Research Article

Analysis of the Distribution and Antibiotic Resistance of Pathogens Causing Infections in Hospitals from 2017 to 2019

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Background. Antibiotic resistance is a global public health problem, leading to high mortality and treatment costs. To achieve more efficient treatment protocols and better patient recovery, the distribution and drug resistance of pathogens in our hospital were investigated, allowing significant clinical guidance for the use of antimicrobials. Methods. In this retrospective study (2017–2019), 3482 positive samples were isolated from 43,981 specimens in 2017; 3750 positive specimens were isolated from 42,923 specimens in 2018; and 3839 positive pathogens were isolated from 46,341 specimens in 2019. These samples were from various parts of the patients, including the respiratory tract, urine, blood, wound secretions, bile, and puncture fluids. The distribution and antibiotic resistance of these isolated pathogens from the whole hospital were analyzed. Results. The results from pathogen isolation showed that Escherichia coli (12.8%), Staphylococcus aureus (11%), Klebsiella pneumoniae (10.8%), Pseudomonas aeruginosa (10.7%), and Acinetobacter baumannii (6.4%) represented the five main pathogenic bacteria in our hospital. Pseudomonas aeruginosa (16.2% and 17.5%) occupied the largest proportion in the central intensive care unit (central ICU) and respiratory intensive care unit (RICU), while Acinetobacter baumannii (15.4%) was the most common pathogen in the emergency intensive care unit (EICU). The resistance rate of Escherichia coli to trimethoprim and minocycline was 100%, and the sensitivity rate to ertapenem, furantoin, and amikacin was above 90%. The resistance rate of Pseudomonas aeruginosa to all antibiotics, such as piperacillin and ciprofloxacin, was under 40%. The sensitivity rate of Acinetobacter baumannii to tigecycline and minocycline was less than 30%, and the resistance rate to many drugs such as piperacillin, ceftazidime, and imipenem was above 60%. Extended-spectrum β-lactamases (ESBLs)-producing Klebsiella pneumoniae (ESBLs-KPN) and carbapenem-resistant Klebsiella pneumoniae (CRE-KPN), ESBLs-producing Escherichia coli (ESBLs-ECO) and carbapenem-resistant Escherichia coli (CRE-ECO), multidrug-resistant Acinetobacter baumannii (MDR-AB), multidrug-resistant Pseudomonas aeruginosa (MDR-PAE), and methicillin-resistant Staphylococcus aureus (MRSA) are all important multidrug-resistant bacteria found in our hospital. The resistance rate of ESBLs-producing Enterobacteriaceae to ceftazidime and ampicillin-sulbactam was above 95%. CRE Enterobacteriaceae bacteria showed the highest resistance to ampicillin-sulbactam (97.1%), and the resistance rates of MDR-AB to cefotaxime, cefepime, and aztreonam were 100%. The resistance rates of MDR-PAE to ceftazidime, imipenem, and levofloxacin were 100%, and the sensitivity rate to polymyxin B was above 98%. The resistance rate of MRSA to oxacillin was 100%, and the sensitivity rate to linezolid and vancomycin was 100%. Conclusion. The distribution of pathogenic bacteria in different hospital departments and sample sources was markedly different. Therefore, targeted prevention and control of key pathogenic bacteria in different hospital departments is necessary, and understanding both drug resistance and multiple drug resistance of the main pathogenic bacteria may provide guidance for the rational use of antibiotics in the clinic.

1. Introduction

Due to the complexity and universality of infectious diseases, antibacterial agents have been widely used in clinical practice. Since the application of antibacterial agents in clinical practice, they have saved the lives of countless patients. However, bacterial resistance caused by overuse not only has a negative impact on individual users but also on the social group as a whole. Globally, various institutes and agencies have recognized this serious public health issue.
Antibiotics are a subset of antimicrobial agents that play a key role in the inhibition of essential bacterial functions and are used widely to treat and prevent bacterial infections in humans and other animals [1]. Treatment by antibiotics is one of the main approaches used by modern medicine to combat infectious diseases [2]. Antibiotics have not only saved countless lives but also have played a pivotal role in achieving significant advances in medicine and surgery and have successfully prevented or treated infections that occur in patients [3]. However, antibiotic resistance has emerged because of their overuse and inappropriate prescribing, as well as their extensive use in agriculture [4]. A minimum of 700,000 people die from antimicrobial-resistant infections each year around the world, and drug-resistant infections are expected to kill 10 million people a year within 30 years, greatly exceeding deaths from cancer. It has also been estimated that this resistance problem will be the biggest challenge facing healthcare systems by 2050 [1]. The rapid and sustained spread of antibiotic resistance poses a growing threat to the public, animal, and environmental health worldwide. The abuse of antibiotics in clinical practice, poor public health conditions, and insufficient public awareness are the main causes cited [5].

Multidrug resistance (MDR) relates to bacteria becoming resistant to multiple classes of antibiotics and [6, 7] is now classified as follows: multidrug resistance (MDR) that is not susceptible to at least one representative from each of the three categories of selected antimicrobial compound families [7]. Extreme drug resistance (XDR) is not susceptible to at least a single representative of all but very few categories of antimicrobial compounds. Pan-drug resistance (PDR) is not susceptible to any of the tested representatives of all known antimicrobial compound families [7]. Compared with other infections, MDR infections are associated with poorer clinical outcomes, resulting in increased morbidity and mortality rates and higher healthcare costs [8]. There is concern that the emergence of pan-resistant strains (pathogens resistant to all available antibiotics) will render some infections untreatable. How to effectively slow down the emergence of multidrug-resistant bacteria and block the spread of multidrug-resistant bacteria has attracted extensive attention from the medical community, government, and society.

In this study, the isolation, culture, and identification of pathogenic microorganisms and antimicrobial sensitivity tests were carried out, the detection results for different pathogenic microorganisms were provided, and the changes to and the mechanism of drug resistance were analyzed. This study provides a theoretical basis for exploring the clinical application of antibacterial drugs and further monitoring bacterial resistance and multidrug-resistant bacteria.

