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ORIGINAL RESEARCH

Distribution and Antimicrobial Resistance Trends of Bloodstream Bacterial Isolates: A 10-year Single-Center Study in China

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Purpose: To analyze the changing distribution and drug resistance of pathogenic bacteria in patients with bloodstream infections (BSIs), thereby providing reference for hospital anti-infection treatment.

Methods: The clinical data, distribution of pathogenic bacteria and antimicrobial susceptibility profiles of patients with positive blood cultures at the First Affiliated Hospital of Xi'an Jiaotong University from January 1, 2015 to December 31, 2024 were collected retrospectively. WHONET 5.6 software was used for data analysis. The χ^2 test and *Fisher* exact test were used for statistical analysis.

Results: A total of 9372 bacterial strains were isolated from blood cultures. Gram-negative bacterial predominated (66.8%), markedly surpassing Gram-positive bacterial (33.2%). The top five pathogens were *Escherichia coli* (30.1%), *Klebsiella pneumoniae* (15.8%), *Enterococcus faecium* (6.9%), coagulase-negative *Staphylococci* (6.3%) and *Staphylococcus aureus* (6.1%). The detection rate of methicillin-resistant *Staphylococcus aureus* ranged from 25.8% to 38.4%, and it remained susceptible to vancomycin, linezolid, and teicoplanin. The detection rate of methicillin-resistant coagulase-negative *Staphylococci* peaked at 77.7% to 82.4%. *Enterococcus faecium* showed resistance to ampicillin exceeding 75%, with resistance rates to vancomycin and linezolid increasing from 0% to 5.8% and 1.2%, respectively. *Escherichia coli* demonstrated high susceptibility to Carbapenems, with imipenem resistance remaining low (1.6–2.2%). The resistance rates of *Klebsiella pneumoniae* to imipenem rose from 3.2% to 25.6%.The resistance rate of carbapenem-resistant *Pseudomonas aeruginosa* decreased from 36.4% in 2015–2016 to 16.5% in 2023–2024. However, the resistance rate of carbapenem-resistant *Acinetobacter baumannii* significantly increased from 47.2% to 75.7% during the same period.

Conclusion: The pathogenic bacteria in blood cultures isolates at this hospital are predominantly Gram-negative, with *Escherichia coli* and *Klebsiella pneumoniae* being the most common pathogens. The increasing trends of carbapenem-resistant *Klebsiella pneumoniae, Acinetobacter baumannii* and methicillin-resistant coagulase-negative *Staphylococci* underscore the urgent need for enhanced surveillance of pathogen distribution and antimicrobial resistance in bloodstream infections to guide rational antimicrobial use.

Keywords: blood culture, antimicrobial resistance, bacterial pathogens, carbapenem-resistant bacteria, antimicrobial susceptibility testing

Introduction

Bloodstream infections (BSIs) are severe systemic infections diseases caused by pathogenic microorganisms entering the bloodstream, which can lead to bacteremia, sepsis, multiple organ dysfunction syndrome (MODS) and high fatality rates.[1] Local epidemiological data play a crucial role in guiding empiric anti-infective therapy and reducing patient mortality. Because BSIs are closely linked with pneumonia, urinary tract infections, and other invasive infections, are aggravated by increasing antimicrobial resistance (AMR), and can directly precipitate sepsis, BSIs have become one of the major global public health burdens.[2] In recent years, extensive use of broad-spectrum antibiotics, the growing number

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of invasive surgical procedures, and wider application of immunosuppressive agents have driven a steady rise in the incidence of bloodstream infections. Currently, the emergence of multidrug-resistant (MDR) strains among these infections has posed formidable challenges for clinical antimicrobial therapy.[3,4]

Blood culture is the gold standard for the diagnosis of BSIs, enabling timely pathogen identification and guiding targeted antimicrobial therapy.[5] The majority of pathogens causing BSIs are bacteria (>90%).[6,7] In China, the predominant causative pathogens include *Escherichia coli, Klebsiella pneumoniae*, coagulase-negative *staphylococci, Staphylococcus aureus, Enterococcus spp., Acinetobacter baumannii, Pseudomonas aeruginosa, Streptococcus spp*. and *Enterobacter spp*.[8] However, the spread of drug-resistant strains has become increasingly severe. For instance, carbapenem-resistant Enterobacterales (CRE) and carbapenem-resistant *Acinetobacter baumannii* (CRAB) have been on the rise in multiple hospitals.[5,9] The emergence of resistant bacteria has severely limited the choice of effective antimicrobial agents and significantly increased the risk of treatment failure.[10]

Although several studies have reported on the species distribution and current resistance patterns of blood-culture isolates in different regions,[5,11] long-term, continuous surveillance data focusing specifically on the epidemiological trends of BSIs in Northwest China remain limited. While the Bacterial Resistant Investigation Collaborative System (BRICS) has conducted nationwide surveillance of bloodstream infection bacterial resistance since 2014, continuous ten-year antimicrobial resistance data are still scarce. Furthermore, China Antimicrobial Surveillance Network (CHINET) primarily emphasizes comprehensive surveillance, with relatively limited data specifically dedicated to bloodstream infections. In this study, we retrospectively analyzed the pathogen distribution and antimicrobial susceptibility trends in blood culture positive specimens from 2015 to 2024, aiming to provide a scientific basis for optimizing clinical antimicrobial use, formulating individualized treatment strategies, and strengthening hospital infection prevention and control programs.

Materials and Methods

Bacterial Isolates

A total of 9372 bacterial strains were collected from positive blood cultures of patients at the First Affiliated Hospital of Xi'an Jiaotong University between January 1, 2015, and December 31, 2024. Duplicate pathogens from multiple cultures of the same patient during the same hospitalization were excluded. Single-positive blood culture isolates of coagulase-negative staphylococci (CoNS) were interpreted as probable contaminants and excluded from the analysis. This retrospective study was approved by the Medical Ethics Committee of the First Affiliated Hospital of Xi'an Jiaotong University, which waived pan-informed consent.

