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ORIGINAL RESEARCH

Distribution and Antimicrobial Resistance Analysis of Blood Culture Isolates at a Chinese National Cardiovascular Regional Medical Center: A 7-Year Retrospective Study

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Purpose: This study aimed to characterize the epidemiological patterns and antimicrobial resistance profiles of bloodstream infections (BSIs) in a cardiovascular specialty hospital and to identify region-specific pathogen distributions, resistance risks, and clinical implications for optimizing empirical therapy and infection control strategies.

Patients and Methods: A retrospective analysis (2018–2024) evaluated 1,055 non-duplicate BSI isolates from 37,576 blood cultures at the Fuwai Central China Cardiovascular Hospital. Researchers investigated both bacterial classification and associated drug resistance through comprehensive analysis.

Results: The study revealed that a total of 1,055 bacterial strains were isolated from blood cultures, with Gram-negative bacteria accounting for 31.5% (332 strains), Gram-positive bacteria for 62.7% (662 strains), and fungi for 5.8% (61 strains). The most frequently isolated pathogens were *Staphylococcus epidermidis* (13.7%), *Staphylococcus hom*inis (8.0%), *Klebsiella pneumoniae* (7.4%), *Escherichia coli* (7.1%), and *Staphylococcus haemolyticus* (6.7%). These pathogens were predominantly isolated from intensive care units (ICUs), with the Coronary Heart Disease ICU (24.7%), General ICU (18.0%), and Adult Cardiac Surgery ICU (8.1%) representing the top three departments for bacterial detection. Among *Staphylococcus* isolates, methicillin-resistant *Staphylococcus aureus* (MRSA) and methicillin-resistant coagulase-negative *Staphylococci* (MRCNS) were identified at rates of 51.6% and 88.7%, respectively. The carbapenem resistance rates of *K. pneumoniae* and *E. coli* were 28.8% and 4.0%, respectively. Non-fermenting Gram-negative bacilli, such as *Acinetobacter baumannii*, showed alarming resistance rates to carbapenems (60.0%) and other β-lactams (≥52%), while *Burkholderia cepacia* and *Stenotrophomonas maltophilia* remained highly susceptible to first-line agents.

Conclusion: Blood culture isolates in our hospital demonstrated a predominance of Gram-positive organisms, with high detection rates of MRSA, MRCNS, and carbapenem-resistant Gram-negative bacilli. Continuous antimicrobial resistance surveillance of bloodstream isolates should be maintained in clinical practice to provide evidence-based data for rational antibiotic use and mitigate the emergence of resistant pathogens.

Keywords: bloodstream infections, antimicrobial resistance, multidrug-resistant organisms, antibacterial drugs

Introduction

Bloodstream infections (BSIs) represent a major cause of morbidity and mortality in both hospital and community settings. The escalating global burden of BSIs is driven by an aging population and an increasing prevalence of comorbidities, including malignancies, end-organ diseases, and diabetes mellitus. Furthermore, the rise in global antimicrobial resistance (AMR) contributes to a higher rate of inappropriate empirical therapy, resulting in increased overall mortality.[1,2] The causative pathogens of BSIs and the AMR profiles exhibit substantial variations across different

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countries. Coagulase-negative Staphylococci (CoNS) are the most frequently isolated organisms causing BSIs in hospitalized children in the United States.[3] Surveillance data on antibiotic resistance from South Korea, Switzerland, and Europe indicate that *Escherichia coli* and *Staphylococcus aureus* are the predominant BSI pathogens.[4–6] In China, the spectrum of pathogens responsible for BSIs varies considerably by region. A study investigating the clinical characteristics of BSIs in hospitals in Northern China identified Gram-positive cocci as the most common causative agents,[7] while in Hunan Province, Southern China, *E. coli* was the predominant BSI pathogen.[8] Recent years have witnessed a significant surge in multidrug-resistant organism (MDRO) prevalence, driven by escalating use of broad-spectrum antimicrobials and invasive medical interventions.[9] Cardiovascular patients face heightened BSI risks due to their immunocompromised status and frequent exposure to interventional procedures. This retrospective study (2018–-2024) analyzed blood culture-positive specimens at Fuwai Central China Cardiovascular Hospital to delineate pathogen distribution, antimicrobial resistance patterns, and temporal resistance trends within this specialized cohort. The findings aim to establish population-specific microbiological characteristics, elucidate dynamic resistance mechanisms, and inform optimized antimicrobial stewardship protocols, along with tailored infection control strategies for cardiovascular care facilities.

Materials and Methods

Data Collection

Fuwai Central China Cardiovascular Hospital, a public Tier-3 Grade-A hospital specializing in cardiovascular disease diagnosis and treatment, was officially inaugurated on December 16, 2017. It is one of China's first pilot National Regional Medical Centers. This study retrospectively analyzed clinically significant bacterial strains isolated from blood cultures of outpatients and inpatients at Fuwai Central China Cardiovascular Hospital between January 1, 2018, and December 31, 2024. Duplicate isolates from the same patient were excluded according to established laboratory protocols. The dataset encompassed critical clinical parameters including blood culture collection dates, microbial identification results, antimicrobial susceptibility testing (AST) profiles, patient demographics (age and sex), and clinical care locations (hospital wards).