2. Samples and Methods

2.1. Source of Pathogenic Samples. Pathogen samples, including sputum, mid-section urine, blood, wound secretions, chest and gastric juices, bile, and puncture fluids, were taken from hospitalized patients from 2017 to 2019. To avoid overestimating antibiotic resistance, duplicate strains obtained from the same patient were deleted from the study. The study protocol was approved by the Ethics Committee of our hospital and given that medical records and patient information were anonymously reviewed and collected in this observational study, informed consent was not needed.

In 2017, the total number of microbial culture samples submitted for inspection was 43,981, and the top five infection sites were the lower respiratory tract (271/28.65%), urinary tract (125/13.21%), upper respiratory tract (107/11.31%), eyes, ears, and oral cavities (677/7.08%), and blood (64/6.77%). Respiratory tract infection, however, has always represented the main site of infection.

In 2018, the total number of microbial culture samples submitted for inspection was 42,923, a slight decrease from last year. The respiratory tract, urine, blood, stool, and female reproductive tract samples ranked in the top five, of which the respiratory tract samples, urine specimens, and blood specimens accounted for 43.93%, 12.35%, and 9.98% of the total, respectively. Stool specimens accounted for 6.73%, and female reproductive tract specimens accounted for 6.12%, a significant increase from last year by 4% and were related to *Streptococcus agalactiae* screening in obstetrics and gynecology.

The total number of microbial culture specimens submitted for inspection in 2019 was 46,341, also representing an increase from last year. The lower respiratory tract, urine, and blood specimens ranked in the top three, accounting for 39.6%, 11.0%, and 8.8% of the total, respectively, and the female reproductive tract specimens accounted for 6.7%, an increase of 6.12% from 2018. The main reason is related to *Streptococcus agalactiae* screening in the obstetrics and gynecology department, and stool specimens accounted for 6.5% and were related to the decline in the number of intestinal outpatients in recent years.

2.2. Strain Isolation, Strain Identification, and Antimicrobial Susceptibility Testing. We isolated and identified bacteria using standard microbiological and biochemical methods. According to the clinical operation requirements of the National Clinical Inspection Operation Regulations (3rd Edition), various specimens were cultured and bacterial identification was performed using a Vitek 2 Company instrument and supporting identification cards with microbiological tubes. Extended-spectrum β-lactamases (ESBLs)-producing *Klebsiella pneumoniae* (ESBLs-KPN), ESBLs-producing *Escherichia coli* (ESBLs-ECO), carbapenem-resistant (CRE) *Klebsiella pneumoniae* (CRE-KPN), CRE *Escherichia coli* (CRE-ECO), multidrug-resistant *Acinetobacter baumannii* (MDR-AB), multidrug-resistant *Pseudomonas aeruginosa* (MDR-PAE), and methicillin-resistant *Staphylococcus aureus* (MRSA) were defined based on their resistance to all antimicrobial agents as reported previously [6].

In addition, instrument drug sensitivity cards and Kirby–Bauer agar diffusion methods were used to define antibiotic resistance. The results were interpreted according to the minimum inhibitory concentration (MIC) interpretive breakpoints recommended by the Clinical and Laboratory
2.3. Monitoring and Analysis of Multidrug-Resistant Bacteria. Our hospital microbiology laboratory uses special statistical software MDR for drug resistance analysis to conduct multidrug resistance analysis on the main pathogenic bacteria (Enterobacteriaceae, Acinetobacter baumannii, Pseudomonas aeruginosa, and Staphylococcus aureus). An interim standard definition of MDR, XDR, and PDR terms coauthored by experts from the United States, Israel, Greece, Switzerland, and Australia [6] was used to identify the drug resistance of the samples.

2.4. Statistical Analyses. Data from our study were analyzed with SPSS (version 22.0, IBM Corp., Armonk, NY) and Microsoft Excel software 2007 (Microsoft Corporation, Redmond, WA). Proportions were used to summarize categorical data as appropriate.

3. Results

3.1. Isolation of Pathogenic Bacteria. According to the results from the pathogen bacteria isolation from the three hospital departments from 2017 to 2019 (Table 1), the top five pathogenic bacteria in three years were always Escherichia coli (12.8%), Staphylococcus aureus (11%), Klebsiella pneumoniae (10.8%), Pseudomonas aeruginosa (10.7%), and Acinetobacter baumannii (6.4%), which were relatively concentrated, and accounted for 51%, 53.4%, and 50.7% of the total cases each year. The average share of Enterococcus faecalis and Enterococcus faecium was 7.1% within three years.

From 2017 to 2019, the results of pathogenic bacterial isolation in the central intensive care unit (central ICU), respiratory intensive care unit (RICU), and emergency intensive care unit (EICU) were surveyed. Within the three ICU departments, Escherichia coli, Staphylococcus aureus, Klebsiella pneumoniae, Pseudomonas aeruginosa, and Acinetobacter baumannii were always in the top eight within the three years. In central ICU, Pseudomonas aeruginosa was ranked first over three years and had the highest proportion between 15.4% and 17.3%, followed by Klebsiella pneumoniae (36/13.7%), and both showed an upward trend from

