

Distribution and Drug Resistance Analysis of 2287 Strains of Pathogenic Bacteria in Children's Blood Culture

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Abstract

Background: Bloodstream infection is a serious infectious disease. In recent years, the drug resistance of pathogenic bacteria to commonly used anti-infective drugs has been widely concerned, which also makes the treatment of bloodstream infection face severe challenges. **Objective:** To explore the distribution characteristics of blood culture-positive pathogens and the resistance to antibacterial drugs, so as to provide clinicians with accurate laboratory evidence, so as to guide clinicians to rationally apply antibiotics, improve clinical treatment effects, and reduce the emergence of drug-resistant strains. **Methods:** From January 2019 to June 2022, 2287 positive blood culture specimens of patients in Guangzhou Women and Children's Medical Center were retrospectively analyzed, and the proportion of different pathogenic bacteria, the distribution of pathogenic bacteria in different departments, and the multi-drug resistance of different pathogenic bacteria were counted. **Results:** Among the 2287 blood culture positive samples, 1560 strains (68.20%) of gram-positive bacteria and 727 strains (31.80%) of gram-negative bacteria were strained. The top three departments in the distribution of pathogenic bacteria were pediatric intensive care unit (600 strains), pediatric internal medicine (514 strains), and pediatric emergency comprehensive ward (400 strains). The pathogens with high detection rates were: *Staphylococcus epidermidis* (24.09%), *Staphylococcus humans* (23.74%), *Escherichia coli* (13.21%) and *Klebsiella pneumoniae* (8.71%). The pathogens with high multi-drug resistance rates were: *Streptococcus pneumoniae* (93%), *Staphylococcus epidermidis* (83.76%), *Enterobacter cloacae* (75.61%) and *Staphylococcus humans* (62.43%). **Conclusion:** In our hospital, gram-positive bacteria were the main pathogenic bacteria in the blood culture of children patients. The children's intensive care unit was the department with the largest distri-

bution of pathogenic bacteria, and the multiple drug resistance rate of *Streptococcus pneumoniae* was the highest.

Keywords

Children, Blood Culture Pathogen, Drug Resistance

1. Introduction

Bloodstream infection refers to the invasion of various pathogenic microorganisms into the blood circulation, reproduction in the blood, production and release of toxins and other metabolites, inducing cytokine release, causing systemic infection, poisoning and systemic inflammation, and even changes in coagulation and fibrinolysis system, causing systemic multi-organ dysfunction syndrome, which is a serious systemic infectious disease [1]. With the irrational use of broad-spectrum antibiotics and the development of invasive diagnosis and treatment, the incidence of bloodstream infection is increasing. Blood culture, as the gold standard for diagnosis of bloodstream infection, can provide accurate and reliable basis for clinical diagnosis of bloodstream infection and rational use of antibiotics.

Our hospital is a tertiary A specialized hospital for women and children, receiving and treating critically ill children transported from the region and surrounding areas all year round, among which infectious diseases occupy a certain proportion. In addition, when the barrier function of the body is damaged, such as surgery, trauma, intravenous indignant needle, arteriovenous catheter, tracheal intubation, etc., it is easy to cause bloodstream infection. Timely and accurate identification of pathogenic bacteria and reasonable and effective anti-infection treatment are crucial to improve the prognosis. This study retrospectively analyzed the microflora distribution, department distribution and multi-drug resistance of 2287 children with blood culture-positive pathogens in our hospital from January 2019 to June 2022, and the results are reported as follows.

2. Data and Methods

2.1. Source of Specimen

A total of 2287 positive blood culture samples of children with bloodstream infection aged 0 months to 18 years were collected from Guangzhou Women and Children Medical Center from January 2019 to June 2020. The inclusion criteria were: 1) Complete clinical data; 2) Under the age of 18. Exclusion criteria: Repeated samples from the same child during the same hospitalization.