Culture Media and Antibiotic Discs

Mueller-Hinton (MH) agar (Guangzhou, Detgerm Microbiogical Science Ltd, Guangzhou, China) was used for antimicrobial susceptibility testing by disc-diffusion method. For streptococci, 5% defibrinated sheep blood MH agar was used.The antibiotic discs, E-test strips, tigecycline and polymyxins were obtained from Wenzhou Kangtai Biotechnology (Wenzhou, China).

Bacterial Identification and Susceptibility Testing

The fully automated bacterial culture system BACTEC FX400 (Becton, Dickinson and Company, America) and BacT/ALERT Virtuo (Marcy Etoile, bioMérieux, France) were used to detect blood culture specimens. Bacterial Isolates were identified by matrix-assisted laser desorption-ionization time-of-flight mass spectrometry (MALDI-TOF MS) and antimicrobial susceptibility testing (AST) was performed using the VITEK-2 system (bioMérieux SA, Marcy l'Etoile, France). For isolates whose susceptibility could not be reliably determined by the automated system, E-test and Kirby-Bauer disk diffusion assay were employed as supplementary methods to ensure accuracy of antimicrobial susceptibility testing results. The interpretation of antimicrobial susceptibility results was performed according to Clinical and Laboratory Standards Institute (CLSI) M100 (2024 edition). Polymyxins interpretation followed the standards of the American Committee on Antimicrobial Susceptibility Testing.[12] While tigecycline interpretation followed the criteria established by the U.S. Food and Drug Administration (FDA).

Quality Control Strains

Escherichia coli (ATCC 25922, ATCC 8739, ATCC 35218), *Pseudomonas aeruginosa* (ATCC 27853), *Staphylococcus aureus* (ATCC 25923, ATCC 29213), *Enterococcus casseliflavus* (ATCC 700327), *Enterobacter cloacae* (ATCC 700323), *Streptococcus pneumoniae* (ATCC 49619), and *Haemophilus influenzae* (ATCC 49247, ATCC 49766) were included in all AST procedures to ensure methodological consistency.

Statistical Analysis

All microbiology data were managed and analyzed using WHONET 5.6 software (China). SPSS 26.0 software was utilized for statistical analysis. The *Fisher's* exact test or chi-square test was used for categorical variables. A P value < 0.05 was considered statistically significant.

Results

Bacterial Distribution

Between January 2015 and December 2024, a total of 9372 distinct pathogenic strains were isolated from the blood cultures of patients (Figure 1). Among these, 3109 strains (33.2%) were Gram-positive bacteria, while 6263 strains (66.8%) were Gram-negative bacteria. The five most prevalent bacterial species were *Escherichia coli* (2825 strains,

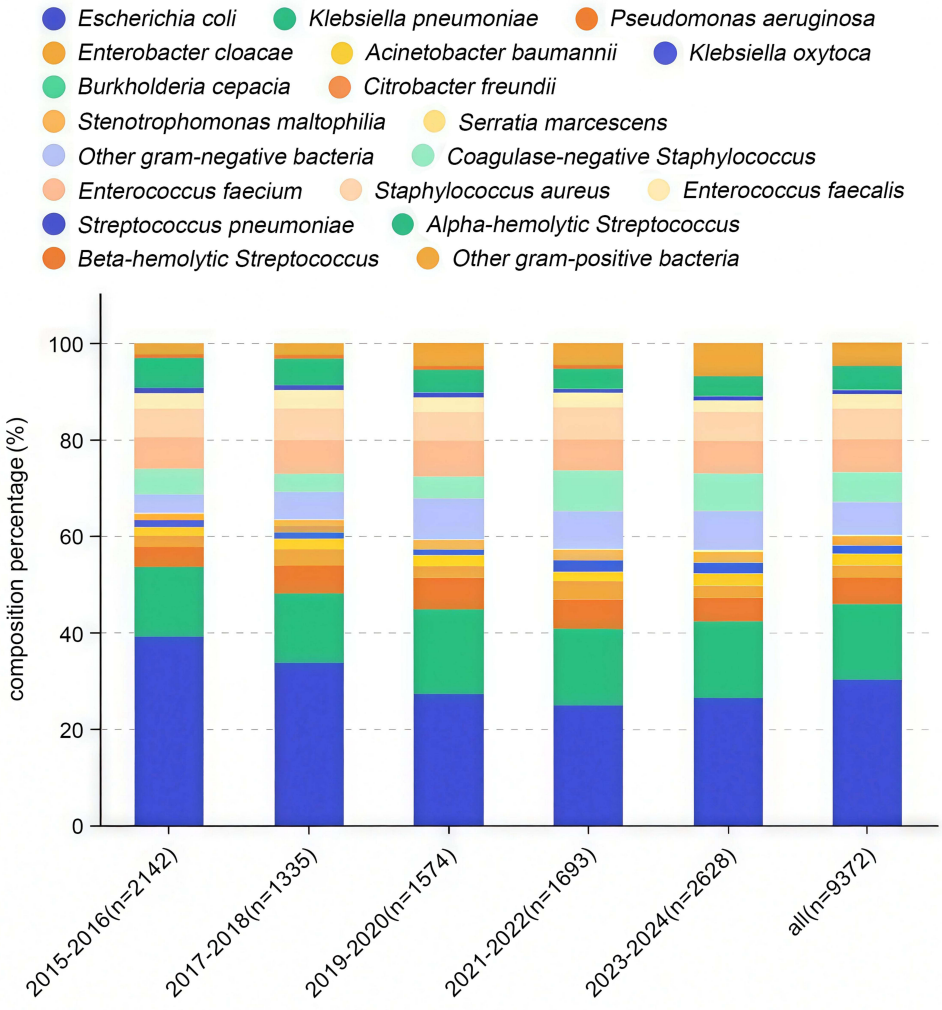

Figure 1 Distribution of 9372 pathogenic bacteria isolated from blood cultures.

