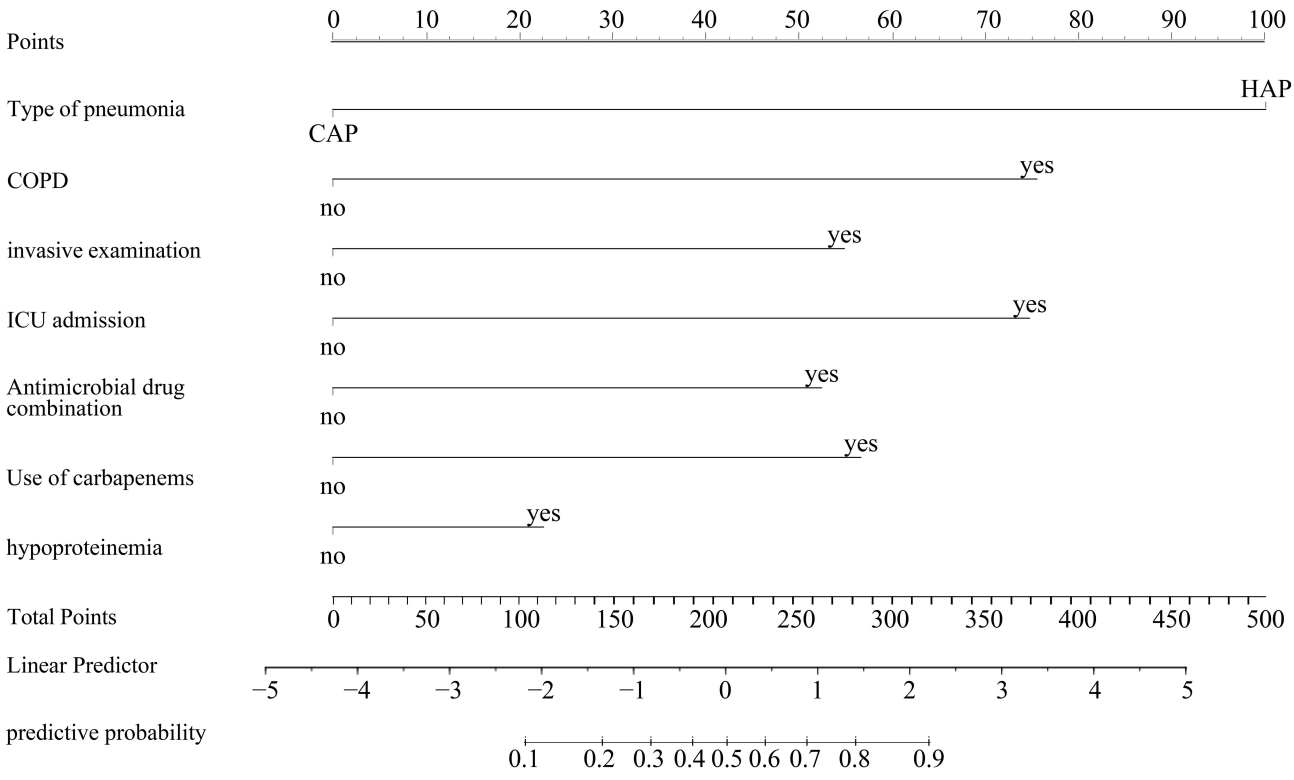

Figure 2 The nomogram model for MDRO infection in SP patients.
Abbreviations: CAP, Community-acquired pneumonia; HAP, Hospital-acquired pneumonia; COPD, Chronic obstructive pulmonary disease.

