Distribution of Pathogenic Bacteria and their Antimicrobial Drug Resistance in the Blood of Patients with HIV/AIDS at a Tertiary Hospital in Hangzhou: An Eight-Year Retrospective Study

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Article

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Abstract

Background: Antimicrobial drug resistance (AMR) is reaching crisis levels worldwide. Patients with HIV/AIDS face the additional challenge of blood infection by antimicrobial-resistant bacteria. However, little information on the pathogenic bacteria distribution and AMR in the blood cultures of patients with HIV/AIDS is available.

Purpose: Herein, we aimed to analyze the distribution and AMR patterns of pathogenic bacteria in blood cultures of patients with HIV/AIDS.

Methods: We carried out an observational, single-center, retrospective, study of all positive blood isolates from patients with HIV/AIDS between 2013 and 2020.

Results: We analyzed 472 isolates from 1864 patients: 185 isolates (39.2%) were gram-positive, 75 isolates (15.9%) were gram-negative, and 173 isolates (36.7%) were fungi. *Staphylococcus* isolates were the most common gram-positive bacteria (155 (83.8%)), and *Salmonella* were the most common gram-negative bacteria (21 (28.0%)). Most of the fungal isolates were *Penicillium marneffei* (108 (62.4%).) Gram-positive bacteria had the highest resistance to penicillin (139 (86.3%) and erythromycin, 126 (78.3%). Coagulase-negative staphylococci had the highest resistance to oxacillin (77.0%), while the resistance of *S. aureus*only was 17.6%. Gram-negative bacteria had high resistance to ampicillin (82.1%) and ampicillin/sulbactam (57.1%). Among the fungal isolates,*Cryptococcus neoformans* was not resistant to amphotericin B, fluconazole, or itraconazole (sensitivity ≈ 100%). Overall, about 51% of isolates showed multidrug resistance, and there was an upward trend of antibiotic resistance in recent years.

Conclusion: Positive blood culture from patients with HIV/AIDS mainly contained gram-positive organisms, followed by fungi. Patients with AIDS with lower T cells counts had a had higher risk of fungal and mycobacterial infection. Gram-positive and gram-negative bacteria had high resistance rates to first-line antibiotics. Several pathogens were multidrug resistant. Culture isolation and microbiology services with susceptibility testing remain key to protecting the HIV/AIDS population from drug-resistant bacterial infections.

1. Introduction

Bloodstream infections are prevalent among patients with AIDS/HIV. Despite the introduction of combined antiretroviral therapy, antimicrobial-resistant bacterial blood infection is a major cause of mortality among patients with AIDS/HIV,[1] which places burdens on developing countries, including China. HIV has a specific capacity to alter B cell function and reduce T cell numbers, resulting in defective immunity and enhanced bacterial infection susceptibility.[2] Bloodstream infections occurs commonly among patients with AIDS/HIV, and are responsible for 13.5% of all AIDS-related deaths.[3] High morbidity bloodstream infections can be caused by gram-positive and gramnegative bacteria; however, gram-positive organisms are the most common pathogens associated with bloodstream infections.[4] For instance, a study showed that 11% of patients with AIDS/HIV in Cambodia had bloodstream infections, and the three most prevalent pathogens were *Escherichia coli*, *Salmonella*, and *Bacillus pseudomallei*, followed by *Staphylococcus aureus*.[5]

Antimicrobial resistance (AMR) is a global problem. Asia, particularly developing countries such as China, has a major problem with AMR.[6] HIV-related immunodeficiency results in a higher incidence and mortality of bloodstream infections in patients with AIDS/HIV compared with that in HIV seronegative patients. In addition, with the emergence of multidrug-resistant bacteria and lack of the infection control measures, patients with AIDS/HIV have an increased risk of bloodstream infection-related death.[4] For clinical management and the rational use of antimicrobials, understanding local AMR data is vital; however, AMR information related to blood culture isolates from patients with AIDS/HIV is limited. Herein, we describe the distribution of pathogenic bacteria and their antimicrobial susceptibility in blood cultures from patients with AIDS/HIV at a tertiary hospital in Hangzhou, China.

2. Materials and methods

2.1 Study area and period

This was an observational, single-center, retrospective study of positive blood isolates from patients with AIDS/HIV admitted to Hangzhou Xixi Hospital, Affiliated to Zhejiang Chinese Medical University, China, between 2013 and 2020. This hospital is a 600-bed tertiary teaching institution dealing with infectious diseases, with an average of 20000 patients with AIDS/HIV attending as outpatients per year and serves about 9620 patients with AIDS/HIV in Hangzhou.

2.2 Data Collection Methods

The hospital's clinical database provided the microbiology data and the patients' records.

2.3 Ethical Statement

The study is original and is not under consideration for publication in another journal. This study has been approved by the ethics committee of Hangzhou Xixi Hospital Affiliated to Zhejiang Chinese Medical University (Approval No. 2023-010). All methods were performed in accordance with the relevant guidelines and regulations and according to the principles laid down in the Declaration of Helsinki. All the authors reviewed and approved the final manuscript.

2.4 Informed Consent

Due to the nature of this retrospective study and the preserved anonymity of patients, a waiver of informed consent was obtained from the ethics committee of Hangzhou Xixi Hospital Affiliated to Zhejiang Chinese Medical University.