| Year | 2017 | 2018 | 2019 |
|------|------|------|------|
| Rankings | Bacteria | Number | Proportion | Bacteria | Number | Proportion | Bacteria | Number | Proportion |
| 1 | Escherichia coli | 456 | 0.131 | Escherichia coli | 497 | 0.133 | Escherichia coli | 465 | 0.121 |
| 2 | Staphylococcus aureus | 384 | 0.11 | Staphylococcus aureus | 462 | 0.123 | Staphylococcus aureus | 410 | 0.107 |
| 3 | Pseudomonas aeruginosa | 370 | 0.106 | Pseudomonas aeruginosa | 420 | 0.112 | Pseudomonas aeruginosa | 409 | 0.107 |
| 4 | Klebsiella pneumoniae | 356 | 0.102 | Klebsiella pneumoniae | 406 | 0.108 | Klebsiella pneumoniae | 382 | 0.1 |
| 5 | Acinetobacter baumannii | 212 | 0.061 | Acinetobacter baumannii | 219 | 0.058 | Acinetobacter baumannii | 282 | 0.073 |
| 6 | Enterococcus faecalis | 156 | 0.045 | Enterococcus faecalis | 176 | 0.047 | Enterococcus faecalis | 251 | 0.065 |
| 7 | Vibrio parahaemolyticus | 135 | 0.039 | Vibrio parahaemolyticus | 147 | 0.039 | Vibrio parahaemolyticus | 149 | 0.039 |
| 8 | Staphylococcus epidermidis | 129 | 0.037 | Staphylococcus epidermidis | 120 | 0.032 | Staphylococcus epidermidis | 129 | 0.034 |
| 9 | Stenotomonas maltophilia | 103 | 0.03 | Stenotomonas maltophilia | 116 | 0.031 | Stenotomonas maltophilia | 123 | 0.032 |
| 10 | Streptococcus agalactiae | 99 | 0.028 | Streptococcus agalactiae | 113 | 0.03 | Streptococcus agalactiae | 122 | 0.032 |
| 11 | Enterobacter cloacae | 92 | 0.026 | Enterobacter cloacae | 87 | 0.023 | Enterobacter cloacae | 101 | 0.026 |
| 12 | Enterococcus faecium | 92 | 0.026 | Enterococcus faecium | 84 | 0.022 | Enterococcus faecium | 69 | 0.018 |
| 13 | Corynebacterium striatum | 68 | 0.02 | Corynebacterium striatum | 68 | 0.018 | Corynebacterium striatum | 68 | 0.018 |
| 14 | Streptococcus pneumoniae | 59 | 0.017 | Streptococcus pneumoniae | 60 | 0.016 | Streptococcus pneumoniae | 64 | 0.017 |
| 15 | Proteus mirabilis | 58 | 0.017 | Proteus mirabilis | 52 | 0.014 | Proteus mirabilis | 53 | 0.014 |
| Other bacteria | Total | 714 | 0.205 | Other bacteria | Total | 723 | 0.193 | Other bacteria | Total | 762 | 0.198 |
| | | 3483 | 1 | | | 3750 | 1 | | | 3839 | 1 |

Table 1: The top 15 isolated pathogens in the three districts of the hospital in 2017, 2018, and 2019.

Standards Institute (CLSI) of 2016. The quality-control strains were Escherichia coli ATCC 25922, Pseudomonas aeruginosa ATCC 27853, Klebsiella pneumoniae ATCC 700603, Acinetobacter baumannii ATCC 19606, Staphylococcus aureus ATCC 25923, Staphylococcus epidermidis ATCC 13518, and Enterococcus faecium ATCC 29212.
2017 to 2019, Acinetobacter baumannii (24 strains) and Escherichia coli (18 strains) came in third and fourth, with a proportion of 9.5% and 6.8%, respectively. Staphylococcus aureus (17/6.5%) and Enterococcus faecalis (15/5.9%) also consistently ranked in the top eight for three years (Table 2). In RICUs, six pathogenic bacteria always ranked in the top eight. Pseudomonas aeruginosa (17/17.5%) had the largest average share over three years among the three ICU departments. The next was Klebsiella pneumoniae (14/14.8%), Escherichia coli (11/11%), Acinetobacter baumannii (7/7.7%), and Staphylococcus aureus (6/6.3%). In addition, Stenotrophomonas maltophilia (9 strains) accounted for 9.1%, and the average proportion was highest in the three ICU departments (Table 3). In EICUs, Acinetobacter baumannii (14/15.4%) had the highest average proportion from 2017 to 2019, followed by Klebsiella pneumoniae (14/14.7%), which ranked second for three consecutive years. Pseudomonas aeruginosa (13/13.7%), Escherichia coli (12/13.4%), Enterococcus faecium (8/8.1%), Staphylococcus aureus (7/7.1%), and Corynebacterium striatum (6/6.7%) are also consistently ranked in the top eight for three years and their average proportion was highest in the three ICU departments, respectively (Table 4).

3.2. Distribution of Isolated Strains from Blood, Urine, and Sputum Samples. The composition of isolates from different sources from 2017 to 2019 was analyzed, and the results are shown in Tables 5–7. From 2017 to 2019, the average proportion of Escherichia coli isolates (61/22.8%) in blood samples was the highest, showing a downward trend. At the same time, Staphylococcus epidermidis (48/18.1%) and Klebsiella pneumoniae (32/12%) occupied the second and third places in each of the three years. The mean proportion of Staphylococcus epidermidis in blood specimens was higher than that seen in urine within the three years, but it was not found in sputum specimens. The composition of blood samples in 2017 and 2019 ranked fourth and Acinetobacter baumannii accounted for about 6.7%, but Staphylococcus hominis ranked fourth in 2018, accounting for 7.5%, Staphylococcus hominis ranked fifth for the three years, accounting for 8.1%, and was unique to blood samples (Table 5).

It was found that Escherichia coli (39.7%), Enterococcus faecium (11.3%), Enterococcus faecalis (9.4%), and Klebsiella pneumoniae (9.1%) ranked in the top four pathogenic bacteria from urine sample isolates. The most predominant pathogen in the urine samples was Escherichia coli accounting for 42.2%, 39.3%, and 37.8% from 2017 to 2019. Within the three years, compared to the blood and sputum samples, Escherichia coli accounted for the highest proportion of the urine samples isolated strains. Enterococcus faecium and Enterococcus faecalis have a higher proportion in urine than in blood samples, and they were not present in samples (Table 6).