Pathogen Identification and Antimicrobial Susceptibility Testing

Blood samples were collected from adult patients using commercially available BACTEC culture bottles (Becton Dickinson, USA), with a combination of aerobic and anaerobic bottles, whereas pediatric patients were sampled using aerobic bottles only, with blood volumes of approximately 8–10 mL and 2–5 mL per bottle, respectively. A BD BACTEC™ FX automated blood culture system with matching culture bottles was used for microbial detection. Bacterial identification and antimicrobial susceptibility testing were performed using the BD Phoenix M50 automated system, whereas fungal identification was performed using the DL-96FUNGUS assay. Antimicrobial susceptibility testing followed the latest Clinical & Laboratory Standards Institute (CLSI) guidelines,[10] supplemented by the disk diffusion method (OXOID, UK) for specific antimicrobials, and was verified with E-test strips (Zhejiang Wenzhou Kangtai Biotechnology Co., Ltd). The BD Phoenix M50 system uses dedicated susceptibility panels. Species-specific media was applied to different pathogens: Mueller–Hinton (MH) agar (Zhengzhou Antu Bioengineering Co., Ltd.) for Moraxella catarrhalis, 5% defibrinated sheep blood-supplemented MH agar for *Streptococcus pneumoniae* susceptibility confirmation, and Haemophilus Test Medium (HTM) for *Haemophilus influenzae*. Interpretive criteria followed the latest CLSI M100 guidelines,[10] with the European Committee on Antimicrobial Susceptibility Testing (EUCAST) breakpoints applied to selected antimicrobials.[11] Tigecycline and colistin susceptibility was assessed according to the Chinese Expert Consensus on Polymyxins, Tigecycline and Ceftazidime/Avibactam Susceptibility Testing.[12] Quality control strains included *E. coli* ATCC 25922 and ATCC 35218, *Pseudomonas aeruginosa* ATCC 27853, *Enterococcus faecalis* ATCC 29212, *S. aureus* ATCC 25923 and ATCC 29213, *S. pneumoniae* ATCC 49619, and *H. influenzae* ATCC 49247, ensuring standardized testing procedures throughout the study.

Statistical Analysis

The data were subjected to descriptive epidemiological analysis, with numerical data processed and analyzed using SPSS 22.0 and GraphPad Prism software (version 10.0). Statistical analysis was performed using the χ^2-test, with a $p < 0.05$ considered statistically significant. The distribution of bacterial species and antimicrobial susceptibility data of isolated pathogens were statistically analyzed using WHONET 5.6 software.

Results

Distribution of Isolated Pathogenic Bacteria

From 2018 to 2024, 37,576 blood culture specimens were collected at the Fuwai Central China Cardiovascular Hospital. After excluding duplicate strains from the same patient, 1,055 positive isolates were identified (positivity rate: 2.8%), all of which were isolated from hospitalized patients. Among these positive cultures, 714 (67.7%) and 341 (32.3%) strains were isolated from the male and female patients, respectively. The blood culture positivity rate was significantly higher in the ≥60-year-old group (47.9%, $p < 0.05$) than that in the 0–17-year and 18–59-year groups (9.7% and 42.5%, respectively). General patient characteristics are summarized in Figure 1.

Of the positive isolates, 332 (31.5%) were Gram-negative bacteria. The top five pathogens were *Klebsiella pneumoniae* (78 isolates, 23%), *E. coli* (75, 23%), *Enterobacter cloacae* (31, 9%), *Acinetobacter baumannii* (25, 8%), and *Burkholderia cepacia* (21, 6%). Gram-positive bacteria accounted for 662 isolates (62.7%), predominantly *S. epidermidis* (144, 23%), *S. hominis* (84, 13%), *S. haemolyticus* (71, 11%), *S. aureus* (54, 9%), and *E. faecium* (36, 6%). Fungal pathogens comprised 61 isolates (5.8%), primarily *Candida albicans* (38%) and *C. glabrata* (21%). Over the seven-year study period, the top ten isolated pathogens were *S. epidermidis, S. hominis, K. pneumoniae, E. coli, S. haemolyticus, S. aureus, E. faecium, E. cloacae, S. capitis*, and *A. baumannii*. The detailed distributions are listed in Table 1.

Department Distributions

The top five departments with pathogens isolated from blood cultures were the coronary heart disease ICU, general ICU, adult cardiac surgery ICU, pediatric cardiac center ICU, and adult cardiac surgery ward III, accounting for 24.74, 18.01,

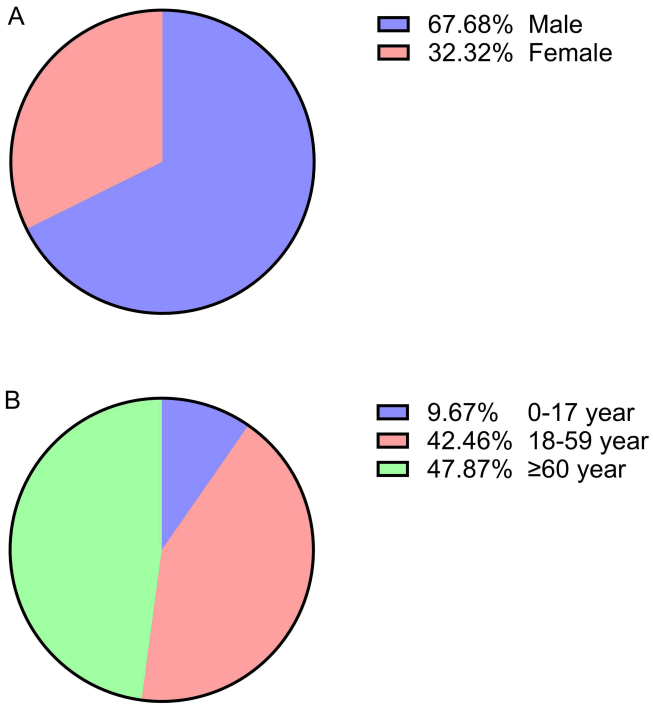

Figure 1 Baseline Data of Patients. (**A**) Gender; (**B**) Age.