2.5 Laboratory techniques

2.5.1 Collection of Blood Samples

We took samples of venous blood (20 mL (adult) and 2–5 mL (children)) from each patient, and each sample was inoculated into a pair of bottles (Becton Dickinson, Franklin Lakes, NJ, USA) (half of the sample in each bottle) using strict aseptic procedures.[7]

2.5.2 Culture and Microorganism Identification

The collected blood samples were incubated for 7 days according to the standards set by the World Health Organization (WHO).[8] Samples were considered negative if they did not produce a positive result after 5 days of common bacterial culture or 14 days of fungal culture. Gram staining was used to identify common strains. *In vitro* strain identification and drug susceptibility tests of isolated colonies were carried out using a VITEK 2 Compact automatic microbial analysis system (bioMérieux, Marcy-l'Étoile, France. *Salmonella* strains were identified using the slide agglutination method, and *Cryptococcus neoformans* strains were identified using the Ink stain. The 4th edition of the "National Guide to Clinical Laboratory Procedures" was followed strictly during all operations, and the M100-S31 document of the Clinical and Laboratory Standards Institute (CLSI) was used to judge the results.[9]

2.5.3 Quality control

Zhengzhou Biocell Biotechnology Liability Company provided the VITEK 2 Compact automatic microbial analysis system, the BacT/ALERT 3D 480 automatic blood culture instrument ((bioMérieux), blood culture bottles, blood agar plates, and MacConkey agar plates. Before the tests, quality control strains (*Escherichia coli* (ATCC® 25922), *Pseudomonas aeruginosa* (ATCC® 27853), and *S. aureus* (ATCC® 25923), provided by the Clinical Laboratory Centre of the Ministry of Health of China, were used to test the sterility and performance of the culture media and the quality of the antimicrobial disks. The manufacturers' standardized operating procedures and instructions were executed strictly.

2.5.4 Analysis of the data

The Statistical Package for Social Sciences version 22.0 (IBM Corp., Armonk, NY, USA) was used for the data analysis. The data were summarized using the mean, frequency, and percentage, as appropriate, followed by presentation of the results using graphs or tables. Statistical significance was indicated by a P value less than 0.05.

3. Results

3.1. Demographic Characteristics

A total of 472 isolates were submitted for examination from 1864 patients with AIDS/HIV from 2013 to 2020. Among the patients providing positive samples, 375 (79.4%) were male and 97 (20.6%) were female. The study participants were 6 to 84 years old (mean ± standard deviation = 41.1± 0.7 years). There was no difference in the age and sex between the positive and negative groups. For the patients with AIDS/HIV, the CD4+count and CD4+/CD8 ratio in those with fungal infection and Mycobacterial infections was significantly lower than in those infected with gram-positive and gram-negative organisms, indicting a lower immune function in patients infected with fungi or *Mycobacteria* compared with those with bacterial infections (Table 1).

3.2 Bacterial Isolates

Figure 1 shows the distribution of pathogenic bacteria in the blood cultures. Among the 472 strains of clinically non-repetitive pathogens, 39.2% were gram-positive bacteria, 36.7% were fungi, 15.9% were gram-negative bacteria, and 8.2% were *Mycobacteria.* Among Gram-positive bacterial isolates, coagulase-negative staphylococci (CoNS; 74.6% (138/185)) were the most predominant, followed by *S. aureus* 17 (9.2%), whereas among the gram-negative isolates, *Salmonella* 21 (28.0%), was predominant. The largest proportion of the fungal isolates comprised *penicillium marneffei,* 108 (62.4%) (Figure 1).

3.3. AMR of Gram-positive Bacteria

S. aureus isolates were highly resistant to penicillin (17(100%)) and erythromycin (12(70.6%)), but only 3 (17.6%) *S. aureus* strains were oxacillin-resistant. Among CoNS, 127 clinically important strains were detected, of which 91.3% (116/127) were penicillin-resistant, approximately 76.4% (97/127) were oxacillin-resistant, and 81.9% (104/127) were erythromycin-resistant. No *Staphylococci* were found to be resistant to vancomycin. *Streptococcus* and *Enterococcus* isolates were observed to be highly resistant to erythromycin, but sensitive to vancomycin and linezolid. Moreover, about 60% of *Corynebacterium* strains exhibited resistance to penicillin and erythromycin (Table 2).

3.4. AMR of Gram-negative Bacteria

E. coli was significantly resistant trimethoprim-sulfamethoxazole (14 (77.8%)) and ampicillin (16 (88.9%)). *Klebsiella pneumoniae* was inherently resistant to ampicillin, and 50% of *K. pneumoniae* isolates were resistant to trimethoprim-sulfamethoxazol, and aztreonam. *Pseudomonas aeruginosa* was resistant to cefotetan and nitrofurantoin (up to 100% resistance), and was inherently resistant to ceftriaxone, trimethoprim-sulfamethoxazole, ampicillin/sulbactam, and ampicillin. In addition, *Salmonella* strains were highly resistant to ampicillin (63.2% (12/19)), and ampicillin/sulbactam (57.9% (11/19)) (Table 3).