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30.1%), *Klebsiella pneumoniae* (1478 strains,15.8%), *Enterococcus faecium* (651 strains, 6.9%), coagulase-negative *Staphylococci* (592 strains, 6.3%) and *Staphylococcus aureus* (571 strains, 6.1%).

Antibiotic Resistances of Major Gram-Positive Bacteria

Staphylococcus Genus

A total of 1163 strains of *Staphylococcus* genus were isolated, comprising 12.4% of all isolated pathogens. Among them, 571 strains were *Staphylococcus aureus*, and 592 strains were coagulase-negative *Staphylococci* (CoNS). The detection rates of methicillin-resistant *Staphylococcus aureus* (MRSA) in 2015–2016, 2017–2018, 2019–2020, 2021–2022 and 2023–2024 were 38.4% (48 strains), 28.1% (25 strains), 25.8% (23 strains), 36.4% (40 strains) and 34.2% (54 strains), respectively. The resistance to gentamicin and rifampin among MRSA isolates demonstrated a consistent and marked decline. In contrast, the resistance rates for the macrolide antibiotics erythromycin and clindamycin remained persistently high throughout the surveillance period. *Staphylococcus aureus* remained susceptible to vancomycin, linezolid, and tigecycline (Table 1). The detection rates of methicillin-resistant coagulase-negative *Staphylococci* (MRCNS) were 77.7% (87strains), 64.1% (34 strains), 79.5% (58 strains), 80.5% (116 strains) and 82.4% (173 strains) during the same period. Resistance to penicillin G and erythromycin remained relatively high among methicillin-sensitive coagulase-negative *Staphylococci* (MSCNS), whereas resistance to levofloxacin and trimethoprim–sulfamethoxazole were low. All CoNS isolates were fully susceptible to vancomycin, linezolid, and tigecycline (Table 2).

Enterococcus Genus

A total of 1056 *Enterococcus* strains were isolated, including 271 strains of *Enterococcus faecalis*, 651 strains of *Enterococcus faecium*, and 134 strains of other *Enterococcus* species. The resistance rate of *Enterococcus faecium* to ampicillin exceeded 75%, but *Enterococcus faecalis* showed low resistance rate to the drug. Moreover, *Enterococcus faecalis* exhibited lower resistance rates to penicillin G, ampicillin, levofloxacin, and erythromycin than those displayed by *Enterococcus faecium*. The resistance rates of *Enterococcus faecium* to vancomycin and linezolid increased from 0% in 2015–2016 to 5.8% and 1.2% by 2023–2024, respectively. No vancomycin resistant isolates were detected and the resistance rate to linezolid was less than 10% among *Enterococcus faecalis* (Tables 3 and 4).

Antibiotic Resistances of Enterobacteriaceae Bacteria

Escherichia coli

During the surveillance period from 2015 to 2024, *Escherichia coli* demonstrated high susceptibility to carbapenem antimicrobials. Resistance rates to piperacillin/tazobactam, cefotetan, and amikacin remained consistently low. In

Table 1 Antimicrobial Resistance Rates of *Staphylococcus aureus* Isolated from Blood Cultures Between 2015 and 2024

Antimicrobial Agent	2015–2016		2017–2018		2019–2020		2021–2022		2023–2024	
	MRSA (n=48)	MSSA (n=77)	MRSA (n=25)	MSSA (n=64)	MRSA (n=23)	MSSA (n=66)	MRSA (n=40)	MSSA (n=70)	MRSA (n=54)	MSSA (n=101)
Penicillin G	100	97.4	100	82.6	100	93.9	100	91.9	100	87
Oxacillin	100	0	100	0	100	0	100	0	100	0
Gentamicin	41.7	16.9	20	17.2	21.7	12.1	15	8.6	9.3	10.9
Clindamycin	68.8	16.9	76	29.7	78.3	45.5	50	25.7	64.8	24.8
Erythromycin	72.9	64.9	92	56.2	78.3	56.1	70	50	75.9	49.5
Vancomycin	0	0	0	0	0	0	0	0	0	0
Linezolid	0	0	0	0	0	0	0	0	0	0
Tigecycline	0	0	0	0	0	0	0	0	0	0
Rifampin	37.5	0	20	0	8.7	0	5	0	0	0
Levofloxacin	37.5	0	20	0	30.4	6.1	35	7.1	24.1	5
Trimethoprim-sulfamethoxazole	16.7	16.9	4	25	4.3	22.7	7.5	24.3	13	21.8

Table 2 Antimicrobial Resistance Rates of Coagulase-Negative Staphylococci Isolated from Blood Cultures Between 2015 and 2024

Antimicrobial Agent	2015–2016		2017–2018		2019–2020		2021–2022		2023–2024	
	MRCNS (n=87)	MSCNS (n=25)	MRCNS (n=34)	MSCNS (n=19)	MRCNS (n=58)	MSCNS (n=15)	MRCNS (n=116)	MSCNS (n=28)	MRCNS (n=173)	MSCNS (n=37)
Penicillin G	100	68.0	100	78.9	100	86.9	100	78.6	100	62.2
Oxacillin	100	0	100	0	100	0	100	0	100	0
Gentamicin	24.1	0	29.4	0	20.7	0	24.1	0	24.8	0
Clindamycin	32.2	16.0	50.0	26.3	62.1	6.7	51.7	10.7	46.2	8.1
Erythromycin	79.3	56.0	88.2	52.6	87.9	60.0	80.2	60.7	83.8	70.3
Vancomycin	0	0	0	0	0	0	0	0	0	0
Linezolid	0	0	0	0	0	0	0	0	0	0
Tigecycline	0	0	0	0	0	0	0	0	0	0
Rifampin	8.0	0	29.4	0	17.2	0	10.3	0	15.6	0
Levofloxacin	63.2	8.0	58.8	26.3	62.1	6.7	68.1	14.3	75.1	5.4
Trimethoprim-sulfamethoxazole	56.3	20.0	64.7	31.5	75.9	33.3	68.1	25.0	69.3	8.1