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Table 1 The Types and Composition of the Main Pathogenic Bacteria with Positive Blood Cultures from 2018 to 2024

Organism	No. of Strains	Proportion/%
Gram-negative bacteria	332	31.47
K. pneumoniae	78	7.39
E. coli	75	7.11
E. cloacae	31	2.94
A. baumannii	25	2.37
B. cepacia	21	1.99
P. aeruginosa	17	1.61
S. marcescens	12	1.14
S. maltophilia	11	1.04
Acinetobacter	8	0.76
K. oxytoca	6	0.57
Other gram-negative bacteria	48	4.55
Gram-positive bacteria	662	62.75
S. epidermidis	144	13.65
S. hominis	84	7.96
S. haemolyticus	71	6.73
S. aureus	54	5.12
E. faecium	36	3.41
S. capitis	30	2.84
S. sanguinis	22	2.09
E. faecalis	20	1.90
S. anginosus	18	1.71
S. gordonii	17	1.61
Other gram-positive bacteria	166	15.73
Fungi	61	5.78
C. albicans	23	2.18
C. glabrata	13	1.23
C. tropicalis	12	1.14
Other fungi	13	1.23
Total	1055	100

8.06, 6.54, and 4.64%, respectively. The coronary heart disease ICU demonstrated a significantly higher blood culture positivity rate than the other wards ($p < 0.05$). The distribution of clinical bacterial isolation departments is shown in Figure 2. The distribution of the pathogen species isolated from each department is presented in Table 2.

Antibiotic Resistance Characteristics of Enterobacterales

Among the carbapenems, the resistance rates of *K. pneumoniae, E. coli, E. cloacae, Serratia marcescens*, and *K. oxytoca* were 28.8, 4.0, 41.9, 0.0, and 0.0%, respectively. The tigecycline resistance rates were 1.3% for *K. pneumoniae* and 3.2% for *E. cloacae*, whereas no resistance (0%) was observed in *E. coli, S. marcescens*, and *K. oxytoca*. Resistance to colistin B was detected in 1.5% of *K. pneumoniae* and *E. coli* isolates, whereas *E. cloacae* and *K. oxytoca* exhibited full susceptibility (0% resistance). Resistance rates to β-lactam/β-lactamase inhibitor combinations, fourth-generation cephalosporins, aminoglycosides, and fluoroquinolones vary across *Enterobacterales* species. Detailed data are presented in Table 3.

Antibiotic Resistance Characteristics of Non-Fermentative Gram-Negative Bacteria

Among the 25 *A. baumannii* isolates, the resistance rates to β-lactams, β-lactam/β-lactamase inhibitor combinations, aminoglycosides, and fluoroquinolones were ≥52%, with carbapenem resistance observed in 60% of isolates. No tigecycline or polymyxin B resistance was observed. For 21 *B. cepacia* isolates, the resistance rates to ceftazidime,

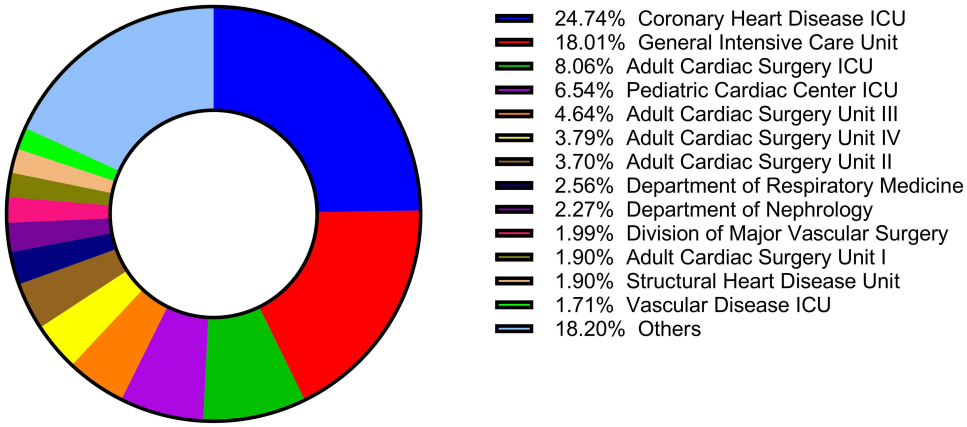

Figure 2 Distribution of clinical isolation bacterial departments.
Abbreviation: ICU, intensive care unit.

levofloxacin, trimethoprim-sulfamethoxazole, and minocycline were <10%, whereas meropenem resistance reached 16.7%. Of 17 *P. aeruginosa* isolates, carbapenem resistance was observed in 31.2% of the 17 *P. aeruginosa* isolates, whereas susceptibility to ceftazidime, piperacillin, piperacillin/tazobactam, cefoperazone/sulbactam, and cefepime remained high (a resistance rate of ≤7.1%). All 11 *S. maltophilia* isolates showed complete susceptibility, with 0% resistance to levofloxacin, trimethoprim-sulfamethoxazole, minocycline, and chloramphenicol. Detailed data are presented in Table 4.