3.5 Changes in Drug Resistance of Common Pathogenic Bacterial Clinical Isolates

The trends of Staphylococcal antibiotic resistance between 2013 and 2020 are shown in Table 4. Resistance to antibiotics peaked in 2017. Staphylococcal resistance to clindamycin, erythromycin, gentamicin, oxacillin, penicillin, and trimethoprim-sulfamethoxazole increased significantly from 50%, 57.1%, 14.3%, 57.1%, 92.9%, and 28.6% in 2013 to 85.7%, 92.9%, 50.0%, 71.4%, 100%, and 57.1% in 2017, respectively. In 2016, the prevalence of oxacillin-resistant *Staphylococcus* was 85.7%, which was much higher than that in 2013 (57.1%). Fortunately, vancomycin-resistant *Staphylococcus* was not observed from 2013 to 2020 (Table 4). From 2017 to 2018, extended spectrum beta-lactamase (ESBL)-producing *E. coli* and *K. pneumoniae* showed prevalences of 0.0% and 25.0%, respectively, which were the lowest in these years (Figure 2). In addition, ertapenem-resistant and imipenem-resistant *E. coli* were not observed from 2013 to 2020. Collectively, there has been an upward trend of resistance to various antibiotics in recent years.

3.6 Multidrug-Resistance Patterns of Bacterial Isolates

Regarding the multidrug-resistance patterns of the bacterial isolates, multidrug resistant (MDR) isolates comprised about 57.3% (126/220) of them, and approximately 34.1% (75/220) of the isolates showed resistance to four or more classes of antibiotics (Table 5). MDR isolates were most common among CoNS 66.9% (85/127), *Enterococcus* 80.0% (4/5), *E. coli* 61.1% (11/18), and *P. Aeruginosa* 80.0% (4/5)(Table 5).

4. Discussion

The distribution of pathogenic bacteria and their antibiotic resistance profile in patients shows wide variation among hospitals; therefore, surveying blood culture data in our institution is essential to provide empirical antibiotic therapy for patients with AIDS/HIV.

Pathogenic microorganism invasion leads to the systemic condition known as bloodstream infection (BSI), which is a common infection among patients with AIDS/HIV.[10] Herein, 20.9% of patients with AIDS/HIV attending our hospital had BSI, which is higher than that reported in Portugal (6.8%)[11] and other parts of China (9.38%)[12]. However, our result is similar to that reported in Nigeria[13], which might be related to the level of medical provision in different regions.

In our study, bacterial BSI (55.1%) was more common than fungal BSI (36.7%). Gram-positive bacteria (39.2%) were the main positive strains, followed by fungi (36.7%), and gram-negative bacteria (15.9%), which is consistent with the report by Mootsikapun[14]. Moreover, with the gradual decrease of $CD4^+$ cells and the patients' immunity, the infection rate of *Mycobacterium* increased. *Mycobacterium* is the most frequent blood culture isolate in hospitalized patients with AIDS/HIV with severe BSI, and is associated with higher mortality.[15]

Susceptibility tests showed that the majority of the isolates were resistant to the antibiotics on test. Gram-positive isolates showed 44.1% and gram-negative isolates showed 51.8% resistance to trimethoprim-sulfamethoxazole, which might be associated with the prophylactic use of trimethoprim-sulfamethoxazole for patients with AIDS/HIV. However, a study in Ethiopia reported a much higher percentage.[16] In addition, 92.4 % of *Staphylococcus* isolates were resistant to penicillin and 80.6% were resistant to erythromycin, which were higher than the percentages reported by Yen et al.[17] More interestingly, all *Staphylococcus* isolates were sensitive to nitrofurantoin, vancomycin, tigecycline and quinupristin-dalfopristin, which was comparable to the results from a study by Alebachew et al.[18] For oxacillin, *S. aureus* showed 17.6% resistance and Cons showed 77.0% resistance, representing oxacillin-resistant *S. aureus* (MRSA) and oxacillin-resistant coagulase-negative *staphylococci* (MR-CoNS). In Italy, Tumbarello et al reported a significantly higher prevalence of MRSA among patients with AIDS/HIV.[19]

Herein, 82.1% of gram-negative bacteria were resistant to ampicillin, but were mostly sensitive to imipenem (94.6%), piperacillin/tazobactam (92.9%), and cefepime (87.5%). This could have been caused by the restricted use of these antibiotics. Besides, one strain of *K. pneumoniae* was resistant to all antibiotics, which would result in great difficulties in clinical treatment. Recent Asian surveillance data showed that the overall prevalence of ESBL among *Enterobacteriaceae* is very high.[20] Herein, the prevalence of ESBL was approximately 50% among *Enterobacteriaceae*, which was in line with the reported rates of ESBL positivity in Cambodia[5], but was higher than that reported in Korea (6.7%)[21]. Although we isolated *Salmonella spp.* from only 19 specimens, we found 6 MDR isolates among them, which were resistant to 3 antimicrobials, such as ampicillin, trimethoprim-sulfamethoxazole, and nitrofurantoin. Fortunately, none of them were resistant to third-generation cephalosporins (ceftazidime, ceftriaxone) or ciprofloxacin. These results agreed with the findings of Shanson.[22]

China has a major problem with antibiotic misuse/overuse, with nearly 70% of inpatients being prescribed with antibiotics, which is double the rate expected by the WHO.[23] Herein, we studied the trend of *Staphylococcus* antimicrobial resistance and found an upward trend of resistance to various antibiotics in recent years. However, antibiotic resistance seemed to decline from 2017 to 2020, which might be related to the actions taken by the hospital, such as improvements in the application of antibiotics and the monitoring system for bacterial resistance, preventing and controlling environmental pollution by antibiotics, and preventing and controlling bacterial resistance. More rational use of antibiotics also decreased the prevalence of ESBL among *Enterobacteriaceae*.