Pseudomonas aeruginosa (22.5%), Klebsiella pneumoniae (20.6%), and Acinetobacter baumannii (16.6%) were the top three in sputum sample isolated strains. Staphylococcus

### Table 2: Isolation of pathogenic bacteria in central intensive care units (central ICUs) in 2017, 2018, and 2019 years.

| Year | Bacteria Number | Proportion | Bacteria Number | Proportion | Bacteria Number | Proportion |
|------|----------------|------------|----------------|------------|----------------|------------|
| 2017 | Pseudomonas aeruginosa | 40 | 0.154 | Pseudomonas aeruginosa | 48 | 0.160 | Pseudomonas aeruginosa | 39 | 0.173 |
|      | Klebsiella pneumoniae | 32 | 0.123 | Klebsiella pneumoniae | 41 | 0.137 | Klebsiella pneumoniae | 34 | 0.150 |
|      | Acinetobacter baumannii | 26 | 0.100 | Escherichia coli | 29 | 0.097 | Acinetobacter baumannii | 25 | 0.111 |
|      | Burkholderia cepacia | 19 | 0.073 | Acinetobacter baumannii | 22 | 0.073 | Staphylococcus aureus | 19 | 0.084 |
|      | Staphylococcus aureus | 16 | 0.062 | Enterococcus faecium | 17 | 0.057 | Burkholderia cepacia | 17 | 0.075 |
|      | Escherichia coli | 14 | 0.054 | Enterococcus faecalis | 16 | 0.053 | Stenotomomas maltophilia | 15 | 0.066 |
|      | Enterococcus faecium | 14 | 0.054 | Staphylococcus aureus | 15 | 0.050 | Enterococcus faecium | 15 | 0.066 |
|      | Enterobacter cloacae | 12 | 0.046 | Enterobacter cloacae | 14 | 0.047 | Escherichia coli | 12 | 0.053 |
|      | Enterococcus faecalis | 10 | 0.038 | Staphylococcus epidermidis | 14 | 0.047 | Enterobacter cloacae | 10 | 0.044 |
|      | Staphylococcus epidermidis | 8 | 0.031 | Burkholderia cepacia | 9 | 0.030 | Staphylococcus epidermidis | 8 | 0.035 |
|      | Stenotomomas maltophilia | 8 | 0.031 | Corynebacterium striatum | 9 | 0.030 | Streplococcus pneumonias | 8 | 0.035 |
|      | Corynebacterium striatum | 8 | 0.031 | Stenotomomas maltophilia | 9 | 0.030 | Enterococcus faecalis | 8 | 0.035 |
|      | Streptococcus pneumoniae | 6 | 0.023 | Haemophilus influenzae | 7 | 0.023 | Corynebacterium striatum | 6 | 0.027 |
|      | Klebsiella aerogenes | 6 | 0.023 | Klebsiella aerogenes | 7 | 0.023 | Klebsiella aerogenes | 6 | 0.027 |
|      | Other bacteria | 41 | 0.158 | Other bacteria | 43 | 0.143 | Other bacteria | 4 | 0.018 |
|      | Total | 260 | 1.000 | Total | 300 | 1.000 | Total | 226 | 1.000 |
### Table 3: Isolation of pathogenic bacteria in respiratory intensive care units (RICUs) in 2017, 2018, and 2019.

| Bacteria             | 2017 | Proportion | Bacteria             | 2018 | Proportion | Bacteria             | 2019 | Proportion |
|----------------------|------|------------|----------------------|------|------------|----------------------|------|------------|
| *Escherichia coli*   | 18   | 0.176      | *Pseudomonas aeruginosa* | 22   | 0.204      | *Escherichia coli*   | 14   | 0.184      |
| *Pseudomonas aeruginosa* | 14   | 0.137      | *Klebsiella pneumoniae* | 17   | 0.157      | *Klebsiella pneumoniae* | 12   | 0.158      |
| *Klebsiella pneumoniae* | 13   | 0.127      | *Stenotomona malophilia* | 11   | 0.102      | *Stenotomona malophilia* | 7    | 0.092      |
| *Stenotomona malophilia* | 8    | 0.078      | *Corynebacterium striatum* | 9    | 0.083      | *Acinetobacter baumannii* | 6    | 0.079      |
| *Acinetobacter baumannii* | 8    | 0.078      | *Acinetobacter baumannii* | 8    | 0.074      | *Escherichia coli*   | 6    | 0.079      |
| *Staphylococcus aureus* | 7    | 0.069      | *Burkholderia cepacia* | 8    | 0.074      | *Staphylococcus aureus* | 5    | 0.066      |
| *Staphylococcus epidermidis* | 7    | 0.069      | *Escherichia coli*   | 8    | 0.074      | *Burkholderia cepacia* | 4    | 0.053      |
| *Enterococcus faecalis* | 6    | 0.059      | *Staphylococcus aureus* | 6    | 0.056      | *Morganella morganii* | 3    | 0.039      |
| *Proteus mirabilis*   | 4    | 0.039      | *Proteus mirabilis*   | 4    | 0.037      | *Staphylococcus epidermidis* | 3    | 0.039      |
| *Enterobacter cloacae* | 3    | 0.029      | *Enterobacter cloacae* | 2    | 0.019      | *Proteus mirabilis*   | 3    | 0.039      |
| *Streptococcus pneumoniae* | 2    | 0.020      | *Enterococcus faecalis* | 2    | 0.019      | *Staphylococcus hominis* | 2    | 0.026      |
| *Corynebacterium striatum* | 2    | 0.020      | *Enterococcus faecium* | 2    | 0.019      | *Corynebacterium striatum* | 2    | 0.026      |
| *Staphylococcus capitis* | 2    | 0.020      | *Streptococcus pneumoniae* | 2    | 0.019      | *Enterobacter cloacae* | 2    | 0.026      |
| *Enterococcus faecium* | 1    | 0.010      | *Staphylococcus capitis* | 1    | 0.009      | *Enterococcus faecalis* | 2    | 0.026      |
| *Other bacteria*      | 7    | 0.069      | *Other bacteria*      | 6    | 0.056      | *Other bacteria*      | 5    | 0.066      |
| **Total**             | 102  | 1.000      | **Total**             | 108  | 1.000      | **Total**             | 76   | 0.704      |