Antibiotic Resistance Characteristics of Staphylococcus

A total of 54 *S. aureus*, 144 *S. epidermidis*, and 210 CoNS isolates were identified in positive blood cultures. The detection rates of methicillin-resistant *S. aureus* (MRSA), methicillin-resistant *S. epidermidis* (MRSE), and methicillin-resistant coagulase-negative *Staphylococci* (MRCNS) were 51.6%, 79.9%, and 88.7%, respectively. Notably, all methicillin-resistant *Staphylococci* (MRS) isolates exhibited complete resistance to penicillin G (100%). In contrast, methicillin-susceptible *Staphylococci* (MSS) demonstrated species-specific resistance variations. MSSA isolates showed a significantly higher penicillin G resistance rate (92.3%) than MSSE (64.7%) and MSCNS (67.7%) ($p < 0.05$).

Table 2 Distribution of Bacterial Sources in Blood Culture and Isolation Departments

Department	Gram-Negative Bacteria	Gram-Positive Bacteria	Fungi	Total
Coronary Heart Disease ICU	80	180	1	261
General ICU	51	126	13	190
Adult Cardiac Surgery ICU	27	51	7	85
Pediatric Cardiac Center ICU	26	37	6	69
Adult Cardiac Surgery Unit III	5	41	3	49
Adult Cardiac Surgery Unit IV	7	27	6	40
Adult Cardiac Surgery Unit II	3	34	2	39
Department of Respiratory Medicine	13	13	1	27
Department of Nephrology	8	14	2	24
Division of Major Vascular Surgery	12	8	1	21
Adult Cardiac Surgery Unit I	7	13	0	20
Structural Heart Disease Unit	5	14	1	20
Vascular Disease ICU	4	10	4	18
Others	84	94	14	192
Total	332	662	61	1055

Abbreviation: ICU, intensive care unit.

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Table 3 The Resistance Rate of Enterobacterales to Antimicrobial Agents

Antimicrobial Agent	*K. pneumoniae*	*E. coli*	*E. cloacae*	*S. marcescens*	*K. oxytoca*
	n=78	n=75	n=31	n=12	n=6
Ampicillin	INR	88.0	INR	INR	INR
Piperacillin	50.7	86.7	58.1	0.0	33.3
Tetracycline	37.5	61.3	41.9	81.8	0.0
Ciprofloxacin	45.8	46.7	45.2	0.0	0.0
Cefoperazone	52.1	64.0	INR	INR	50.0
Levofloxacin	30.1	42.7	41.9	0.0	0.0
Cefuroxime	47.4	51.4	50.0	INR	20.0
Cefotaxime	47.9	52.0	51.6	0.0	16.7
Trimethoprim-sulfamethoxazole	31.5	60.0	16.1	8.3	0.0
Cefepime	42.5	44.6	48.4	0.0	16.7
Gentamicin	28.8	37.3	32.3	0.0	0.0
Aztreonam	40.3	26.7	45.2	0.0	0.0
Ampicillin-sulbactam	40.3	26.7	INR	INR	33.3
Chloramphenicol	20.0	18.3	7.1	18.2	16.7
Ceftazidime	39.7	16.0	48.4	0.0	0.0
Cefoperazone-sulbactam	30.3	6.8	45.2	0.0	16.7
Amoxicillin-clavulanic acid	36.1	13.3	INR	INR	0.0
Piperacillin-tazobactam	32.9	8.0	45.2	0.0	16.7
Imipenem	28.8	4.0	41.9	0.0	0.0
Meropenem	28.8	4.0	41.9	0.0	0.0
Amikacin	16.4	2.7	0.0	0.0	0.0
Polymyxin B	1.5	1.5	0.0	INR	0.0
Tigecycline	1.3	0.0	3.2	0.0	0.0

Abbreviation: INR, intrinsic resistance.

Table 4 The Resistance Rate of Non-Fermentative Gram-Negative Bacilli to Antimicrobial Agents

Antimicrobial Agent	*A. baumannii*	*B. cepacia*	*P. aeruginosa*	*S. maltophilia*
	n=25	n=21	n=17	n=11
Ceftazidime	60.0	10.0	6.2	NA
Piperacillin	60.0	INR	7.1	INR
Ciprofloxacin	60.0	NA	18.8	NA
Levofloxacin	56.0	10.0	25.0	0.0
Cefotaxime	60.0	INR	INR	INR
Cefepime	60.0	INR	6.2	NA
Piperacillin-tazobactam	60.0	INR	6.2	INR
Imipenem	60.0	INR	31.2	INR
Meropenem	60.0	16.7	25.0	INR
Gentamicin	64.0	INR	10.0	INR
Ampicillin-sulbactam	60.0	INR	INR	INR
Cefoperazone-sulbactam	52.2	NA	7.1	NA
Amikacin	52.0	INR	10.0	INR
Trimethoprim-sulfamethoxazole	52.0	10.0	INR	0.0
Minocycline	30.0	8.3	NA	0.0
Tigecycline	0.0	NA	NA	NA
Polymyxin B	0.0	INR	0.0	NA

(*Continued*)

Table 4 (Continued).

Antimicrobial Agent	*A. baumannii*	*B. cepacia*	*P. aeruginosa*	*S. maltophilia*
	n=25	n=21	n=17	n=11
Aztreonam	INR	INR	12.5	INR
Chloramphenicol	INR	0.0	INR	0.0

Abbreviation: NA, not available.