Antibiotic susceptibility testing demonstrated that 25.0% of gram-negative isolates showed resistance to five or more antibiotics, which was significantly lower than value in Northwest Ethiopia (40.7%)[7]. There might be many reasons why the bacteria that infect patients with AIDS/HIV show high antimicrobial drug resistance. The main reasons might be inappropriate antibiotic use and lack of antimicrobial resistance surveillance system.

There were several limitations to this study. First, this was a retrospective single-center study and the sample size was relatively small; therefore, we cannot exclude potential confounders. Second, as a single center study, the findings are probably most appropriate to guide local physicians. Third, resource constraints meant that we did not determine the antimicrobial resistance profile of certain bacterial isolates, including *Mycobacterium* and *penicillium marneffei*.

5. Conclusion

In conclusion, we observed that the prevalence of bloodstream infections and bacterial antimicrobial resistance patterns in patients with AIDS/HIV were high. For gram-positive bacteria, vancomycin and linezolid represent active antibacterial agents, while imipenem, piperacillin/tazobactam, and cefepime remain effective against gram-negative bacteria. In this study, 57.3% of the isolated bacterial strains showed MDR, including resistance to trimethoprim-sulfamethoxazole, which can reduce morbidity and mortality among patients with AIDS/HIV. Consequently, it is recommended that the distribution of pathogenic bacteria, their AMR, and changes in drug resistance during bloodstream infection among patients with AIDS/HIV receive close attention, so as to guide the rational use of antibiotics and prevent the outbreak of drug-resistant strains. We recommend an additional study of other populations at the most risk of life-threatening infections by resistant bacteria, such as the elderly, neonates, and patients suffering from diabetes. Besides, in the study area, we plan to implement continuous antimicrobial susceptibility surveillance on a larger scale.

Abbreviations

AMR, Antimicrobial drug resistance; P, penicillin; OX, oxacillin; GM, gentamicin; LEV, levofloxacin; SXT, trimethoprim-sulfamethoxazole; E, erythromycin; LZD, linezolid; VA, vancomycin; TE, tetracycline; *S. aureus*, *Staphylococcus aureus*; CoNS, Coagulase-negative *staphylococci*; S, susceptible; I, intermediate; R, resistance; IMP, imipenem; TOB, tobramycin; CTT, cefotetan; CAZ, ceftazidime; CRO, ceftriaxone; FEP, cefepime; GM, gentamicin; TZP, piperacillin/tazobactam; CIP, ciprofloxacin; SXT, trimethoprim-sulfamethoxazole; F, nitrofurantoin; ETP, ertapenem; ATM, aztreonam; SAM, ampicillin/sulbactam; AMP, ampicillin; AN, amikacin; ESBL, extended-Spectrum β-Lactamases; *E.coli*, *Escherichia coli*; *K. pneumoniae*, *Klebsiella pneumoniae*; *P. Aeruginosa*, *Pseudomonas aeruginosa*; CM, clindamycin.

Declarations

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Author Contributions

Z.Y.F. designed the study and collected the data, C.J.H. contributed to manuscript writing and revised the final manuscript. Z.M.L. contributed to supervision and visualization. L.C.D., L.S.B., S.B., and Z.J.J. made a contribution to patients' selection and clinical data acquisition. All authors read and approved the final manuscript.

Data Sharing Statement

The datasets generated during and/or analysed during the current study are available from the corresponding author on reasonable request.

Disclosure

The author reports no conflicts of interest in this work.

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Tables

Table 1

Demographical characteristics of patients with HIV/AIDS with bacterial bloodstream infections

Patient Characteristics	G-positive bacteria (n = 185)	G-negative bacteria (n = 75)	Mycobacteria (n = 39)	Fungi (n = 173)	p-Value
Male sex, n (%)	136 (73.5)	52 (69.3)	32 (82.0)	155 (89.6)	NS
Age, median (IQR)	41 (33–51)	41 (32–57)	39 (30–50)	35 (28–45)	NS
$CD4^+$count (/μL), median (IQR)	50 (12–198)	51 (19–192)	9 (4–30)	15 (6–31)	P < 0.001*
$CD8^+$count (/μL), median (IQR)	458 (210–731)	336 (196–749)	241 (154–394)	249 (153–411)	P < 0.05†
$CD4^+$/CD8 ratio, median (IQR)$^+$	0.13 (0.04–0.36)	0.18 (0.06–0.46)	0.05 (0.01–0.16)	0.06 (0.03–0.1)	P < 0.001*
$CD19^+$count (/μL), median (IQR)	62 (22–135)	35 (13–117)	16 (6–36)	25 (12–69)	P < 0.05†
$CD16^+$, $CD56^+$ count (/μL), median (IQR)	81 (50–132)	77 (29–160)	59 (33–105)	44 (23–74)	P < 0.001‡

Note: *The $CD4^+$count and $CD4^+$/CD8 ratio of patients with AIDS with fungi infections and Mycobacteria infections was significantly lower than those with gram-positive (G-positive) and gram-negative (G-negative) organism infections.

†The $CD8^+$, $CD19^+$count of patients with AIDS with Mycobacteria infections was significantly lower than those with gram-positive and gram-negative organism infections.

‡The $CD16^+$, $CD56^+$ count of patients with AIDS with Mycobacteria infections was significantly lower than those with gram-positive and gram-negative organism infections.

IQR, interquartile range.