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Table 3 Antimicrobial Resistance Rates of *Enterococcus faecium* Isolated from Blood Cultures Between 2015 and 2024

Antimicrobial Agent	2015–2016 (n=148)	2017–2018 (n=88)	2019–2020 (n=120)	2021–2022 (n=114)	2023–2024 (n=175)
Penicillin G	87.2	79.2	80.7	89.5	89.6
Ampicillin	83.8	79.5	80	89.5	89
Gentamicin-high	0	1.7	5	18.8	29.1
Levofloxacin	75.7	79.5	78.7	88.2	87.2
Erythromycin	87.2	81.8	85.8	88.6	89.6
Linezolid	0	0	0	0	1.2
Vancomycin	0	1.1	4.2	1.8	5.8
Teicoplanin	0	0	4.2	1.8	1.9

Table 4 Antimicrobial Resistance Rates of *Enterococcus faecalis* Isolated from Blood Culture Between 2015 and 2024

Antimicrobial Agent	2015–2016 (n=65)	2017–2018 (n=48)	2019–2020 (n=45)	2021–2022 (n=49)	2023–2024 (n=64)
Penicillin G	13.8	7	6.8	6.1	3.2
Ampicillin	6.2	2.1	0	0	1.6
Gentamicin-high	0	7.7	2.3	22.4	30.2
Levofloxacin	23.1	22.9	27.5	27.5	27.3
Erythromycin	60	62.5	52.3	53.1	49.2
Linezolid	0	4.2	6.8	4.1	9.5
Vancomycin	0	0	0	0	0
Teicoplanin	0	0	0	0	0

contrast, Resistance rates to multiple cephalosporins, including cefuroxime, cefazolin and ceftriaxone, remained persistently high, whereas those for ceftazidime ranged from 25.1% to 36%. Resistance to piperacillin, ampicillin/sulbactam, cefuroxime, ceftazidime, ceftriaxone, cefepime, aztreonam, gentamicin, tobramycin, ciprofloxacin, levofloxacin and trimethoprim/sulfamethoxazole exhibited significant annual variation. However, no tigecycline-resistant isolates were detected during the study period (Table 5).

Klebsiella pneumoniae

From 2015–2016 to 2023–2024, the resistance rate of *Klebsiella pneumoniae* to most routine antibiotics remained below 45%, with resistance rates to cefazolin, cefuroxime, and ceftriaxone being lower those that of *Escherichia coli*. However, a statistically significant increase in carbapenem resistance was observed, with resistance to both imipenem and meropenem rising substantially. Concurrently, resistance to several other antibacterial agents also showed significant upward trends ($P < 0.05$) (Table 6).

Table 5 Antimicrobial Resistance Rates of *Escherichia coli* Isolated from Blood Cultures Between 2015 and 2024

Antimicrobial Agent	2015–2016 (n=837)	2017–2018 (n=450)	2019–2020 (n=426)	2021–2022 (n=421)	2023–2024 (n=691)	χ^2	*P*
Ampicillin	88.1	85.7	87.4	83.1	87.4	9.96	0.041
Piperacillin	66.5	64.2	65.7	59.7	54.9	24.45	<0.001
Ampicillin-Sulbactam	68.1	62.6	58.7	51.1	45.6	96.30	<0.001
Piperacillin-Tazobactam	3.2	4	4.7	4.1	1.7	7.47	0.113
Cefazolin	70.9	65.7	65.5	65	64.4	9.34	0.053
Cefuroxime	68.1	60.5	61.4	61.5	60.3	13.49	<0.001
Ceftazidime	36	29.6	27.1	29.1	25.1	22.43	<0.001
Ceftriaxone	67.1	60.8	60	60.6	58.9	13.19	0.010

(*Continued*)

Table 5 (Continued).

Antimicrobial Agent	2015–2016 (n=837)	2017–2018 (n=450)	2019–2020 (n=426)	2021–2022 (n=421)	2023–2024 (n=691)	χ^2	*P*
Cefepime	28.1	22	16.3	17.4	14.7	48.93	<0.001
Cefotetan	3.3	4.5	2.9	4.2	2.1	6.27	0.180
Aztreonam	47.2	41.3	38.9	38.4	35.5	24.26	<0.001
Imipenem	1.6	2	1.7	2.1	2.2	1.01	0.908
Meropenem	1.3	2	1.4	2.1	1.7	1.76	0.780
Amikacin	3.3	2.5	1.2	2.4	1.6	4.90	0.298
Gentamicin	51.5	37	40	39.3	33.5	58.51	<0.001
Tobramycin	21	14.3	13.9	14.1	12.4	25.89	<0.001
Ciprofloxacin	64.3	59.8	62.7	57	55.2	15.37	0.004
Levofloxacin	61.8	58	60.8	55.4	70.2	37.70	<0.001
Trime-thoprim /sulfamethoxazole	64.8	53.4	58.3	52.4	52.9	34.24	<0.001
Tigecycline	NA	0	0	0	0	-	-
Polymyxin B	NA	0	0	0.2	0	-	-

Table 6 Antimicrobial Resistance Rates of *Klebsiella pneumoniae* Isolated from Blood Cultures Between 2015 and 2024