2.2. Identification of Bacteria

Zhuhai Deere BL-BT112 automatic blood culture instrument and VITEK2 compact automatic bacterial analysis system were used to detect pathogenic

bacteria and drug sensitivity in children's blood culture specimens. Drug sensitivity test paper was purchased from Kangtai Biotechnology Co., LTD. Blood AGAR plate, MacConkey plate, chocolate plate, Shabao's plate are purchased from Guangzhou Dejing Company.

2.3. Drug Sensitivity Test

1 - 3 mL of venous blood was collected aseptically into a blood culture bottle and sent to the laboratory. Deere BL-BT112 automatic blood culture instrument was used to culture the bacteria for 5 days. Gram stains are performed on cultures of positive specimens and microscopic results are reported to the doctor. At the same time, the bacteria liquid in the blood culture bottle of the positive specimens was transferred to the blood AGAR plate, MacConkey plate and chocolate plate. After 18 h, the VITEK2 compact automatic bacterial analysis system was used for pathogen detection and drug sensitivity detection. Multidrug-resistant bacteria refer to a type of bacteria resistant to three or more types of antibacterial drugs.

2.4. Quality Control

The quality control strains were *Escherichia coli* ATCC25922, *Staphylococcus aureus* ATCC25923, *Staphylococcus aureus* ATCC29213, *Enterococcus faecalis* ATCC29212, *Streptococcus pneumoniae* ATCC49619, and the quality control strains were provided by the Temporary Inspection Center of the Ministry of Health.

2.5. Statistical Analysis

Whonet 5.6 software was used for statistical analysis of blood cultures. SPSS 26.0 software was used for statistical analysis of data. Measurement data are expressed as (Mean \pm SD), and counting data is expressed as Numeric value and percentage (N, %).

3. Results

3.1. Distribution of Pathogenic Bacteria Detected

Among the 2287 blood-culture-positive pathogens, 1560 strains (68.20%) were gram-positive bacteria and 727 strains (31.80%) were gram-negative bacteria. The first few strains of gram-positive bacteria were *Staphylococcus epidermidis* (24.09%), Human staphylococcus (23.74%), *Staphylococcus aureus* (7.26%), and *Streptococcus pneumoniae* (4.37%). The first few strains of gram-negative bacteria are *Escherichia coli* (13.21%), *Klebsiella pneumoniae* (8.71%), *Pseudomonas aeruginosa* (3.06%), *Enterobacter cloacae* (1.79%), and *Acinetobacter baumannii* (1.79%). The specific distribution of various pathogenic bacteria is shown in **Table 1**.

3.2. Department Distribution

The departments where the positive blood culture samples were located in our

Table 1. Distribution of 2287 blood-positive pathogenic bacteria.

Pathogenic bacteria	Number	Percentage (%)
Gram-positive bacteria		
<i>Staphylococcus aureus</i>	166	7.26
<i>Enterococcus faecium</i>	44	1.92
<i>Streptococcus pneumoniae</i>	100	4.37
<i>Enterococcus faecalis</i>	84	3.67
<i>Staphylococcus epidermidis</i>	551	24.09
<i>Human staphylococcus</i>	543	23.74
Other Gram-positive bacteria (<i>Streptococcus parahaemoides</i> , <i>Streptococcus pyogenes</i> , <i>Streptococcus oral</i> , <i>Streptococcus green</i> , <i>Streptococcus haematoides</i> , <i>Streptococcus pharyngiae</i>)	72	3.15
Gram-negative bacteria		
<i>Escherichia coli</i>	302	13.21
<i>Klebsiella pneumoniae</i>	199	8.71
<i>Pseudomonas aeruginosa</i>	70	3.06
<i>Enterobacter cloacae</i>	41	1.79
<i>Acinetobacter baumannii</i>	41	1.79
Other Gram-negative bacteria (<i>Salmonella enteritidis</i> , <i>Salmonella Typhimurium</i> , <i>Enterobacter aeri-producing</i> , <i>Klebsiella aeri-producing</i> , <i>Campylobacter Escherichia coli</i> , <i>Haemophilus influenzae</i> , <i>Proteus mirabilis</i> , <i>Acinetobacter Joni</i>)	74	3.24
Total	2287	100