Table 2

Antibiotic resistance patterns of gram-positive bacterial isolates

Name of antibiotics	P	OX	GM	LEV	SXT	E	LZD	VA	TE
S. aureus (n = 17)									
S	0 (0)	14 (82.4)	14 (82.4)	16 (94.1)	15 (88.2)	5 (29.4)	17 (100)	17 (100)	14 (82.4)
I	0(0)	0(0)	0 (0)	0 (0)	0 (0)	0 (0)	0(0)	0(0)	0(0)
R	17 (100)	3 (17.6)	3 (17.6)	1 (5.9)	2 (11.8)	12 (70.6)	0(0)	0(0)	3 (17.6)
CoNS (n = 127)									
S	10 (7.9)	29 (23.0)	88 (69.3)	52 (40.9)	56 (44.1)	23 (18.1)	124 (99.2)	127 (100)	90 (71.4)
I	0(0)	0(0)	12 (9.4)	33 (26.0)	3 (2.4)	0 (0)	0(0)	0(0)	0(0)
R	116 (92.1)	97 (77.0)	27 (21.3)	42 (33.1)	68 (53.5)	104 (81.9)	1 (0.8)	0 (0)	36 (28.6)
Corynebacterium (n = 5)									
S	2 (40.0)	/	4 (80.0)	3 (60.0)	5 (100)	1 (25.0)	4 (100)	5 (100)	3 (75.0)
I	0(0)	/	0 (0)	1 (20.0)	0 (0)	0 (0)	0(0)	0(0)	1 (25.0)
R	3 (60.0)	/	1 (20.0)	1 (20.0)	0 (0)	3 (75.0)	0(0)	0(0)	0 (0)
Streptococcus (n = 6)									
S	2 (33.3)	/	0 (0)	4 (66.7)	2 (33.1)	2 (33.1)	4 (66.7)	5 (83.3)	3 (50.0)
I	0 (0)	/	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)
R	0(0)	/	1 (16.7)	1 (16.7)	1 (16.7)	3 (50.0)	0 (0)	0 (0)	2 (33.3)
Enterococcus (n = 6)									
S	3 (50.0)	/	3 (50.0)	3 (50.0)	/	1 (16.7)	6 (100)	6 (100)	2 (33.3)
I	0 (0)	/	0 (0)	0 (0)	/	1 (16.7)	0 (0)	0 (0)	0 (0)
R	3 (50.0)	/	1 (16.7)	1 (16.7)	/	4 (66.7)	0 (0)	0 (0)	2 (33.3)
Total (n = 161)									
S	17 (10.6)	/	109 (67.7)	78 (48.4)	78 (48.4)	32 (19.9)	155 (96.3)	161 (100)	112 (69.6)
I	0 (0)	/	12 (7.5)	34 (21.1)	3 (1.9)	1 (0.6)	0 (0)	0 (0)	1 (0.6)
R	139 (86.3)	/	33 (20.5)	46 (28.6)	71 (44.1)	126 (78.3)	1 (0.6)	0 (0)	43 (26.7)

Abbreviations: P, penicillin; OX, oxacillin; GM, gentamicin; LEV, levofloxacin; SXT, trimethoprim-sulfamethoxazole; E, erythromycin; LZD, linezolid; VA, vancomycin; TE, tetracycline; S. aureus, Staphylococcus aureus; CoNS, Coagulase-negative staphylococci; S, susceptible; I, intermediate; R, resistance

Table 3

Antibiotic resistance patterns of gram-negative bacterial isolates

Antibiotics	LEV	IMP	TOB	CTT	CAZ	CRO	FEP	GM	TZP	CIP	SXT	F	ETP	ATM	SAM
E. coli (n = 18)															
S	**9 (50.0)**	**18 (100)**	**12 (66.7)**	**17 (94.4)**	**14 (77.8)**	**12 (66.7)**	**15 (83.3)**	**12 (66.7)**	**17 (94.4)**	**10 (55.6)**	**4 (22.2)**	**17 (94.4)**	**18 (100)**	**14 (77.8)**	**3 (16.7)**
I	2 (11.1)	0 (0)	6 (33.3)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	1 (5.6)	1 (5.6)	0 (0)	1 (5.6)	0 (0)	1 (5.6)	3 (16.7)
R	7 (38.9)	0 (0)	0 (0)	1 (5.6)	4 (22.2)	6 (33.3)	3 (16.7)	6 (33.3)	0 (0)	7 (38.9)	14 (77.8)	0 (0)	0 (0)	3 (16.7)	12 (66.7)
K. pneumoniae (n = 14)															
S	9 (64.3)	12 (85.7)	10 (71.4)	12 (85.7)	8 (57.1)	8 (57.1)	10 (71.4)	11 (78.6)	12 (85.7)	9 (64.3)	7 (50.0)	7 (53.8)	11 (78.6)	7 (50.0)	7 (50.0)
I	1 (7.1)	0(0)	1 (7.1)	0 (0)	0(0)	0(0)	0(0)	0 (0)	0 (0)	0(0)	0 (0)	0 (0)	0(0)	0(0)	2(14.3)
R	4 (28.6)	2 (14.3)	3 (21.4)	2 (14.3)	6 (42.9)	6 (42.9)	4 (28.6)	3 (21.4)	2 (14.3)	5 (35.7)	7 (50.0)	6 (46.2)	3 (21.4)	7 (50.0)	5 (35.7)
Salmonella (n = 19)															
S	19 (100)	19 (100)	/	/	18 (100)	19 (100)	19 (100)	/	19 (100)	18 (94.7)	15 (78.9)	7 (36.8)	19 (100)	19 (100)	6 (31.6)
I	0 (0)	0(0)	/	/	0(0)	0(0)	0(0)	/	0(0)	1 (5.3)	0 (0)	6 (31.6)	0 (0)	0 (0)	2(10.5)
R	0(0)	0(0)	/	/	0(0)	0 (0)	0 (0)	/	0(0)	0 (0)	4 (21.1)	6 (31.6)	0 (0)	0 (0)	11 (57.9)
P. Aeruginosa (n = 5)															
S	4 (100)	4 (80.0)	4 (100)	0 (0)	4 (80.0)	0 (0)	5 (100)	5 (100)	4 (80.0)	5 (100)	0 (0)	0 (0)	/	/	0(0)
I	0(0)	0(0)	0 (0)	0 (0)	1 (20.0)	0 (0)	0 (0)	0 (0)	1 (20.0)	0(0)	0 (0)	0 (0)	/	/	0(0)
R	0(0)	1 (20.0)	0 (0)	4 (100)	0(0)	4 (100)	0 (0)	0(0)	0(0)	0 (0)	4 (100)	4 (100)	/	/	4 (100)
Total (n = 56)															
S	41 (73.2)	53 (94.6)	26 (46.4)	29 (51.8)	44 (78.6)	39 (69.6)	49 (87.5)	28 (50.0)	52 (92.9)	42 (75.0)	26 (46.4)	31 (55.4)	48 (85.7)	40 (71.4)	16 (28.6)
I	3 (5.9)	0 (0)	7 (12.5)	0 (0)	1 (1.8)	0 (0)	0 (0)	0 (0)	2(3.6)	2(3.6)	0 (0)	7 (12.5)	0 (0)	1 (1.8)	7 (12.5)
R	11 (19.6)	3 (5.4)	3 (5.4)	7 (12.5)	10 (17.9)	16 (28.6)	7 (12.5)	9 (16.1)	2 (3.6)	12 (21.4)	29 (51.8)	16 (28.6)	3 (5.4)	10 (17.9)	32 (57.1)