### Table 4: Isolation of pathogenic bacteria in emergency intensive care units (EICUs) in 2017, 2018, and 2019.

| Bacteria             | 2017 | Proportion | Bacteria             | 2018 | Proportion | Bacteria             | 2019 | Proportion |
|----------------------|------|------------|----------------------|------|------------|----------------------|------|------------|
| *Pseudomonas aeruginosa* | 15   | 0.140      | *Acinetobacter baumannii* | 19   | 0.200      | *Escherichia coli*   | 13   | 0.163      |
| *Klebsiella pneumoniae* | 13   | 0.121      | *Klebsiella pneumoniae* | 16   | 0.168      | *Klebsiella pneumoniae* | 12   | 0.150      |
| *Acinetobacter baumannii* | 12   | 0.112      | *Pseudomonas aeruginosa* | 15   | 0.158      | *Acinetobacter baumannii* | 12   | 0.150      |
| *Escherichia coli*   | 12   | 0.112      | *Escherichia coli*   | 12   | 0.126      | *Pseudomonas aeruginosa* | 9    | 0.113      |
| *Enterococcus faecium* | 10   | 0.093      | *Enterococcus faecium* | 6    | 0.063      | *Enterococcus faecium* | 7    | 0.088      |
| *Staphylococcus aureus* | 8    | 0.075      | *Staphylococcus aureus* | 6    | 0.063      | *Staphylococcus aureus* | 6    | 0.075      |
| *Corynebacterium striatum* | 8    | 0.075      | *Corynebacterium striatum* | 5    | 0.053      | *Corynebacterium striatum* | 6    | 0.075      |
| *Stenotomona malophilia* | 8    | 0.075      | *Stenotomona malophilia* | 4    | 0.042      | *Stenotomona malophilia* | 4    | 0.050      |
| *Enterococcus faecalis* | 6    | 0.056      | *Proteus mirabilis*   | 3    | 0.032      | *Enterococcus faecalis* | 2    | 0.025      |
| *Burkholderia cepacia* | 4    | 0.037      | *Burkholderia cepacia* | 2    | 0.021      | *Staphylococcus epidermidis* | 2    | 0.025      |
| *Proteus mirabilis*   | 2    | 0.019      | *Enterococcus faecalis* | 2    | 0.021      | *Proteus mirabilis*   | 2    | 0.025      |
| *Staphylococcus haemolyticus* | 1    | 0.009      | *Staphylococcus haemolyticus* | 1    | 0.011      | *Staphylococcus haemolyticus* | 1    | 0.013      |
| *Corynebacterium afermentans* | 1    | 0.009      | *Corynebacterium urealyticum* | 1    | 0.011      | *Staphylococcus capitis* | 1    | 0.013      |
| *Staphylococcus capitis* | 1    | 0.009      | *Enterobacter avium*  | 1    | 0.011      | *Saprophytic staphylococcus* | 1    | 0.013      |
| *Other bacteria*      | 6    | 0.056      | *Other bacteria*      | 2    | 0.021      | *Other bacteria*      | 0    | 0.000      |
| **Total**             | 107  | 1.000      | **Total**             | 95   | 1.000      | **Total**             | 80   | 1.000      |
aureus (8.3%) and Stenotrophomonas maltophilia (6.1%) were also common in sputum specimens and ranked fourth and fifth. Moreover, Stenotrophomonas maltophilia is a pathogen specific to sputum samples, and its proportion was increasing from 5.2% to 7.7% during 2017 to 2019 (Table 7).

3.3. Antibiotic Resistance Analysis. Combining the isolation of the pathogenic bacteria from the three hospital departments from 2017 to 2019 and the distribution of isolated strains from blood, urine and sputum specimens, it can be seen that the bacteria that are susceptible and have a high titer in each specimen were mainly *Escherichia coli*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, *Staphylococcus aureus*, and *Acinetobacter baumannii* and their antibiotic resistance was found to be unchanged.

From 2017 to 2019, *Escherichia coli* was generally resistant to trimethoprim and minocycline, with a resistance rate of up to 100% and with high sensitivity to imipenem, amikacin, ertapenem, and other drugs (Table 8). The resistance rate of *Klebsiella pneumoniae* to trimethoprim, cefuroxime, piperacillin, piperacillin-sulbactam, and

| Table 5: Composition of blood specimen isolates in 2017, 2018, and 2019 years. |
|-------------------------------------------------|-------------------------------------------------|-------------------------------------------------|
| Bacteria | Number | Proportion | Bacteria | Number | Proportion | Bacteria | Number | Proportion |
|-------------------------------------------------|-------------------------------------------------|-------------------------------------------------|
| Escherichia coli | 62 | 0.238 | Escherichia coli | 70 | 0.228 | Escherichia coli | 50 | 0.218 |
| Staphylococcus epidermidis | 45 | 0.173 | Staphylococcus epidermidis | 57 | 0.186 | Staphylococcus epidermidis | 42 | 0.183 |
| Klebsiella pneumoniae | 30 | 0.115 | Klebsiella pneumoniae | 42 | 0.137 | Klebsiella pneumoniae | 25 | 0.109 |
| Acinetobacter baumannii | 20 | 0.077 | Staphylococcus hominis | 23 | 0.075 | Acinetobacter baumannii | 13 | 0.057 |
| Pseudomonas aeruginosa | 12 | 0.046 | Staphylococcus aureus | 13 | 0.042 | Staphylococcus hominis | 11 | 0.048 |
| Staphylococcus aureus | 11 | 0.042 | Enterococcus faecalis | 12 | 0.039 | Enterococcus faecalis | 10 | 0.044 |
| Staphylococcus hominis | 10 | 0.038 | Acinetobacter baumannii | 11 | 0.036 | Staphylococcus aureus | 9 | 0.039 |
| Enterobacter cloacae | 9 | 0.035 | Pseudomonas aeruginosa | 7 | 0.023 | Staphylococcus haemolyticus | 9 | 0.039 |
| Enterococcus faecium | 8 | 0.031 | Enterobacter cloacae | 6 | 0.020 | Pseudomonas aeruginosa | 7 | 0.031 |
| Staphylococcus haemolyticus | 4 | 0.015 | Enterococcus faecalis | 4 | 0.013 | *Burkholderia cepacia* | 3 | 0.013 |
| Other bacteria | 49 | 0.188 | Other bacteria | 62 | 0.202 | Other bacteria | 50 | 0.218 |
| Total | 260 | 1.000 | Total | 307 | 1.000 | Total | 229 | 1.000 |