Susceptibility analysis further revealed that MRS isolates exhibited a statistically significant trend toward higher resistance to multiple antimicrobial classes, including macrolides, fluoroquinolones, and sulfonamides, than MSS isolates, suggesting a potential association between β-lactam resistance and multidrug-resistant phenotypes. No vancomycin-resistant *Staphylococci* were detected. Resistance to teicoplanin and linezolid was observed in 3.6% and 4.8% of MRCNS isolates, respectively, with no resistance detected in other staphylococcal groups. The detailed resistance data are summarized in Table 5.

Antibiotic Resistance Characteristics of Enterococcus

Sixty *Enterococcus* isolates were recovered from the clinical specimens, with the following species distributions: *E. faecalis* (20 isolates, 33.3%), *E. faecium* (36 isolates, 60.0%), and other *Enterococcus* species (4 isolates, 6.7%). *E. faecium* demonstrated markedly elevated resistance profiles compared to *E. faecalis* across multiple antimicrobial classes, including erythromycin (86.7% vs 50.0%), penicillin G (97.1% vs 47.1%), ampicillin (88.9% vs 10.5%), and high-level gentamicin (36.0% vs 14.3%). The disparity in β-lactam resistance was particularly striking, with *E. faecium* exhibiting an 8.5-fold higher ampicillin resistance rate (88.9% vs 10.5%) and twice the penicillin G resistance rate (97.1% vs 47.1%) than *E. faecalis*. Notably, amoxicillin/clavulanic acid retained full activity against both species. Glycopeptide susceptibility analysis revealed no detectable vancomycin or teicoplanin resistance in *E. faecalis*. For *E. faecium*, a low vancomycin resistance rate of 2.8% was observed, whereas teicoplanin maintained 100% susceptibility. These findings highlight critical interspecies differences in antimicrobial resistance patterns, particularly the heightened β-lactam resistance in *E. faecium*, underscoring the need for species-level identification to guide therapeutic decisions (Table 6).

Table 5 The Resistance Rate of Staphylococcus to Antimicrobial Agents

Antimicrobial Agent	MSSA	MRSA	MSSE	MRSE	MSCNS	MRCNS
	n=26	n=28	n=29	n=115	n=40	n=314
Oxacillin	0.0	100.0	0.0	100.0	0.0	100.0
Penicillin G	92.3	100.0	64.7	100.0	67.7	100.0
Erythromycin	53.8	82.1	47.1	75.8	55.6	84.3
Clindamycin	19.2	60.7	5.9	47.6	8.3	53.4
Tobramycin	27.8	21.1	20.0	63.9	10.0	70.4
Trimethoprim-sulfamethoxazole	19.2	21.4	47.1	76.6	25.0	72.1
Tetracycline	3.8	28.6	5.9	16.4	11.4	17.2
Levofloxacin	0.0	17.9	20.0	63.3	9.1	70.8
Ciprofloxacin	0.0	17.9	29.4	56.2	11.1	66.5
Gentamicin	15.4	17.9	17.6	42.6	5.6	49.2
Amikacin	3.8	3.6	0.0	12.3	0.0	5.2
Rifampicin	0.0	3.6	0.0	17.7	0.0	21.1
Mupirocin	0.0	11.5	NA	NA	NA	NA
Linezolid	0.0	0.0	0.0	0.0	0.0	4.8
Vancomycin	0.0	0.0	0.0	0.0	0.0	0.0
Teicoplanin	0.0	0.0	0.0	0.0	0.0	3.6

Abbreviations: MSSA, Methicillin-resistant Staphylococcus aureus; MRSA, Methicillin-resistant Staphylococcus epidermidis; MSSE, methicillin-resistant Staphylococcus epidermidis; MRSE, methicillin-resistant Staphylococcus epidermidis; MSCNS, methicillin-resistant Staphylococcus epidermidis; MRCNS, methicillin-resistant coagulase-negative Staphylococci.

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Table 6 The Resistance Rate of *E. faecalis* and *E. faecium* to Antimicrobial Agents

Antimicrobial Agent	*E. faecalis*	*E. faecium*
	n=20	n=36
Erythromycin	50.0	86.7
Penicillin G	47.1	97.1
Gentamicin-high	14.3	36.0
Ampicillin	10.5	88.9
Amoxicillin/clavulanic Acid	0.0	0.0
Vancomycin	0.0	2.8
Teicoplanin	0.0	0.0
Linezolid	0.0	0.0

Antibiotic Resistance Characteristics of Streptococcus

Antimicrobial susceptibility testing revealed that all four β-hemolytic streptococcal isolates from blood cultures demonstrated 100% resistance to erythromycin, clindamycin, and levofloxacin, while maintaining complete sensitivity to ampicillin, penicillin G, and tetracycline, although the limited sample size necessitates cautious interpretation of these findings. Similarly, four *S. pneumoniae* blood culture isolates exhibited universal resistance (100%) to tetracycline, erythromycin, azithromycin, and clindamycin but remained fully susceptible to levofloxacin, moxifloxacin, and third-generation cephalosporins (cefotaxime/ceftriaxone). Among the 110 viridans streptococci isolates, high resistance rates were observed for erythromycin (77.9%), clindamycin (66.2%), and tetracycline (61.5%), whereas significantly lower resistance was documented for β-lactams (5.6% to ampicillin) and fluoroquinolones (5.1% to levofloxacin). Notably, vancomycin, linezolid, and meropenem maintained complete antimicrobial activity against all tested streptococcal species, with no emerging resistance detected in the study cohort. These findings underscore the preserved efficacy of β-lactams and glycopeptides against *streptococci* despite escalating resistance to macrolides, lincosamides, and tetracyclines, particularly in viridans (Table 7).