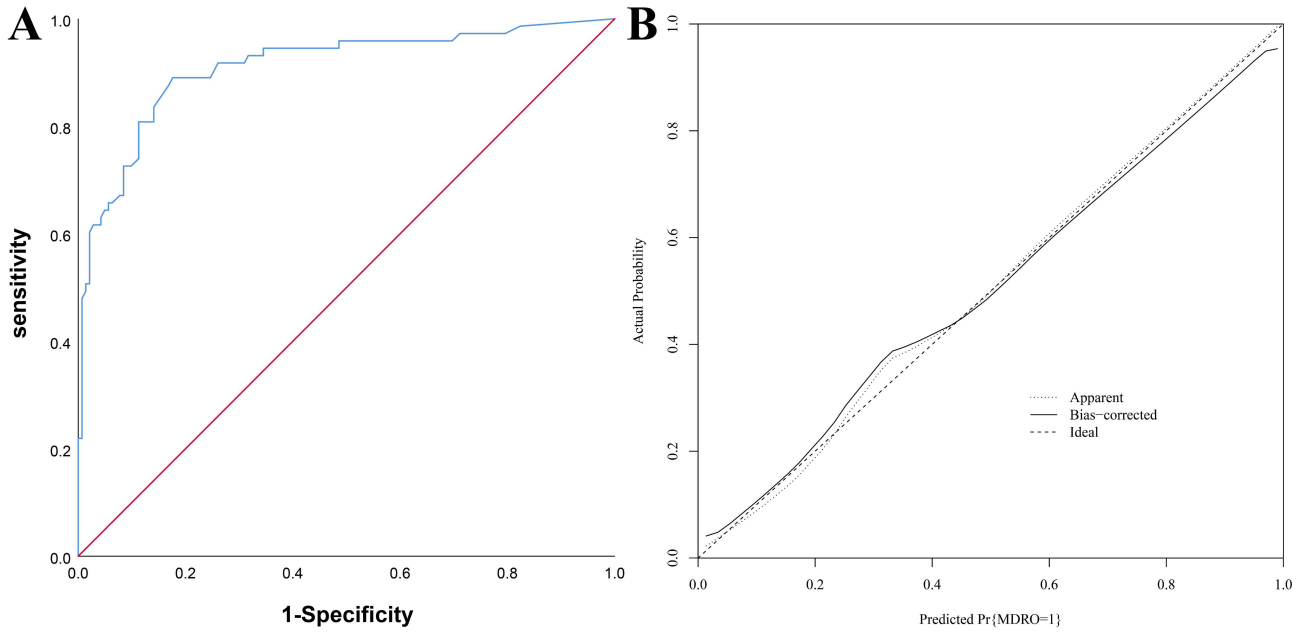

Figure 3 Internal validation of the nomogram model for MDRO infection in SP patients (**A**) ROC curve of modeling group; (**B**) Calibration curve of modeling group.

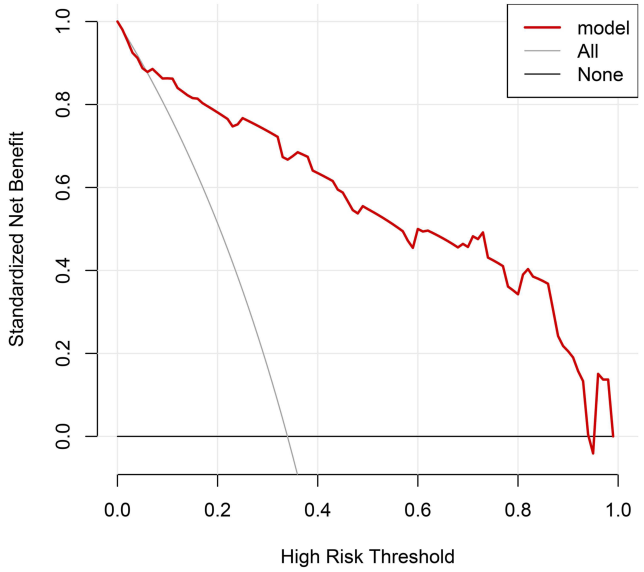

Figure 4 DCA curve for the nomogram.