| Table 6: Composition of urine specimen isolates in 2017, 2018, and 2019. |
|-------------------------------------------------|-------------------------------------------------|-------------------------------------------------|
| Bacteria | Number | Proportion | Bacteria | Number | Proportion | Bacteria | Number | Proportion |
|-------------------------------------------------|-------------------------------------------------|-------------------------------------------------|
| Escherichia coli | 258 | 0.422 | Escherichia coli | 262 | 0.393 | Escherichia coli | 265 | 0.377 |
| Klebsiella pneumoniae | 75 | 0.123 | Enterococcus faecalis | 69 | 0.103 | Enterococcus faecalis | 86 | 0.123 |
| Enterococcus faecalis | 70 | 0.114 | Enterococcus faecalis | 63 | 0.094 | Enterococcus faecalis | 59 | 0.084 |
| Enterococcus faecalis | 63 | 0.103 | Klebsiella pneumoniae | 51 | 0.076 | Klebsiella pneumoniae | 51 | 0.073 |
| Pseudomonas aeruginosa | 34 | 0.056 | Pseudomonas aeruginosa | 34 | 0.051 | Pseudomonas aeruginosa | 34 | 0.048 |
| Staphylococcus epidermidis | 22 | 0.036 | Staphylococcus epidermidis | 21 | 0.031 | Staphylococcus epidermidis | 28 | 0.040 |
| Proteus mirabilis | 17 | 0.028 | Proteus mirabilis | 18 | 0.027 | Proteus mirabilis | 15 | 0.021 |
| Enterobacter cloacae | 15 | 0.025 | Streptococcus agalactiae | 16 | 0.024 | Proteus mirabilis | 15 | 0.021 |
| Streptococcus agalactiae | 14 | 0.023 | Morganella morganii | 12 | 0.018 | Acinetobacter haemolyticus | 14 | 0.020 |
| Acinetobacter haemolyticus | 11 | 0.018 | Corynebacterium glutamicum | 11 | 0.016 | Enterobacter cloacae | 12 | 0.017 |
| Other bacteria | 33 | 0.054 | Other bacteria | 110 | 0.165 | Other bacteria | 120 | 0.171 |
| Total | 612 | 1.000 | Total | 667 | 1.000 | Total | 702 | 1.000 |
ampicillin was higher than 90%. However, its resistance to cefoperazone-sulbactam, ertapenem, and amikacin was lower than 40% (Table 9). The resistance of *Pseudomonas aeruginosa* to most antibiotics such as piperacillin, ciprofloxacin, amikacin, and tobramycin was less than 30%, and resistance to polymyxin B was less than 5%, and even reached a sensitivity of 100% in 2018 and 2019 (Table 10). *Acinetobacter baumannii* had high sensitivity to tigecycline.

Table 7: Composition of sputum specimen isolates in 2017, 2018, and 2019.

| Bacteria                      | 2017     |         | Bacteria                      | 2018     |         | Bacteria                      | 2019     |         |
|-------------------------------|----------|---------|-------------------------------|----------|---------|-------------------------------|----------|---------|
|                               | Number   | Proportion |                               | Number   | Proportion |                               | Number   | Proportion |
| *Pseudomonas aeruginosa*      | 280      | 0.233    | *Klebsiella pneumoniae*       | 286      | 0.224    | *Pseudomonas aeruginosa*      | 295      | 0.220    |
| *Klebsiella pneumoniae*       | 262      | 0.218    |                               | 282      | 0.221    | *Acinetobacter baumannii*     | 247      | 0.185    |
| *Acinetobacter baumannii*     | 203      | 0.169    | *Acinetobacter baumannii*     | 183      | 0.143    | *Klebsiella pneumoniae*       | 234      | 0.175    |
| *Staphylococcus aureus*       | 100      | 0.083    | *Staphylococcus aureus*       | 110      | 0.086    | *Staphylococcus aureus*       | 108      | 0.081    |
| *Escherichia coli*            | 85       | 0.071    |                               | 71       | 0.056    | *Stenotomomas maltophilia*    | 103      | 0.077    |
| *Stenotomomas maltophilia*    | 62       | 0.052    | *Escherichia coli*            | 60       | 0.047    | *Escherichia coli*            | 59       | 0.044    |
| *Corynebacterium striatum*    | 48       | 0.040    |                               | 50       | 0.039    | *Enterobacter cloacae*        | 52       | 0.039    |
| *Enterobacter cloacae*        | 41       | 0.034    |                               | 48       | 0.038    | *Corynebacterium striatum*    | 42       | 0.031    |
| *Streptococcus pneumoniae*    | 36       | 0.030    | *Streptococcus pneumoniae*    | 33       | 0.026    |                               | 40       | 0.030    |
| *Burkholderia cepacia*        | 29       | 0.024    | *Burkholderia cepacia*        | 31       | 0.024    |                               | 30       | 0.022    |
| Other bacteria                | 54       | 0.045    | Other bacteria                | 123      | 0.096    | Other bacteria                | 128      | 0.096    |
| Total                         | 1200     | 1.000    | Total                         | 1277     | 1.000    | Total                         | 1338     | 1.000    |

Table 8: Drug resistance rates of *Escherichia coli* from 2017 to 2019.