hospital were mainly concentrated in the pediatric intensive care unit, pediatric internal medicine and pediatric emergency comprehensive ward, accounting for 26.24%, 22.47% and 17.49% respectively. The pathogens of pediatric intensive care unit, pediatric surgery, pediatric internal medicine, and pediatric emergency comprehensive ward were mainly gram-positive bacteria, and the pathogens of neonatology and pediatric hematology and oncology were mainly gram-negative bacteria. The specific distribution of pathogenic bacteria is shown in **Table 2**.

3.3. Multiple Drug Resistance of Different Pathogens

Among gram-positive bacteria, the pathogens with high multiple drug resistance rate were *Streptococcus pneumoniae*, *Staphylococcus epidermidis* and *Staphylococcus human*, and the multiple drug resistance rates were 93%, 83.67% and 62.43%, respectively. Among Gram-negative bacteria, *Enterobacter cloacae* had high multiple drug resistance rate, and its multiple drug resistance rate was 75.61%. The multiple drug resistance of each pathogen is shown in **Table 3**.

Table 2. Distribution of 2287 blood-culture-positive pathogenic bacteria.

Department distribution	Gram-positive bacteria	Gram-negative bacteria	Total	Percentage (%)
Pediatric Intensive Care Unit	382	218	600	26.24
Pediatric Surgery	224	51	275	12.02
Pediatric Internal Medicine	435	79	514	22.47
Neonatology	105	112	217	9.49
Pediatric Hematology Oncology	132	149	281	12.29
Children's Emergency Comprehensive Ward	283	117	400	17.49

Table 3. Multiple drug resistance of 2287 blood culture positive pathogenic bacteria.

Pathogenic bacteria	Multidrug resistance	Non-multidrug-resistant	Total	Multidrug resistance rates
Gram-positive bacteria				
<i>Staphylococcus aureus</i>	66	100	166	39.76%
<i>Enterococcus faecium</i>	10	34	44	22.73%
<i>Streptococcus pneumoniae</i>	93	7	100	93%
<i>Enterococcus faecalis</i>	18	66	84	21.43%
<i>Staphylococcus epidermidis</i>	461	90	551	83.67%
<i>Human staphylococcus</i>	339	204	543	62.43%
Other Gram-positive bacteria (<i>Streptococcus parahaemoides</i> , <i>Streptococcus pyogenes</i> , <i>Streptococcus oral</i> , <i>Streptococcus green</i> , <i>Streptococcus haematoides</i> , <i>Streptococcus pharyngiae</i>)	31	41	72	43.06%
Gram-negative bacteria				
<i>Escherichia coli</i>	131	171	302	43.38%
<i>Klebsiella pneumoniae</i>	94	105	199	47.24%
<i>Pseudomonas aeruginosa</i>	15	55	70	21.43%
<i>Enterobacter cloacae</i>	31	10	41	75.61%
<i>Acinetobacter baumannii</i>	9	32	41	21.95%
Other Gram-negative bacteria (<i>Salmonella enteritidis</i> , <i>Salmonella Typhimurium</i> , <i>Enterobacter aeri-producing</i> , <i>Klebsiella aeri-producing</i> , <i>Campylobacter Escherichia coli</i> , <i>Haemophilus influenzae</i> , <i>Proteus mirabilis</i> , <i>Acinetobacter Joni</i>)	44	30	74	59.46%

4. Discussion

Bloodstream infection is a kind of blood infection caused by various pathogenic microorganisms and/or toxins invading the bloodstream, which can cause se-

rious systemic infectious diseases with high mortality. Blood culture results are the gold standard for the diagnosis of bloodstream infections. In recent years, the incidence of bloodstream infections in hospitals has also increased year by year [2] [3], especially multi-drug-resistant bacteria such as carbapenem-resistant gram-negative bacteria, which increase the treatment difficulty, high mortality and heavy patient burden [4]. Timely summary and analysis of the bacteria and drug sensitivity detected in bloodstream infection specimens can provide scientific reference for clinical experience medication.