Comparison of Clinical Data Between MDRO and Non-MDRO Groups in the Validation Group

Significant differences were observed between the MDRO and non-MDRO groups in terms of pneumonia type, COPD, invasive procedures, ICU admission, combination antibiotic therapy, carbapenems use, and hypoproteinemia ($P < 0.05$). No significant differences were found in other clinical data ($P > 0.05$). See Table 7.

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Table 7 Comparison of Clinical Data Between MDRO and Non-MDRO Groups in the Validation Group

Factor	MDRO Group (n=30)	Non-MDRO Group (n=62)	t/χ^2	*P*
Age			0.138	0.710
≥60years old	21 (70.00)	41 (66.13)		
<60 years old	9 (30.00)	21 (33.87)		
Gender			0.014	0.905
Male	18 (60.00)	38 (61.29)		
Female	12 (40.00)	24 (38.71)		
BMI			0.004	0.950
≥24kg/m^2	9 (30.00)	19 (30.65)		
<24kg/m^2	21 (70.00)	43 (69.35)		
Length of stay (d)	16.33±3.01	16.22±3.08	0.162	0.872
Heat generation time (d)	7.46±1.89	7.38±1.78	0.198	0.843
Duration of use of antipneumonia drugs (d)	16.06±3.37	16.09±3.15	0.042	0.967
Diabetes			0.631	0.427
Yes	5 (16.67)	8 (12.90)		
No	25 (83.33)	54 (87.10)		
Hypertensive			0.195	0.659
Yes	7 (23.33)	12 (19.35)		
No	23 (76.67)	50 (80.65)		
Hyperlipidemia			0.080	0.777
Yes	4 (13.33)	7 (11.29)		
No	26 (86.67)	55 (88.71)		
Coronary heart disease			0.131	0.717
Yes	2 (6.67)	3 (4.84)		
No	28 (93.33)	59 (95.16)		
Drinking history			0.528	0.467
Yes	14 (46.67)	24 (38.71)		
No	16 (53.33)	38 (61.29)		
Types of Pneumonia			8.817	0.003
HAP	22 (73.33)	25 (40.32)		
CAP	8 (26.67)	37 (59.68)		
COPD			19.059	<0.001
Yes	16 (53.33)	7 (11.29)		
No	14 (46.67)	55 (88.71)		
Invasive examination			6.347	0.012
Yes	19 (63.33)	22 (35.48)		
No	11 (36.67)	40 (64.52)		
Indwelling catheterization			0.233	0.629
Yes	19 (63.33)	36 (58.06)		
No	11 (36.67)	26 (41.94)		
ICU admission			11.657	0.001
Yes	23 (76.67)	24 (38.71)		
No	7 (23.33)	38 (61.29)		
Antimicrobial drug combination			9.985	0.002
Yes	24 (80.00)	28 (45.16)		
No	6 (20.00)	34 (54.84)		
Use of carbapenems			8.701	0.003
Yes	16 (53.33)	14 (22.58)		
No	14 (46.67)	48 (77.42)		

(*Continued*)

Table 7 (Continued).

Factor	MDRO Group (n=30)	Non-MDRO Group (n=62)	t/χ^2	*P*
Disorders of consciousness			0.006	0.939
Yes	8 (26.67)	17 (27.42)		
No	22 (73.33)	45 (72.58)		
Hypoproteinemia			7.138	0.008
Yes	7 (23.33)	3 (4.84)		
No	23 (76.67)	59 (95.16)		
Deep vein cannulation			1.759	0.185
Yes	16 (53.33)	24 (38.71)		
No	14 (46.67)	38 (61.29)		
GCS score	7.71±1.31	7.91±1.41	0.652	0.516
Coma	13 (43.33)	24 (38.71)	0.180	0.672
Body temperature (°C)	36.87±0.62	36.91±0.67	0.275	0.784
Endotracheal intubation	10 (33.33)	14 (22.58)	1.212	0.271
Central venous catheter	8 (26.67)	14 (22.58)	0.186	0.667
Mechanical ventilation time (d)	3.42±0.86	3.34±0.85	0.422	0.674
WBC (×109/L)	7.10±1.53	7.09±1.43	0.031	0.976
PLT (×109/L)	132.49±21.46	131.65±18.96	0.191	0.849
FBG (mmol/L)	7.12±1.24	6.96±1.21	0.590	0.557
TG (mmol/L)	1.08±0.24	1.09±0.22	0.198	0.843
TC (mmol/L)	4.54±1.13	4.52±1.12	0.080	0.936
Hb (g/L)	124.63±15.42	125.12±16.04	0.139	0.890
APACHE II score	18.65±2.51	17.89±2.34	1.426	0.157