Antimicrobial Agent	2015–2016 (n=311)	2017–2018 (n=193)	2019–2020 (n=279)	2021–2022 (n=271)	2023–2024 (n=424)	χ^2	*P*
Piperacillin	26	30.1	28.6	27.6	41.8	27.71	<0.001
Ampicillin-Sulbactam	28.3	35	36.7	30.7	44.7	25.80	<0.001
Piperacillin-Tazobactam	3.5	9.4	22.8	17.8	26.8	83.40	<0.001
Cefazolin	27.3	31.9	31.5	28	43.5	28.22	<0.001
Cefuroxime	25.4	32.1	33.7	26.8	43.8	35.06	<0.001
Ceftazidime	11.6	18.8	29	28.6	33.3	53.67	<0.001
Ceftriaxone	25.7	29.3	27.6	23.6	42.1	37.65	<0.001
Cefepime	7.1	15.1	25	25	28.7	61.41	<0.001
Cefotetan	3.3	4.4	3.5	4.7	25.7	158.28	<0.001
Aztreonam	15.8	22.5	31.9	29.6	37.1	45.48	<0.001
Imipenem	3.2	9.9	19.9	13	25.6	80.14	<0.001
Meropenem	3.2	7.9	19.9	13.3	25.4	83.43	<0.001
Amikacin	3.5	5.7	15.9	13.3	21.1	59.86	<0.001
Gentamicin	20.6	17.5	18.1	12.6	27.1	24.26	<0.001
Tobramycin	5	11	18.8	17.8	24.4	54.05	<0.001
Ciprofloxacin	15.1	17.8	34.8	26.7	33.9	50.23	<0.001
Levofloxacin	11.6	14.1	33.3	24.8	36.7	82.44	<0.001
Trime-thoprim /sulfamethoxazole	27.3	28.1	42.8	33.7	39.7	23.63	<0.001
Tigecycline	NA	0	0.7	0.7	0.2	-	-
Polymyxin B	NA	0	0.7	1.5	7.8	-	-

Enterobacter cloacae

The resistance rate of *Enterobacter cloacae* to carbapenem antibiotics and trimethoprim-sulfamethoxazole showed an upward trend. Resistance rates to piperacillin-tazobactam, ceftazidime, ceftriaxone, cefepime, aztreonam, imipenem, meropenem, tobramycin, ciprofloxacin and levofloxacin exhibited significant annual variation ($P < 0.05$). In contrast, resistance rates to piperacillin and amikacin remained relatively stable over the study period (Table 7).

Table 7 Antimicrobial Resistance Rates of *Enterobacter cloacae* Isolated from Blood Cultures Between 2015 and 2024

Antimicrobial Agent	2015–2016 (n=54)	2017–2018 (n=42)	2019–2020 (n=36)	2021–2022 (n=59)	2023–2024 (n=61)	χ^2	*P*
Piperacillin	29.6	19.5	22.9	23.7	31	2.70	0.609
Piperacillin-tazobactam	11.1	2.4	5.6	18.6	13.1	28.52	<0.001
Ceftazidime	27.8	19	19.4	37.3	39.3	77.99	<0.001
Ceftriaxone	40.7	19.5	22.9	31.6	40.7	59.29	<0.001
Cefepime	14.8	9.5	8.3	13.6	18	23.86	<0.001
Aztreonam	27.8	16.7	19.4	32.2	36.1	64.72	<0.001
Imipenem	3.7	0	8.3	8.5	13.1	29.20	<0.001
Meropenem	3.7	0	8.3	8.5	13.1	29.20	<0.001
Amikacin	1.9	0	0	1.7	1.6	2.97	0.564
Gentamicin	9.3	4.9	11.4	5.3	11.9	15.40	0.004
Tobramycin	13	7.1	8.3	5.1	11.5	10.99	0.027
Ciprofloxacin	14.8	11.9	2.8	10.2	19.7	25.57	<0.001
Levofloxacin	7.4	11.9	2.8	10.2	13.2	24.68	<0.001
Trime-thoprim /sulfamethoxazole	9.3	19	19.4	18.6	24.6	56.46	<0.001
Tigecycline	NA	0	0	0	0	-	-
Polymyxin B	NA	NA	0	0	0	-	-

Antibiotic Resistances of Non-Fermenting Gram-Negative Bacteria

Pseudomonas aeruginosa

Compared with 2015–2016, the resistance rates of *Pseudomonas aeruginosa* to imipenem and meropenem showed a significant decline in 2023–2024. Resistance to piperacillin–tazobactam, ceftazidime, cefepime, aztreonam, amikacin, and tobramycin remained below 30% throughout the study period, although statistically significant annual differences in resistance rates were observed. In contrast, resistance to ciprofloxacin and levofloxacin remained stable at approximately 10.0%, with no statistically significant annual variation observed. No colistin-resistant isolates were detected (Table 8).

Acinetobacter baumannii

Acinetobacter baumannii exhibited alarmingly high resistance rates to most commonly used antibacterial agents. Resistance to Carbapenems demonstrated a sharp and substantial increase from 2015–2016 to 2021–2022. Although a slight decline was observed in 2023–2024, the resistance rate remained above 75.7%. Temporal variations in resistance rates to piperacillin/tazobactam, imipenem, meropenem, amikacin, ciprofloxacin, and levofloxacin were statistically

Table 8 Antimicrobial Resistance Rates of *Pseudomonas aeruginosa* Isolated from Blood Cultures Between 2015 and 2024

Antimicrobial Agent	2015–2016 (n=88)	2017–2018 (n=76)	2019–2020 (n=103)	2021–2022 (n=101)	2023–2024 (n=127)	χ^2	*P*
Piperacillin-tazobactam	12.5	3.9	2.1	12.9	12.8	13.68	0.008
Ceftazidime	26.1	7.9	8.8	12.9	10.4	17.77	0.001
Cefepime	27.3	5.3	4.9	7.9	8.8	33.21	<0.001
Aztreonam	26.4	15.8	16.8	10	8.8	15.03	0.005
Imipenem	39.1	15.8	23.5	19.8	20.8	15.18	0.004
Meropenem	36.8	13.7	19.6	17.8	15.2	19.29	<0.001
Amikacin	3.4	0	0	7.9	8.5	23.08	<0.001
Tobramycin	20.5	1.4	2	8	6.5	30.45	<0.001
Ciprofloxacin	6.8	5.3	2.9	7	8	2.83	0.586
Levofloxacin	8	3.9	3.9	9.9	10.4	5.58	0.233
Polymyxin B	NA	0	0	0	0	-	-