| Escherichia coli | Drugs                          | 2017 Drug resistance rate (%) | 2018 Drug resistance rate (%) | 2019 Drug resistance rate (%) |
|------------------|--------------------------------|------------------------------|------------------------------|------------------------------|
|                  | Trimethoprim                   | 100                          | 71.3                         | 76.8                         |
|                  | Minocycline                    | 100                          | 60.4                         | Cefuroxime                    | 54.3                         |
|                  | Cefazolin                      | 90.27                        | 55.9                         | Ciprofloxacin                 | 54.1                         |
|                  | Ampicillin                     | 87.7                         | 55.2                         | Levofoxacin                   | 49.9                         |
|                  | Ceftriazone                    | 78                           | 49.5                         | Ceftriazone                   | 48.3                         |
|                  | Ciprofloxacin                  | 78                           | 39.6                         | Cotrimoxazole                 | 45.3                         |
|                  | Levofloxacin                   | 73.2                         | 36.5                         | Gentamicin                    | 34.9                         |
|                  | Ampicillin-sulbactam           | 65.9                         | 26.4                         | Cefazidime                    | 27.9                         |
|                  | Compound sulfadiazine          | 64                           | 23.3                         | Cefazidime                    | 20.3                         |
|                  | Aztreonam                      | 55.2                         | 14.3                         | Cefepime                      | 17.4                         |
|                  | Piperacillin                   | 50                           | 7.9                          | Tobramycin                    | 10.5                         |
|                  | Tobramycin                     | 49.2                         | 7                            | Fosfomycin                    | 7.0                          |
|                  | Cefepime                       | 36.4                         | 5.2                          | Tobramycin                    | 3.4                          |
|                  | Gentamicin                     | 36.3                         | Piperacillin                  | 4.6                          | Nitrofurantoin                | 2.5                          |
|                  | Cefotaxime                     | 32.4                         | Imipenem                     | 4                            | Piperacillin-tazobactam       | 2.4                          |
|                  | Ceftazidime                    | 32                           | Nitrofurantoin               | 2.9                          | Amikacin                      | 1.7                          |
|                  |                                |                              |                              |                               | Ertapenem                     | 0.7                          |
|                  |                                |                              |                              |                               | Imipenem                      | 0.6                          |
### Table 9: Drug resistance rates of *Klebsiella pneumoniae* from 2017 to 2019.

|          | 2017 Drug resistance rate (%) | 2018 Drug resistance rate (%) | 2019 Drug resistance rate (%) |
|----------|-------------------------------|--------------------------------|-------------------------------|
| **Klebsiella pneumoniae** |                               |                                |                               |
| Trimethoprim | 100                           | Ampicillin-sulbactam 71.7      | Ampicillin-sulbactam 66.7     |
| Cefuroxime | 100                           | Nitrofurantoin 34.8            | Nitrofurantoin 33.9           |
| Piperacillin | 100                           | Fosfomycin 34.1                | Cotrimoxazole 29.6            |
| Piperacillin-sulbactam | 100                      | Ceftriaxone 30                 | Aztreonam 26.7                |
| Ampicillin | 96.3                          | Cotrimoxazole 27               | Cotrimoxazole 23.8            |
| Cefazolin | 81.7                          | Levofloxacin 25.6              | Ciprofloxacin 22.2            |
| Nitrofurantoin | 78.8                        | Aztreonam 25.2                | Cefazidime 20.9               |
| Fosfomycin | 72.5                          | Ciprofloxacin 25.1             | Levofloxacin 19.9             |
| Ampicillin-sulbactam | 70.8              | Ceftazidime 23.9               | Gentamicin 18.9               |
| Ceftriaxone | 65.7                          | Gentamicin 22.7                | Cefepime 17.1                 |
| Cefepime | 53.5                          | Cefepime 22.2                 | Tobramycin 13.5               |
| Tobramycin | 52.6                          | Tobramycin 19                 | Imipenem 11.8                 |
| Aztreonam | 51.3                          | Cefoperazone-sulbactam 18.9    | Ciprofloxacin-tazobactam 11.3 |
| Compound sulfadiazine | 50.8                     | Imipenem 17.8                  | Cefoperazone-sulbactam 11.1   |
| Ceftazidime | 50                            | Ertapenem 17.3                | Ertapenem 8.8                 |
| Cefotaxime | 50                            | Piperacillin-tazobactam 17     | Amikacin 6.0                  |
| Ciprofloxacin | 49.2                         | Amikacin 12.2                 | Tigecycline 0.0               |
| Cefoperazone | 48.6                         |                                |                               |
| Levofloxacin | 47.2                         |                                |                               |
| Gentamicin | 46.1                          |                                |                               |
| Piperacillin-tazobactam | 44.3                      |                                |                               |
| Imipenem | 40.2                          |                                |                               |
| Cefoperazone-sulbactam | 32.4                      |                                |                               |

### Table 10: Drug resistance rates of *Pseudomonas aeruginosa* from 2017 to 2019.

|          | 2017 Drug resistance rate (%) | 2018 Drug resistance rate (%) | 2019 Drug resistance rate (%) |
|----------|-------------------------------|--------------------------------|-------------------------------|
| **Pseudomonas aeruginosa** |                               |                                |                               |
| Aztreonam | 37.2                          | Meropenem 22                    | Meropenem 18.4                |
| Cefepime | 34                            | Aztreonam 18.8                  | Imipenem 15.8                 |
| Imipenem | 33.5                          | Levofloxacin 18.8               | Levofloxacin 13.7             |
| Piperacillin | 29.1                         | Cefepime 18.7                  | Aztreonam 13.4                |
| Meropenem | 27.1                          | Imipenem 18.2                  | Gentamicin 12.2               |
| Gentamicin | 25.2                          | Gentamicin 15.6                | Cefepime 12.1                 |
| Piperacillin-sulbactam | 25.1                          | Ciprofloxacin 13.5             | Piperacillin 11.6             |
| Ceftazidime | 23.7                          | Piperacillin 12.8               | Cefoperazone-sulbactam 9.2    |
| Levofloxacin | 20                            | Ceftazidime 12.2                | Ciprofloxacin 8.6             |
| Ciprofloxacin | 18.4                         | Cefoperazone-sulbactam 11.1    | Tobramycin 7.7                |
| Tobramycin | 13.5                          | Tobramycin 9.9                 | Piperacillin-tazobactam 7.2   |
| Amikacin | 10                            | Amikacin 9.2                   | Cefazidime 6.8                |
| Polymyxin B | 2.5                           | Piperacillin-tazobactam 8.6    | Amikacin 3.5                  |
| Polymyxin B | 0                              |                                | Polymyxin B 0.0               |
and minocycline of less than 30%, and the resistance rate to tigecycline was zero but was greater than 60% resistant to many drugs such as piperacillin, ceftazidime, gentamicin, and imipenem (Table 11). *Staphylococcus aureus* had the highest resistance rate to penicillin, at more than 80%, and the resistance rate to erythromycin was approximately 60%. However, no strains were resistant to antibiotics such as vancomycin, teicoplanin, tigecycline, and linezolid (Table 12).