Abbreviations:BMI, Body mass index; CAP, Community-acquired pneumonia; HAP, Hospital-acquired pneumonia; COPD, Chronic obstructive pulmonary disease; WBC, White blood cell count; PLT, Platelet count; FBG, Fasting blood glucose; TG, Triglycerides; TC, Total cholesterol; Hb, Hemoglobin.

External Validation of the Nomogram Model for MDRO Infection in SP Patients

The ROC curve was plotted, with an external validation AUC of 0.953 (95% CI = 0.914–0.992) in the validation group, as shown in Figure 5A. The Hosmer-Lemeshow test yielded $\chi^2 = 7.032$ (P = 0.741), as shown in Figure 5B.

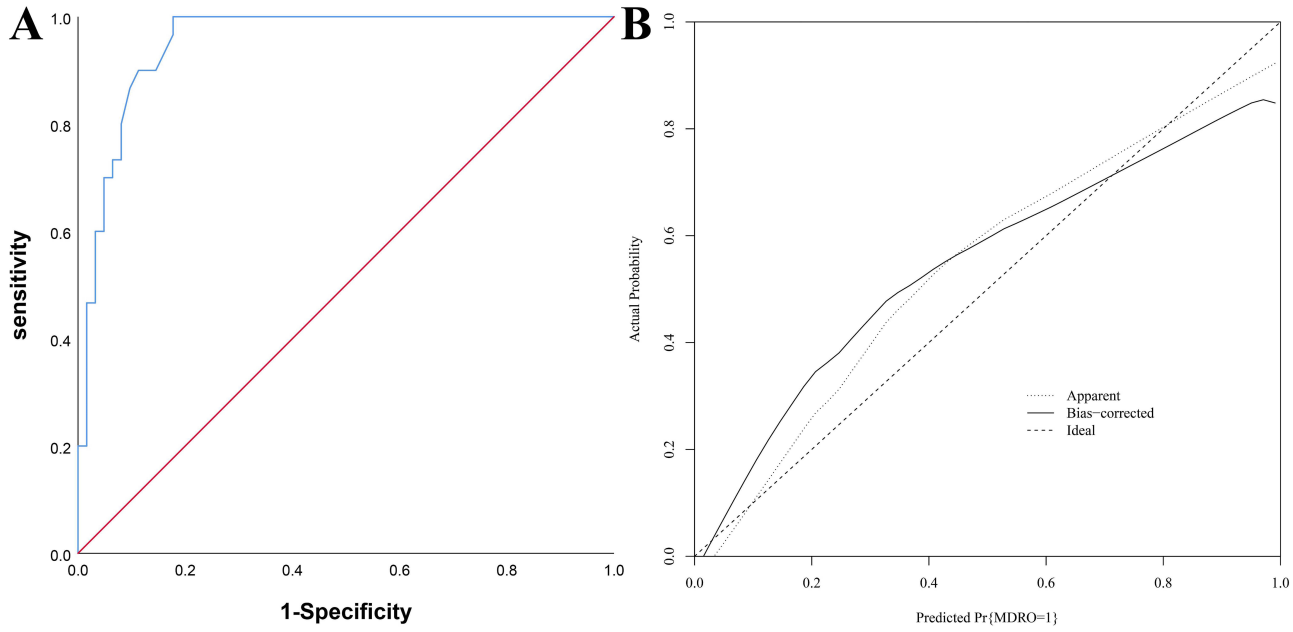

Figure 5 External validation of the nomogram model for MDRO infection in SP patients (**A**) ROC curve of validation group; (**B**): Calibration curve of modeling group.