Table 7 The Resistance Rate of Streptococcus Species to Antimicrobial Agents

Antimicrobial Agent	β-haemolytic *Streptococcus*	*S. pneumoniae*	*S. viridans*
	n=4	n=4	n=110
Erythromycin	100.0	100.0	77.9
Clindamycin	100.0	100.0	66.2
Tetracycline	0.0	100.0	61.5
Ampicillin	0.0	NA	5.6
Levofloxacin	100.0	0.0	5.1
Penicillin G	0.0	0.0	2.8
Chloramphenicol	0.0	0.0	1.3
Cefotaxime	0.0	0.0	1.3
Ceftriaxone	0.0	0.0	1.3
Cefepime	0.0	0.0	1.2
Linezolid	0.0	0.0	0.0
Vancomycin	0.0	0.0	0.0
Meropenem	0.0	0.0	0.0
Trimethoprim/sulfamethoxazole	NA	0.0	NA
Cefuroxime	NA	0.0	NA
Azithromycin	NA	100.0	NA
Moxifloxacin	NA	0.0	NA

Temporal Shifts in Multidrug-Resistant Organism Detection Rates

Longitudinal surveillance (2018–2024) revealed dynamic shifts in MDRO epidemiology. CRABA maintained persistently high rates (>50% in 5/7 years), peaking at 75% (2019,2021), while CRKPN exhibited marked fluctuations with a concerning surge to 47.1% in 2023 after a 2020 nadir (14.3%). Notably, CRPAE, absent during 2019–2022, re-emerged at 33.3% (2023) and 20% (2024). Extended-spectrum cephalosporin resistance demonstrated divergent patterns: Cefotaxime- and Ceftriaxone-Resistant *K. pneumoniae* (CTX-CRO-R-KPN) paralleled CRKPN trends (peak 58.8% in 2023), whereas Cefotaxime- and Ceftriaxone-Resistant *E. coli* (CTX-CRO-R-ECO) fluctuated drastically from 20% (2019) to 80% (2021). Quinolone-resistant *E. coli* (QNR-ECO) oscillated between 20% and 53.3% without clear temporal direction. Gram-positive pathogens showed contrasting trajectories: MRCNS climbed from 83.8% (2018) to >90% during 2020–2023 (peak 95.1% in 2022), contrasting with declining MRSA rates falling from 75% (2018) to 40% (2024) despite transient rebounds. The marked fluctuations in multidrug resistance rates, particularly the dramatic oscillations observed in CTX-CRO-R-ECO (20–80%) and CRPAE (0–33.3%), may be partially attributable to limited annual isolates of target pathogens, which reduces statistical power and amplifies variability in resistance rate estimates. Detailed data are presented in Figure 3.

Discussion

Bloodstream infections represent a critical mortality determinant in critically ill cardiovascular patients, where evolving etiological profiles and antimicrobial resistance patterns not only dictate empirical antibiotic selection but also profoundly impact clinical outcomes and healthcare resource utilization.[13] Within the BSI diagnostic framework, standardized blood culture protocols form the cornerstone of laboratory diagnostics, with rapid pathogen identification enabling clinicians to implement targeted antimicrobial therapy—a decisive factor in mortality reduction.[14] This investigation systematically analyzed 1055 blood culture-positive isolates from Fuwai Central China Cardiovascular Hospital (2018–2024), delineating distinctive pathogen distributions and resistance patterns characteristic of specialized cardiovascular care settings, thereby providing critical insights for optimizing antimicrobial stewardship in high-risk populations.

Over a seven-year surveillance period, 1055 clinically significant bacterial isolates were recovered from blood cultures at our institution, with Gram-positive organisms predominating (62.7%), a proportion substantially exceeding the 48.8% reported in the 2015–2021 China Antimicrobial Surveillance Network (CHINET) multicenter surveillance of bloodstream isolates from 52 Chinese medical facilities and data from other tertiary general hospitals.[15–17] This distinctive epidemiological profile likely reflects cardiovascular-specific risk factors, including the high prevalence of intravascular devices (cardiac pacemakers and prosthetic valves), post-cardiopulmonary bypass immunosuppression, and frequent central venous catheter utilization. The causative agents of BSIs exhibit geographic variations across countries,

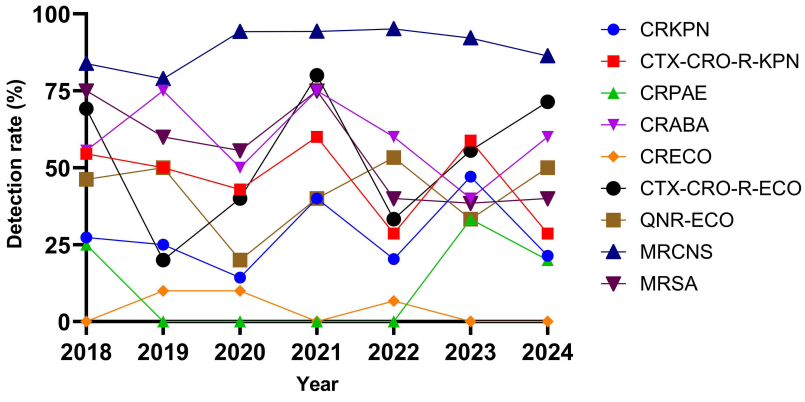

Figure 3 Trend of detection rate of multidrug-resistant bacteria in 2018–2024.