Table 9 Antimicrobial Resistance Rates of *Acinetobacter baumannii* Isolated from Blood Cultures Between 2015 and 2024

Antimicrobial Agent	2015–2016 (n=36)	2017–2018 (n=34)	2019–2020 (n=37)	2021–2022 (n=38)	2023–2024 (n=70)	χ^2	*P*
Ampicillin/Sulbactam	47.2	62.1	50.4	66.7	75.7	10.97	0.270
Piperacillin-tazobactam	44.4	61.8	86.2	86.1	75.7	23.86	<0.001
Ceftazidime	55.6	67.6	79.4	84.2	75.7	9.29	0.054
Cefepime	55.6	67.6	77.1	81.6	70	7.38	0.117
Imipenem	47.2	67.6	80	84.2	75.7	16.26	0.003
Meropenem	47.2	67.6	80	84.2	75.7	16.12	0.003
Amikacin	38.2	61.8	39.4	63.2	71.5	15.78	0.003
Tobramycin	50	70.6	60	63.2	58.5	3.31	0.507
Ciprofloxacin	52.8	70.6	80	84.2	75.7	11.59	0.021
Levofloxacin	25	44.1	65.7	63.2	44.2	15.94	0.003
Trime-thoprim /sulfamethoxazole	41.7	47.1	68.6	57.9	48.6	6.32	0.176
Tigecycline	NA	0	0	0	0	-	-
Polymyxin B	NA	0	0	0	0	-	-

significant ($P < 0.05$). Notably, no resistance to tigecycline and colistin were detected among *Acinetobacter baumannii* isolates (Table 9).

Carbapenem-Resistant Gram-Negative Bacilli

The prevalence of Gram-negative bacteria varied across different periods. Carbapenem-resistant organisms (CRO) isolates accounted for 3.0%, 4.64%,7.68%, 6.91%, and 7.95% of the total bacterial isolates in 2015–2016, 2017–2018, 2019–2020, 2021–2022, and 2023–2024, respectively. The detection rates of CRE showed a consistent upward trend. In contrast, the detection rates of carbapenem-resistant *Pseudomonas aeruginosa* (CRPA) gradually decreased from an initially high level, whereas detection rates of CRAB remained persistently high, consistently exceeding 70%. Except for tigecycline and colistin, CRE exhibited resistance rates greater than 40% to all commonly tested antimicrobial agents throughout 2015–2024. CRPA isolates exhibited rising resistance to amikacin and fluoroquinolones over time. CRAB isolates demonstrated uniformly high resistance to most agents, with a slight downward trend observed for amikacin. Notably, no isolates of CRE, CRPA, or CRAB resistant to tigecycline or colistin were detected (Figure 2).

Discussion

Bloodstream infections (BSIs) are life-threatening conditions with high prevalence worldwide.[13,14] The majority of patients with bacteremia require hospital admission and 30-day mortality is still as high as 12–17%.[13–15] A total of 9372 strains were isolated from positive blood cultures of patients between 2015 and 2024. The results showed that the isolation rate of Gram-negative bacteria (66.8%) was higher than that of Gram-positive bacteria (33.2%), a pattern similar to findings from a Chinese multicenter study and a report from Ethiopia.[5,6] Species distribution showed *Escherichia coli* (2825 isolates, 30.1%) ranked first, followed by *Klebsiella pneumoniae* (1478, 15.8%), *Enterococcus faecium* (651, 6.9%), coagulase-negative *staphylococci* (592, 6.3%) and *Staphylococcus aureus* (571, 6.1%). This distribution largely mirrors data from a domestic investigation,[9] but differs from overseas studies in which *Acinetobacter baumannii* was the most common Gram-negative species, followed by *Pseudomonas aeruginosa* and *Klebsiella pneumoniae*.[5]

Enterococcus faecium was the predominant Gram-positive pathogens causing bloodstream infections, followed by Coagulase-negative *staphylococci* (CoNS). This distribution differs slightly from findings in Southwest China,[16] where CoNS were reported as the most common Gram-positive pathogens. CoNS are commensal bacteria that colonize human skin and have traditionally been regarded as contaminants rather than causes of bloodstream infections. However, they can be harmful in immunocompromised hosts. Most CoNS strains can form biofilms, especially those that carry the