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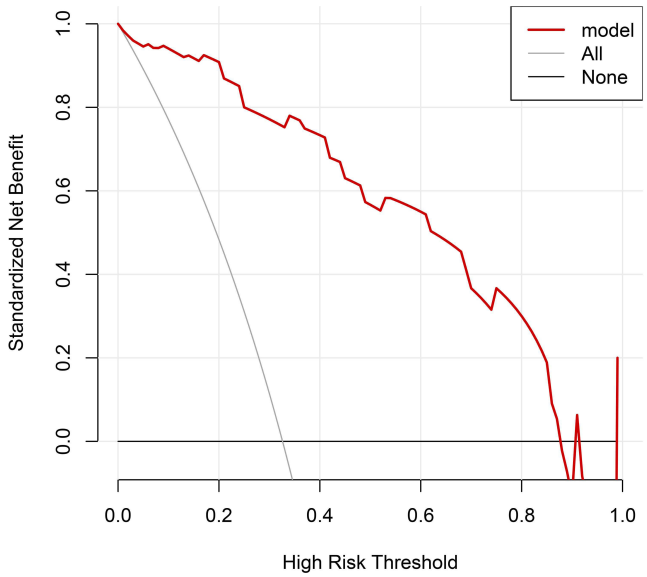

Figure 6 External validation of the nomogram model by DCA.

External Validation of the Nomogram Model by Decision Curve Analysis

As shown in the DCA curve, when the probability ranged from 0.07 to 0.89, the nomogram model had a positive net benefit and good clinical utility in evaluating MDRO infection in SP patients. See Figure 6.

Discussion

SP progresses relatively rapidly. During disease progression, patients may develop complications such as respiratory failure and disturbance of consciousness. Moreover, when SP patients develop MDRO infection, it exacerbates the disease and increases the difficulty of treatment. The reasons for MDRO infection in SP patients are relatively complex and may be influenced by disease status, antibacterial drugs, and other factors.[13,14] This study found that among 306 patients, 101 developed MDRO (33.01%), and among the 214 patients in the modeling group, 72 developed MDRO (33.64%), indicating a relatively high infection rate. The pathogens isolated from MDRO infected patients were mainly Gram-negative bacteria, with *Acinetobacter baumannii* accounting for the highest proportion. This may be because it is an opportunistic pathogen that is widely distributed in hospitals, can resist ultraviolet radiation, and is therefore difficult to eradicate.[15] Through analyzing the drug resistance of the main Gram-negative and Gram-positive bacteria, it was found that Gram-negative bacteria had the highest resistance to piperacillin-tazobactam and piperacillin, while being more sensitive to cefiderocol and colistin, indicating relatively good sensitivity to cefiderocol and colistin, which can be prioritized for clinical treatment.Gram-positive bacteria showed a high resistance rate to penicillin but was more sensitive to oxacillin, norvancomycin, vancomycin, fosfomycin, rifampin, teicoplanin, and tigecycline. Therefore, penicillin should be avoided as much as possible in these patients.[16]