Abbreviations: CRKPN, carbapenem-resistant Klebsiella pneumoniae; CTX-CRO-R-KPN, Cefotaxime- and Ceftriaxone-Resistant K. pneumoniae; CRPAE, carbapenem-resistant Pseudomonas aeruginosa; CRABA, carbapenem-resistant Acinetobacter baumannii; CRECO, carbapenem-resistant Escherichia coli; CTX-CRO-R-ECO, Cefotaxime- and Ceftriaxone-Resistant E. coli; QNR-ECO, quinolone-resistant E. coli; MRCNS, methicillin-resistant coagulase-negative Staphylococci; MRSA, methicillin-resistant Staphylococcus aureus.

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with distinct epidemiological profiles. Musicha et al[18] in Malawi, Koupetori et al[19] in Greece, and Bouza et al[20] in Spain have attributed BSIs predominantly to Gram-negative bacteria, whereas Wasihun et al[21] in Ethiopia, Bassetti et al[22] in Italy, and Kolonitsiou et al[23] in Greece challenged these results and identified Gram-positive bacteria as the primary causative agents. The predominance of *E. coli* in BSIs reported by Opota et al,[24] Obeng-Nkrumah et al,[25] and Labi et al[26] stands in sharp contrast to investigations from certain Italian and African hospitals, where CoNS and *Salmonella* spp. have been consistently established as the predominant BSI pathogens.[27,28] These divergent findings may be multifactorial and potentially attributable to differences in specimen collection volumes, geographic disparities, and distinct community lifestyles.

The most frequently isolated pathogens at our institution were CoNS, *K. pneumoniae, E. coli, Enterococcus* spp., and *S. aureus*. This finding aligns closely with the distribution data of clinically isolated bacteria from blood specimens reported by CHINET between 2015 and 2021.[15] This microbial ecology may be attributed to multifactorial determinants: (1) the predominance of CoNS as commensal skin flora is strongly associated with iatrogenic infections from invasive procedures (eg, central line placements) and their propensity for biofilm formation on medical devices, predisposing to persistent bacteremia; (2) the elevated isolation rates of *K. pneumoniae* and *E. coli* likely reflect nosocomial transmission of extended-spectrum β-lactamase (ESBL)-producing and carbapenemase-expressing *Enterobacteriaceae* strains, which disproportionately cause bloodstream infections in immunocompromised hosts; and (3) *S. aureus* prevalence underscores rising community-acquired and healthcare-associated MRSA burdens, particularly in patients with diabetes mellitus or secondary bacteremia complicating skin/soft tissue infections. Pathophysiological drivers enabling the hematogenous dissemination of these opportunistic pathogens include inappropriate broad-spectrum antibiotic use, compromised mucosal barriers in critically ill patients, and expanding the implementation of immunosuppressive therapies.

This study elucidates the antimicrobial resistance profiles of clinically prevalent *Enterobacteriaceae* pathogens and provides critical evidence to guide empirical therapies for infectious diseases. Notably, the predominant pathogens, including *K. pneumoniae* and *E. coli* exhibit widespread resistance to conventional β-lactam antibiotics, with ampicillin resistance reaching 88.0% in *E. coli*, aligning with the global dissemination of ESBL-producing strains. Although piperacillin-tazobactam maintained relatively low resistance (8.0%) against *E. coli*, its resistance rate increased to 32.9% in *K. pneumoniae*, emphasizing the necessity of incorporating regional epidemiological data when selecting empirical regimens for severe infections. Carbapenem resistance rates reached 28.8 and 4.0% in *K. pneumoniae* and *E. coli*, respectively, exceeding those reported in CHINET bloodstream isolate surveillance data (2015–2021) and surveillance data from other countries.[15,27,29] In contrast, *E. cloacae* demonstrated persistent carbapenem resistance (41.9%), a phenomenon potentially attributable to its intrinsic AmpC β-lactamase overexpression mechanism.[30] The last-line agents polymyxin B and tigecycline retained potent activity against multidrug-resistant strains (resistance rates of <3.2%), although vigilant monitoring is warranted given the risk of resistance gene dissemination with widespread clinical use. Distinct interspecies resistance patterns emerged: *S. marcescens* exhibited pan-susceptibility across the tested agents, possibly related to its lower clinical prevalence and limited horizontal gene transfer capacity, whereas *K. oxytoca* demonstrated moderate β-lactam resistance (16.7–50.0%), along with preserved susceptibility to aminoglycosides and fluoroquinolones, offering alternative therapeutic options. Notably, fourth-generation cephalosporin cefepime showed comparable resistance rates (16.7–48.4%) to third-generation cephalosporins across species, suggesting the diminished empirical utility of conventional cephalosporins for severe *Enterobacteriaceae* infections in this region.