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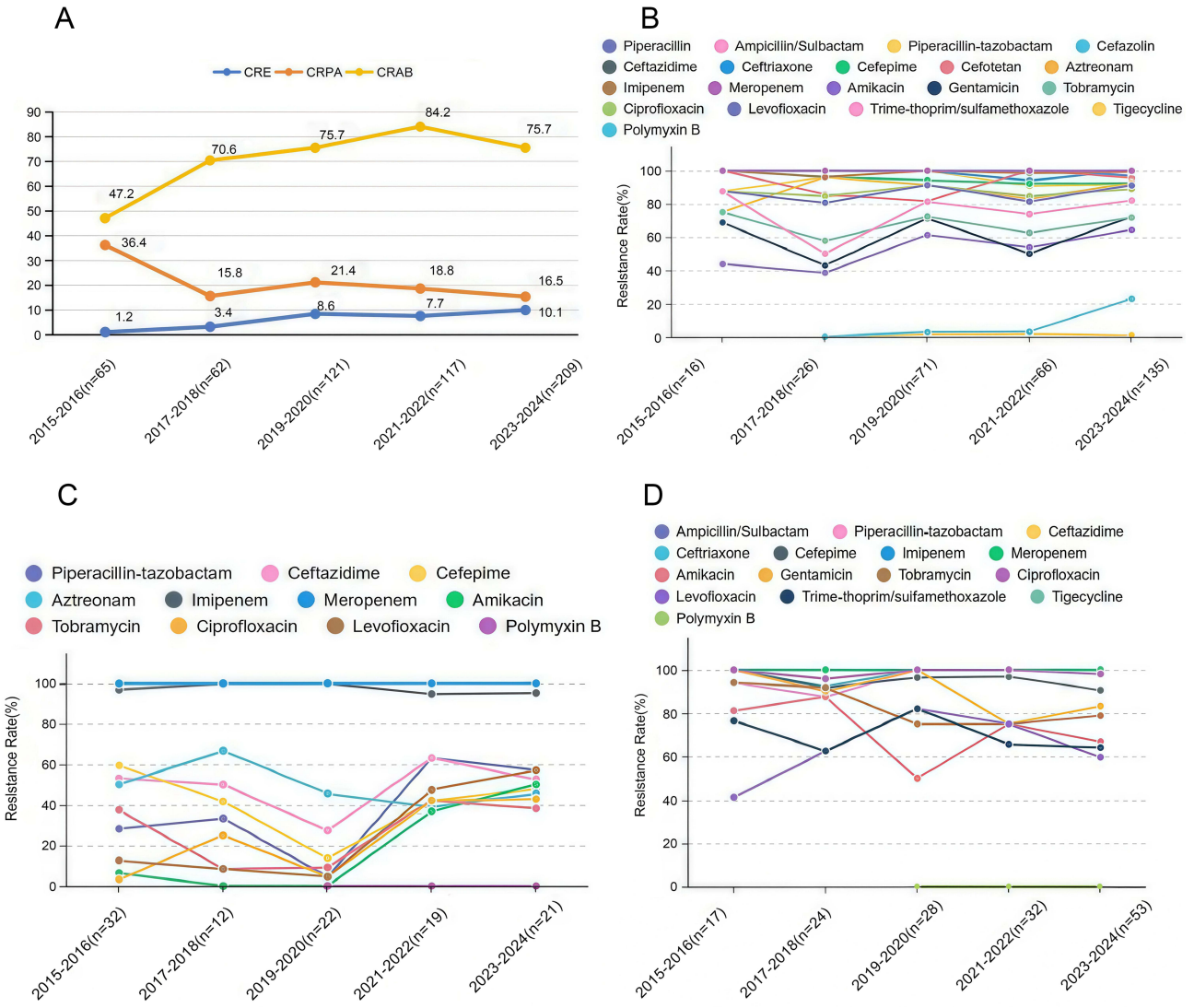

Figure 2 Detection rates (**A**) and antimicrobial resistance rates of CRE (**B**) CRPA (**C**) and CRAB (**D**) isolated from blood cultures between 2015 and 2024.
Abbreviations: CRE, Carbapenem-resistant Enterobacterales; CRPA, Carbapenem-resistant *Pseudomonas aeruginosa*; CRAB, Carbapenem-resistant *Acinetobacter baumannii*.

complete ica operon, which significantly enhancing their pathogenicity. These strains are closely linked to catheter colonization, bacteremia, and sepsis. Previous studies have indicated that the proportion of bloodstream infections caused by CoNS is increasing, particularly among patients with temporary or permanent medical device implantation,[17,18] and similar findings were observed in the present study. The detection rate of methicillin-resistant *Staphylococcus aureus* (MRSA) fluctuated between 25.8% and 38.4% across different periods. With the emergence and spread of MRSA, Gopikrishnan et al have carried out that the resistance mechanisms of MRSA strains are complex and diverse, including target modification, efflux pump activation, and drug degradation or inactivation, posing a formidable challenge to clinical therapy.[16] Of note, MRSA showed a marked decline in resistance to gentamicin and rifampicin, but resistance to macrolides such as erythromycin and clindamycin remained high (50–92%), largely attributable to the widespread erythromycin ribosome methylase (erm)-mediated macrolide-lincosamide-streptogramin B (MLSB) phenotype.[19] All *Staphylococcus aureus* and CoNS isolates retained full susceptibility to vancomycin, linezolid and tigecycline, mirroring findings by Abdel Halim et al in Egyptian pediatric patients,[20] and confirming these agents as first-line options for MRSA infections. *Enterococcus spp*. constituted 11.32% of all isolates in our hospital, with *Enterococcus faecium* (6.9%) recovered more frequently than *Enterococcus faecalis* (2.9%). Previous studies demonstrated that the increasing

incidence of *Enterococcus faecium* bloodstream infections is closely linked to acquisition of the pilA gene and enhanced biofilm-forming capacity,[21] suggesting a corresponding genotypic resistance profile. *Enterococcus faecium* displayed higher resistance rates to most antimicrobial agents than *Enterococcus faecalis*, although the proportion of vancomycin-resistant isolates is rising,but it remains lower than that reported in a recent two-year international survey.[22] Notably, 30-days mortality among patients with vancomycin-resistant *Enterococcus faecium* (36.6%) was significantly higher than those infected with vancomycin-susceptible strains (31.8%),[23] which underscores the prognostic value of accurate species identification and continuous antimicrobial resistance surveillance.