This study identified seven factors influencing MDRO infection in SP patients, and the reasons are as follows: (1) Studies have shown that among different types of pneumonia, hospital-acquired pneumonia (HAP) is more prone to infection. Patients often develop pulmonary parenchymal inflammation and mixed infections after 48 hours of hospitalization, placing them at a higher risk of infection with MDRO.[17] This finding is consistent with the results of the present study. The reason may be that pathogens are more densely distributed in the hospital environment. Patients who are hospitalized for prolonged periods may experience reduced immune function due to steroid use, invasive procedures, etc., thereby increasing the risk of MDRO infection.[18] (2) Among SP patients with COPD, there may be other underlying conditions, and they tend to experience repeated infections, requiring multiple types of medication, thus increasing the infection risk.[19] Furthermore, patients with acute exacerbations of COPD often need endotracheal intubation, which affects the ciliary function of the respiratory tract, damages the airways, and may increase the risk of infection,[20] which is

similar to the results of this study. Therefore, for such patients, it is advisable to make a comprehensive assessment of pathogen drug resistance, choose appropriate antimicrobial agents, and use steroids judiciously to reduce the risk of infection. (3) This study found that invasive procedures are a factor influencing MDRO infection in patients with SP. Because,SP patients undergoing invasive procedures face varying degrees of risk and potential injury to the body, which compromises the integrity and defense functions of the body, allowing pathogens to invade, increasing the burden on the body, and thereby raising the risk of infection.[21] (4) The ICU is also a high-risk area for MDRO. When patients are admitted to the ICU for surgery and medication, the risk of MDRO infection increases. Thus, it is necessary to emphasize disinfection among healthcare professionals, isolate and manage patients with MDRO, and strengthen the supervision of antimicrobial drug use to minimize MDRO transmission.[22] Similar to the findings of this study. (5) Although combination antibiotic therapy can alleviate infection to some extent and inhibit pathogen proliferation, it can also promote the abnormal growth of multidrug-resistant bacteria, increasing drug tolerance. Moreover, the expanded use of antibacterial agents can amplify the suppression of non-pathogenic flora, affect the structure of the oropharyngeal microbiota, facilitate pathogen colonization, and elevate the risk of infection.[23] (6) Carbapenems are broad-spectrum antibiotics with strong antibacterial activity; however, they can alter the body's microbiological ecology and cause an imbalance in the flora. Under pharmacological pressure, this may increase the risk of resistant strains and thereby raise the risk of MDRO infection.[11] Therefore, carbapenems can be used initially for SP infection, followed later by rational drug selection based on pathogen detection results to reduce the risk of infection. (7) Albumin, synthesized by hepatocytes, plays a crucial role in maintaining plasma osmotic pressure and nutritional functions. A decrease in albumin levels indicates hepatic dysfunction and compromised immunity.In patients with hypoproteinemia, immune function is diminished, leaving them unable to resist external pathogens, thus increasing the risk of pathogen invasion.[24,25]

Based on the results of Logistic analysis, this study constructed a nomogram model that can help medical staff intuitively understand the various risk factors. The nomogram constructed in this study yielded AUC values of 0.910 and 0.953 for the two groups, and the H-L test indicated a good fit, suggesting strong predictive ability. When the DCA curve probability ranged from 0.07 to 0.94 and 0.07 to 0.89, the nomogram model for assessing MDRO infection in SP patients showed high clinical applicability, which can help clinicians select high-risk groups based on identified influencing factors and carry out targeted interventions,effectively improving patients' quality of life.

Conclusions

In summary, pneumonia type, COPD, invasive procedures, ICU admission, combination antibiotic therapy, carbapenems use, and hypoproteinemia are factors influencing MDRO infection in SP patients. The nomogram based on these factors can effectively evaluate the risk of MDRO infection, with good discrimination and clinical applicability. However, there are limitations to this study as it is retrospective, single-center in design, and has a small sample size, possibly introducing bias into the findings,and did not further address potential confounding effects of disease severity and treatment indications. Further verification through multi-center prospective studies with expanded sample sizes is warranted.

Research Involving Human Participants

The study was approved by the Ethics Committee of Ganzhou People's Hospital (No.GZSRMYY2025010018) and with the 1964 Helsinki Declaration. Written informed consent to participate in this study was provided by the participants.

Data Sharing Statement

The datasets in this study are available from the corresponding author.

Consent for Publication

All authors give consent for publication.

Disclosure

The authors declared no conflicts of interest in this work.

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