The results of this study showed that there were 2287 blood culture-positive non-duplicate strains in Guangzhou Women's and Children's Medical Center from January 2019 to June 2022, mainly Gram-positive bacteria (1560 strains, 68.20%) and Gram-negative bacteria (727 strains, 31.80%). This is consistent with the results of relevant domestic studies [5] [6]. *Staphylococcus epidermidis* (551 strains, 24.09%) and *Staphylococcus human* (543 strains, 23.74%) accounted for the highest proportion of pathogenic bacteria distribution. Both *Staphylococcus epidermidis* and *Staphylococcus human* belong to coagulase negative staphylococcus. Coagulase negative staphylococcus is a conditional pathogen, and the immune defense function of children has not been fully developed. When the skin is damaged or there are other iatrogenic operations, it is easy to enter the blood through various ways and lead to bloodstream infection. Secondly, coagulase negative staphylococcus, mainly *Staphylococcus epidermidis*, as a normal skin bacterium, is easy to become a common contaminating bacterium in blood culture when blood samples are not thoroughly collected after skin disinfection, which is difficult for children, especially children, and also greatly increases the risk of contamination. Although coagulase negative staphylococcus is a common contaminated bacteria in blood culture, the diseases caused by it cannot be ignored. Therefore, it is very important to take effective measures to distinguish the contaminated bacteria from the pathogenic bacteria in the late clinical diagnosis and treatment. A positive result of coagulase negative staphylococcus in blood culture requires comprehensive diagnosis by clinicians combined with the patient's condition. The laboratory and clinical departments should strengthen communication and pay attention to the quality control before blood culture test. Whether coagulase negative *Staphylococcus aureus* is a contaminative bacterium with bloodstream infection needs to be comprehensively determined based on positive detection time, clinical manifestations and other laboratory examination indicators such as procalcitonin and neutrophil percentage [7].

The data in this paper showed that the departments where the blood culture positive specimens were collected were mainly concentrated in the children's intensive care unit, children's internal medicine unit and children's emergency general ward of our hospital. The children's intensive care unit was the most important ward for bloodstream infection (26.24%), which may be related to the underlying diseases and low immunity of patients and other factors. The higher proportion of positive blood culture samples in pediatric department (22.47%)

and pediatric emergency general ward (17.49%) may be related to the fact that the diseases treated in the ward were mainly infectious diseases. Statistical analysis of drug susceptibility results of different pathogens showed that the pathogens with high multiple drug resistance rate were *Streptococcus pneumoniae* (93%), *Staphylococcus epidermidis* (83.67%) and *Enterobacter cloacae* (75.61%). In 2019, the World Health Organization listed antibiotic resistance as one of the top ten problems threatening global health security. The emergence of multi-drug resistant strains is a severe clinical challenge. Timely analysis of blood culture results combined with epidemiology and genomics can effectively prevent its outbreak and achieve immediate management and control.

5. Conclusion

Bloodstream infection is a serious systemic infectious disease, the course of the disease develops rapidly, timely and accurate empirical antibacterial treatment has a great impact on the prognosis of patients. In recent years, with the wide application of antibiotics, bacterial drug resistance has become increasingly serious, and there are some differences in the drug resistance of pathogenic bacteria in different regions. Understanding the composition and drug resistance of blood culture isolates in this region can provide an important basis for rational clinical selection of antibiotics, and can reduce the mortality of severe infection and save the lives of patients.

Limitations

The current study has some limitations that should be noted. Firstly, this study was retrospective and may have selection bias, and second, the study was a single-centre study, which may have an impact on the results. Future multi-center collaborative studies are needed to more accurately evaluate blood culture results and bacterial multidrug resistance data in the region.

Conflicts of Interest

The authors declare no conflicts of interest regarding the publication of this paper.

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