A decade of surveillance data identifies *Escherichia coli* and *Klebsiella pneumoniae* as the commonest Gram-negative pathogens causing bloodstream infections. *Escherichia coli* has preserved high susceptibility to carbapenems and to most β-lactam/β-lactamase-inhibitor combinations, whereas resistance to third-generation cephalosporins and fluoroquinolones remains substantial. This phenotypic resistance pattern is consistent with that reported in previous studies to be primarily driven by ESBL or AmpC enzymes.[24] In sharp contrast, the carbapenem- resistance rate in *Klebsiella pneumoniae* has risen steeply from 3.2% in 2015–2016 to 25.6% in 2023–2024, a trend linked to carbapenemase production, loss or down regulation of outer-membrane porins, and over-expressed efflux pumps.[25] Previous studies have identified IncFII/IncR and IncC plasmids as the principal vehicles for carbapenemase genes in this species.[4,26] The horizontal spread among strains has greatly accelerated the dissemination of resistance. Mobile genetic elements such as IS26-containing integrons can capture, rearrange and express resistance cassettes, thereby providing ready platforms for the accumulation and transfer of resistance determinants.[27] The high prevalence of carbapenem resistance in *Klebsiella pneumoniae* observed in our study suggests a genotypic resistance profile similar to previous studies. A retrospective ICU cohort demonstrated significantly higher 30-days mortality in patients with CRKP bloodstream infection than in those infected with the carbapenem-susceptible strains, regardless of colistin susceptibility.[28] Consequently, the ensuing proliferation of CRKP infections has markedly restricted therapeutic options and has worsened patient outcomes. In the face of multidrug resistance and limited clinical antimicrobial options, combination therapy with one or more agents including ceftazidime–avibactam, aztreonam, and aminoglycosides is increasingly becoming the optimal choice. Continuous resistance monitoring, molecular-epidemiology-guided infection-control measures, prudent antimicrobial stewardship and the development of novel therapeutics are all essential to curtail CRKP spread and improve prognosis. Likewise, the carbapenem-resistant rate among *Enterobacter cloacae* has climbed noticeably, mirroring global reports[29] and reflecting the species ongoing evolution under antibiotic pressure. This trend is driven not only by the clonal expansion of resistant genotypes but also by hospital environments and host factors. Strengthened surveillance, optimization of antimicrobial use and introduction of new treatment modalities are urgently required to contain further dissemination.

Among non-fermenting Gram-negative bacilli, *Pseudomonas aeruginosa* and *Acinetobacter baumannii* are the leading pathogens. Carbapenems have long been regarded as the last-line therapy for *Pseudomonas aeruginosa* bloodstream infections. However, their widespread use has driven a global increase in CRPA, with the highest prevalence (64.6%) reported in Latin America.[30] A 7-year Chinese retrospective study showed that the CRPA rate in bloodstream isolates rose from 26% in 2017 to 49% in 2020, it then fell to 29% in 2021, and rebounded sharply to 47% in 2023.[31] In contrast, our data indicate that the carbapenem-resistance rate among *Pseudomonas aeruginosa* declined between 2015–2016 and 2023–2024, a trend consistent with the findings of Zeshi Liu.[32] Domestic studies have demonstrated that oprD loss-of-function mutations and over-active efflux pumps remain the dominant resistance mechanisms in CRPA causing bloodstream infection, while carbapenemase production is emerging as an increasingly important secondary driver of resistance.[33] Notably, our phenotypic analysis cannot confirm the genetic basis of CRPA resistance in our isolates; however, the observed resistance phenotype suggests a similar genotypic resistance profile to that reported in these domestic studies. All *Pseudomonas aeruginosa* isolates in our survey remained susceptible to colistin, mirroring the results reported by Fišerová et al[34] In China, approximately 2.8% of nosocomial bloodstream infections are caused by *Acinetobacter baumannii*; despite this low isolation rate, associated mortality exceeds 60%.[35,36] The organism displays high levels of resistance, with the national CRAB rate approaching 70%.[37] Over the past decade, the carbapenem resistance rate of *Acinetobacter baumannii* has continued to rise, increasing from 47.2% in 2015–2016 to 84.2% in 2021–2022; although it has fallen slightly in 2023–2024, but it still exceeds 75%. Once carbapenem resistance is acquired, the organism usually becomes resistant to most other antimicrobial agents, leaving few therapeutic options. In

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our dataset, CRAB isolates remained fully susceptible to tigecycline and colistin, whereas resistance to all other agents was high,underscoring the critical role of these two agents as salvage therapy. In addition to antibiotic resistance, *Acinetobacter baumannii* thrives in the nosocomial environment because it persists on surfaces: it tolerates disinfectants and desiccation, forms robust biofilms, and exhibits motility.[36] Global molecular epidemiology indicates that genes such as blaOXA-23 and blaOXA-24/40 are frequently associated with the carbapenem-resistant phenotype in CRAB.[37] This suggests that our isolates may also carry these genes, which would imply a shared resistance mechanism. Hospitals should enhance the infection control management of *Acinetobacter baumannii*. In addition, implementing hand hygiene, environmental disinfection, contact precautions, and environmental screening can help reduce the incidence of hospital-acquired antimicrobial-resistant organisms.

This study has several limitations. First, it is a single-center, retrospective analysis, so the findings may not be generalizable. Multi-center studies are needed to elucidate temporal changes in resistance patterns. Second, no molecular biology techniques were integrated, precluding a detailed description of resistance mechanisms or potential routes of transmission, further work on the molecular basis of multidrug resistance is essential to inform empirical therapy of bloodstream infections. Finally, this study focused solely on bacterial pathogens and their resistance profiles; the spectrum of fungal bloodstream infections was not examined, particularly the distribution of Candida species and their antifungal susceptibilities.

Conclusion

Over the past decade, Gram-negative bacteria have been the predominant causative agents of bloodstream infections in our hospital. The isolation rates of CRKP, CRAB, and MRCNS have increased, whereas the isolation rate of CRPA has decreased slightly. These findings not only provide valuable guidance for clinical anti-infective therapy but also offer a scientific basis for healthcare institutions to formulate antimicrobial stewardship strategies.

Data Sharing Statement

All data generated or analyzed in the study are included in the article and further inquiries can be directly contacted with the corresponding author Xiaoqin Wang via e-mail.

Ethics Approval

This retrospective study was approved by the Medical Ethics Committee of the First Affiliated Hospital of Xi'an Jiaotong University (XJTU1AF2023LSK-167), which waived pan-informed consent. All methods were carried out in accordance with Declaration of Helsinki.

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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