Our study revealed significantly higher detection rates of MRCNS (88.7%) and MRSA (51.6%) than both the CHINET bloodstream surveillance data (2015–2021) and other parts of the world.[15,31,32] Notably, CoNS was isolated at a substantially higher frequency than *S. aureus* in our clinical setting. Although traditionally regarded as blood culture contaminants, CoNS demand particular attention for their pathogenic potential in immunocompromised hosts, having evolved into significant nosocomial pathogens through increasing utilization of invasive medical procedures (central venous catheterization, prosthetic joint replacement) and heightened risk of biofilm-associated infections in critically ill populations.[33–35] Penicillin G exhibited 92.3% resistance in MSSA, highlighting ubiquitous β-lactamase production within this population.[36] Macrolide resistance patterns revealed erythromycin resistance in 82.1% of MRSA cases versus 53.8% in MSSA cases, potentially associated with erm-mediated ribosomal methylation. High clindamycin resistance (60.7%) in MRSA suggests prevalent constitutive or inducible MLSB-resistant phenotypes necessitating D-test guidance

for clinical application.[37] Amikacin maintained low resistance rates (≤12.3% across all strains), particularly <3.8% in MSSA and MSSE, attributable to its structural resistance against aminoglycoside-modifying enzymes. Trimethoprim-sulfamethoxazole demonstrated markedly higher resistance in MRCNS (72.1%) than MRSA (21.4%), underscoring its limited therapeutic value against CoNS infections. As a last-resort antibiotic, vancomycin maintained 100% susceptibility across all isolates, confirming its status as a cornerstone therapy for severe MRSA and MR-CNS infections. However, the emerging resistance rates of 4.8% for linezolid and 3.6% for teicoplanin observed in MRCNS necessitate a stricter stewardship of these antimicrobial agents.

This study revealed extensive multidrug resistance in *A. baumannii*, demonstrating resistance rates exceeding 50% to β-lactams (ceftazidime 60.0%) and aminoglycosides (gentamicin 64.0%), while maintaining complete susceptibility to tigecycline and polymyxin B. Notably, carbapenem resistance in *A. baumannii* (60.0%) was lower than that reported in CHINET bloodstream surveillance data (>72.0%)[15] and comparable to the 60.8% resistance rate documented at a Vietnamese hospital.[38] *P. aeruginosa* exhibited favorable sensitivity to third-generation cephalosporins (ceftazidime 6.2%) and β-lactam/β-lactamase inhibitor combinations (piperacillin-tazobactam 6.2%), although its carbapenem resistance (31.2%) surpassed historical CHINET benchmarks and a tertiary care hospital in Beijing,[39] suggesting potential carbapenemase production requires vigilance. *B. cepacia complex* and *S. maltophilia* demonstrated preferable antibiotic susceptibility profiles, with sulfonamides or fluoroquinolones recommended as first-line options. Enterococci exhibited marked interspecies resistance divergence: *E. faecalis* retained a higher susceptibility to ampicillin (10.5% resistance) and penicillin G (47.1% resistance), whereas *E. faecium* demonstrated resistance rates of 88.9% and 97.1%, respectively. Overall, vancomycin resistance remained low (2.8%), with complete susceptibility to amoxicillin-clavulanate, teicoplanin, and linezolid, providing effective therapeutic alternatives for severe infections. β-Hemolytic streptococci and *S. pneumoniae* exhibited universal resistance to erythromycin and clindamycin, indicating widespread erm-mediated MLSB resistance phenotypes,[40] while viridans group streptococci showed similarly elevated resistance rates (77.9% and 66.2%, respectively). Penicillin G maintained full activity against β-hemolytic streptococci and *S. pneumoniae*, though 2.8% resistance emerged in viridans group streptococci, potentially associated with penicillin-binding protein (PBP) gene modifications.[41] Fluoroquinolone susceptibility patterns demonstrated complete levofloxacin resistance in β-hemolytic streptococci versus minimal resistance (0–5.1%) in *S. pneumoniae* and viridans group streptococci, possibly reflecting differential accumulation of parC/gyrA mutations across species.[42] Third-generation cephalosporins (cefotaxime, ceftriaxone), vancomycin, and linezolid maintained universal susceptibility across all streptococcal species, offering reliable options for severe infections. These findings underscore the critical need to avoid macrolides owing to their universal resistance risks, prioritize β-lactams or glycopeptides as empirical therapy, and implement species-specific treatment strategies based on distinct resistance profiles.

Limitations of This Study

It should be noted that our evaluation and discussion are limited to the cohort from our single institution, which may not be fully representative of broader patterns. In future studies, we intend to conduct a multicenter investigation to obtain a more comprehensive understanding.

Conclusion

In summary, our data demonstrate alarming antimicrobial resistance rates among predominant bloodstream isolates to first-line antibiotics. The persistent emergence of novel MDROs poses substantial therapeutic challenges for the management of BSIs. These findings underscore the critical need to sustain antimicrobial resistance surveillance programs, optimize antibiotic stewardship protocols, and reinforce hospital infection control measures to curb the spread and transmission of resistant pathogens.

Data Sharing Statement

All data used to analyze and generate the results of this study are included in this article.

Ethics Approval and Consent to Participate

The study was approved by the Ethics Committee of Fuwai Central China Cardiovascular Hospital (approval number: 2023-LS-84). Prior to the commencement of the study, all participants were fully informed of the purpose, procedures, potential risks, and benefits of the study and signed an informed consent form. Participants had the right to withdraw from the study at any time without any adverse consequences. The research adhered fully to the principles outlined in the Declaration of Helsinki.

Consent for Publication

All authors have read the manuscript and consent to publish.

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Author Contributions

All authors made a significant contribution to the work reported, whether that is in the conception, study design, execution, acquisition of data, analysis and interpretation, or in all these areas; took part in drafting, revising or critically reviewing the article; gave final approval of the version to be published; have agreed on the journal to which the article has been submitted; and agree to be accountable for all aspects of the work.

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Disclosure

The authors report no conflicts of interest in this work.

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