Abbreviation: LEV, levofloxacin; IMP, imipenem; TOB, tobramycin; CTT, cefotetan; CAZ, ceftazidime; CRO, ceftriaxone; FEP, cefepime; GM, gentamicin; TZP, pip CIP, ciprofloxacin; SXT, trimethoprim-sulfamethoxazole; F, nitrofurantoin; ETP, ertapenem; ATM, aztreonam; SAM, ampicillin/sulbactam; AMP, ampicillin; AN, a extended-Spectrum β-Lactamases; E. coli, Escherichia coli; K. pneumoniae, Klebsiella pneumoniae; P. Aeruginosa, Pseudomonas aeruginosa; S, susceptible; resistance.

Table 4
Antibiotic resistance of Staphylococcus at Xixi Hospital, Hangzhou, China, 2013–2020

Antibiotic	2013 (n = 14)	2014 (n = 16)	2015 (n = 15)	2016 (n = 21)	2017 (n = 14)	2018 (n = 22)	2019 (n = 23)	2020 (n = 19)	Total (n = 144)
CM	7 (50.0)	5 (31.3)	8 (53.3)	12 (57.1)	12 (85.7)	11 (50.0)	19 (82.6)	10 (52.6)	84 (58.3)
E	8 (57.1)	13 (81.3)	12 (80.0)	18 (85.7)	13 (92.9)	18 (81.8)	19 (82.6)	15 (78.9)	116 (80.6)
GM	2 (14.3)	3 (18.8)	3 (20. 0)	9 (42.9)	7 (50.0)	3 (13.6)	2 (8.7)	1 (5.3)	30 (20.8)
LZD	2 (14.3)	0 (0)	0 (0)	0(0)	1(7.1)	0(0)	0 (0)	0(0)	3(2.1)
OX	8 (57.1)	11 (68.8)	11 (73.3)	18 (85.7)	10 (71.4)	13 (59.1)	16 (69.6)	13 (68.4)	100 (69.4)
P	13 (92.9)	16 (100)	13 (86.7)	20 (95.2)	14 (100)	18 (81.8)	20 (87.0)	19 (100)	133 (92.4)
SXT	4 (28.6)	10 (62.5)	10 (66.7)	12 (57.1)	8 (57.1)	9 (40.9)	10 (43.5)	7 (36.8)	70 (48.6)
TE	3 (21.4)	4 (25.0)	7 (46.7)	4 (19.0)	3 (21.4)	4 (18.2)	9 (39.1)	5 (26.3)	39 (27.1)
VA	0 (0)	0 (0)	0 (0)	0(0)	0(0)	0(0)	0 (0)	0(0)	0(0)
LEV	3 (21.4)	4 (25.0)	4 (26.7)	9 (42.9)	3 (21.4)	7 (31.8)	5 (21.7)	8 (42.1)	43 (29.9)

Abbreviation: P, penicillin; OX, oxacillin; GM, gentamicin; LEV: levofloxacin; SXT: trimethoprimsulfamethoxazole; E: erythromycin; LZD: linezolid; VA: vancomycin; TE: tetracycline; CM: clindamycin.

Table 5
Multidrug-resistant patterns of the bacterial isolates among patients with HIV/AIDS at Hangzhou Xixi Hospital Affiliated to Zhejiang Chinese Medical University.

Bacterial Isolate	R0 (N%)	R1 (N%)	R2 (N%)	R3 (N%)	R4 (N%)	R5 (N%)	≥R6 (N%)	Overall MDR (%)
gram-positive								
S. aureus(n = 17)	0 (0)	4 (23.5)	8 (47.1)	4 (23.5)	1 (5.9)	0 (0)	0 (0)	5 (29.4)
CoNs (n = 127)	4 (3.1)	10 (7.9)	28 (22.0)	31 (24.4)	29 (22.8)	19 (15.0)	6 (4.7)	85 (66.9)
Corynebacterium (n = 5)	0 (0)	2 (40.0)	2 (40.0)	1 (20.0)	0 (0)	0 (0)	0 (0)	1 (20.0)
Enterococcus (n = 5)	0 (0)	0 (0)	1 (20.0)	3 (60.0)	0 (0)	1 (20.0)	0 (0)	4 (80.0)
Streptococcus (n = 5)	1 (20.0)	3 (60.0)	0 (0)	1 (20.0)	0 (0)	0 (0)	0 (0)	1 (20.0)
Total (n = 159)	5 (3.1)	19 (11.9)	39 (24.5)	40 (25.2)	30 (18.9)	20 (12.6)	6 (3.8)	96 (60.4)
gram-negative								
E. coli (n = 18)	0 (0)	2 (11.1)	2 (11.1)	5 (27.8)	4 (22.2)	4 (22.2)	1 (5.6)	14 (77.8)
K. pneumoniae (n = 14)	0 (0)	5 (35.7)	3 (21.4)	0 (0)	1 (7.1)	1 (7.1)	4 (28.6)	6 (42.9)
Salmonella (n = 19)	4 (21.1)	3 (15.8)	6 (31.6)	6 (31.6)	0 (0)	0 (0)	0 (0)	6 (31.6)
P. Aeruginosa (n = 5)	1 (20.0)	0 (0)	0 (0)	0 (0)	0 (0)	3 (60.0)	1 (20.0)	4 (80.0)
Total (n = 56)	5 (8.9)	10 (17.9)	11 (19.6)	11 (19.6)	5 (8.9)	8 (14.3)	6 (10.7)	30 (53.6)
Fungus								
Candida (n = 5)	5 (100)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)
Overall (n = 220)	15 (6.8)	29 (13.2)	50 (22.7)	51 (23.2)	35 (15.9)	28 (12.7)	12 (5.5)	126 (57.3)

Abbreviation: R0, nonresistance; R1, resistance for 1 antibiotic; R2, resistance for 2 antibiotics; R3, resistance for 3 antibiotics; R4, resistance for 4 antibiotics; R5, resistance for 5 antibiotics; R6, resistance for 6 and above; S. aureus, Staphylococcus aureus; CoNS, Coagulase-negative staphylococci; E. coli, Escherichia coli; K. pneumoniae, Klebsiella pneumoniae; P. Aeruginosa, Pseudomonas aeruginosa; MDR, multi drug resistance.

Figures

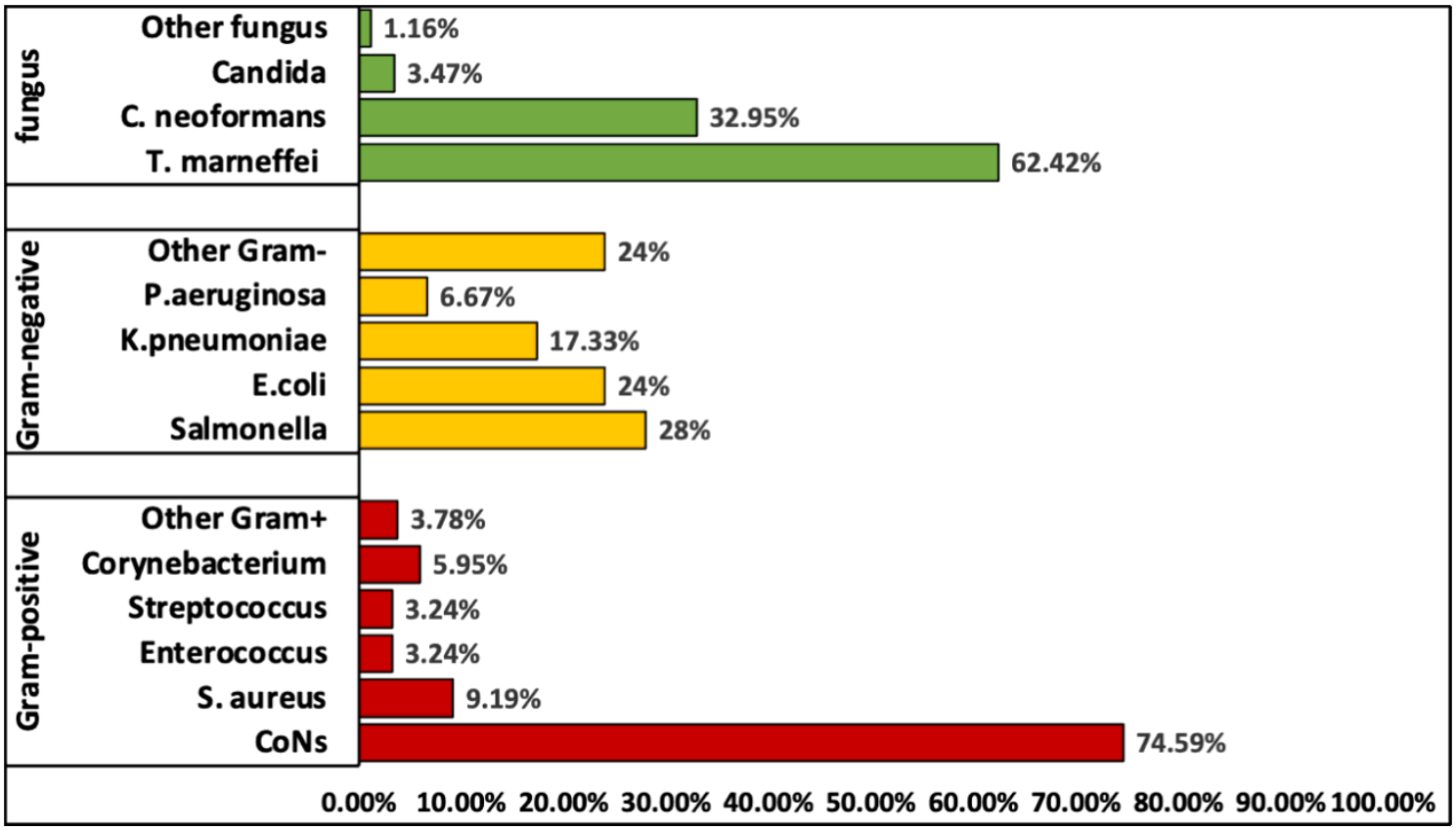

Figure 1

Bacterial isolate distributions in patients with HIV/AIDS with positive blood cultures at Hangzhou Xixi Hospital Affiliated to Zhejiang Chinese Medical University.

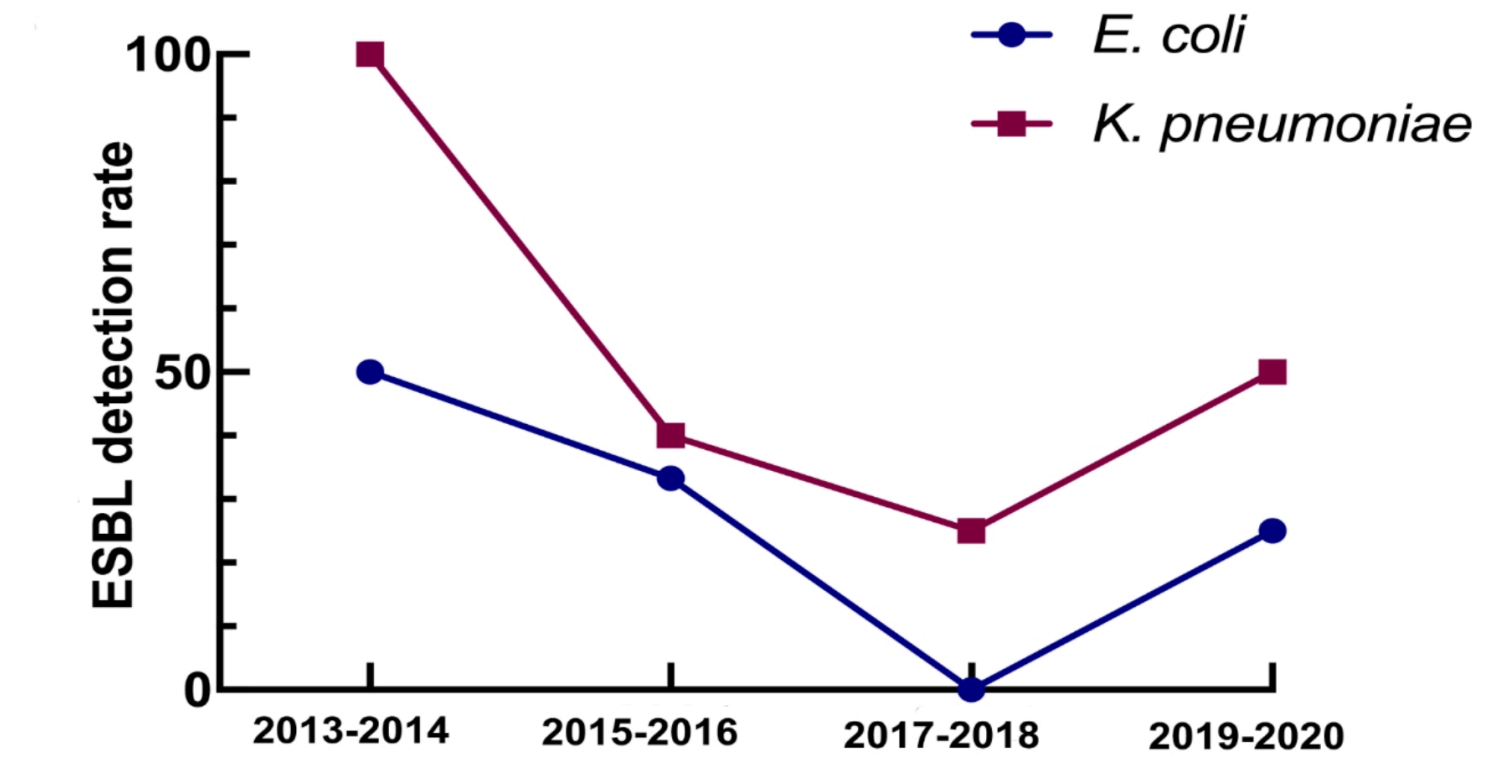

Figure 2

Change trends for the prevalence of *K. pneumoniae* and ESBL-producing *E. coli* between 2013 and 2020.