### 3.4. Multidrug Resistance Analysis

Analysis of multiple drug resistance for the main pathogenic bacteria in our hospital in 2017 is shown in Figure 1. In 2017, a total of 1181 multidrug-resistant bacterial strains of *Enterobacteriaceae* were isolated, accounting for the largest proportion of the detected multidrug-resistant strains; of which 491 strains of multidrug-resistant organisms (MDRO) accounted for 41.6%, and no XDR and PDR strains were found (Figure 1(a)). ESBLs-KPN is highly resistant to amoxicillin and ceftriaxone, with resistance rates of 100% and 99.4%, respectively, and the sensitivity to ertapenem, imipenem, and piperacillin/tazobactam was above 95% (Table 13). The resistance rate of CRE-KPN to all drugs was above 50%, among which ampicillin, cefoperazone-sulbactam, ampicillin-sulbactam, ceftazidime, and ceftriaxone were all resistant by 100%. The resistance rates to nitrofurantoin, ciprofloxacin, levofloxacin, and linezolid were all greater than 95% (Table 14) and the resistance rates of ESBLs-producing *Escherichia coli* (ESBLs-ECO) to ampicillin and ceftriaxone were over 99%, and sensitivities to drugs such as amikacin, tigecycline, and minocycline were zero but was greater than 60% resistant to many drugs such as piperacillin, ceftazidime, gentamicin, and imipenem (Table 11). *Staphylococcus aureus* had the highest resistance rate to penicillin, at more than 80%, and the resistance rate to erythromycin was approximately 60%. However, no strains were resistant to antibiotics such as vancomycin, teicoplanin, tigecycline, and linezolid (Table 12).

### Table 11: Drug resistance rates of *Acinetobacter baumannii* from 2017 to 2019.

|          | 2017 Drug resistance rate (%) | 2018 Drug resistance rate (%) | 2019 Drug resistance rate (%) |
|----------|-------------------------------|-------------------------------|-------------------------------|
| Acinetobacter baumannii |                               |                               |                               |
| Piperacillin | 73.5                          | Piperacillin | 63                          | Piperacillin | 73.2          |
| Moxifloxacin | 74.7                          | Moxifloxacin | 63.8                        | Imipenem    | 72.2          |
| Cefepime   | 73.6                          | Cefepime    | 63.7                        | Piperacillin-tazobactam | 71.2        |
| Piperacillin-tazobactam | 74.6                      | Piperacillin-tazobactam | 63.6                        | Cefepime    | 70.0          |
| Ceftazidime| 73.9                          | Ceftazidime | 63.6                        | Ceftazidime | 69.8          |
| Imipenem   | 73.1                          | Imipenem    | 62.7                        | Gentamicin  | 69.6          |
| Levofloxacin | 72.5                         | Levofloxacin | 62.6                        | Ciprofloxacin | 67.7        |
| Gentamicin | 69.7                          | Gentamicin  | 60.6                        | Levofloxacin | 61.5          |
| Amikacin   | 66.5                          | Amikacin    | 58.1                        | Tobramycin  | 55.4          |
| Tobramycin | 65.3                          | Tobramycin  | 57.2                        | Amikacin    | 42.2          |
| Cefoperazone-sulbactam  | 37.3                        | Cefoperazone-sulbactam  | 32.9                        | Minocycline | 27.3          |
| Minocycline | 25.6                          | Minocycline | 21.5                        | Tigecycline | 0.0           |
| Tigecycline | 0                             | Tigecycline  | 0                           |              |               |

### Table 12: Drug resistance rates of *Staphylococcus aureus* from 2017 to 2019.

|          | 2017 Drug resistance rate (%) | 2018 Drug resistance rate (%) | 2019 Drug resistance rate (%) |
|----------|-------------------------------|-------------------------------|-------------------------------|
| *Staphylococcus aureus* |                               |                               |                               |
| Penicillin | 91.3                          | Penicillin    | 87.6                        | Penicillin    | 89.6          |
| Erythromycin | 61.8                         | Erythromycin  | 59.8                        | Erythromycin  | 62.7          |
| Clindamycin | 58.6                          | Clindamycin   | 57.1                        | Clindamycin  | 58.4          |
| Oxacillin  | 35.2                          | Oxacillin     | 32.3                        | Oxacillin     | 36.8          |
| Tetracycline | 24.2                         | Tetracycline  | 23.2                        | Cotrimoxazole | 24.1        |
| Cotrimoxazole | 17.3                        | Cotrimoxazole | 16.3                        | Tetracycline  | 18.3          |
| Ciprofloxacin | 16.5                         | Ciprofloxacin | 15                          | Ciprofloxacin | 18.0          |
| Gentamicin | 14.8                          | Gentamicin    | 14                          | Moxifloxacin  | 15.7          |
| Moxifloxacin | 14                            | Moxifloxacin  | 13.3                        | Levofloxacin  | 14.2          |
| Levofloxacin | 13                            | Levofloxacin  | 10                          | Gentamicin   | 14.1          |
| Rifampicin | 3.5                           | Rifampicin    | 3.3                         | Rifampicin    | 3.7           |
| Nitrofurantoin | 1.2                         | Nitrofurantoin | 0.8                       | Nitrofurantoin | 0.8        |
| Linezolid  | 0                             | Linezolid     | 0                           | Linezolid    | 0.0           |
| Vancomycin | 0                             | Vancomycin    | 0                           | Vancomycin   | 0.0           |
| Teicoplanin | 0                             | Teicoplanin   | 0                           | Teicoplanin  | 0.0           |
| Tigecycline | 0                             | Tigecycline   | 0                           | Tigecycline  | 0.0           |
Table 13: Analysis of multiple drug resistance rate of ESBLs-KPN in 2017.

| Drugs                | Drug resistance rate (%) |
|----------------------|--------------------------|
| ESBLs-KPN            |                          |
| Ertapenem            | 1.8                      |
| Imipenem             | 2.8                      |
| Piperacillin-tazobactam | 8                    |
| Amikacin             | 9.7                      |
| Cefoperazone-sulbactam | 21.7                 |
| Tobramycin           | 27.8                     |
| Gentamicin           | 40.9                     |
| Fosfomycin           | 42.3                     |
| Nitrofurantoin       | 48.3                     |
| Levofoxacin          | 49.4                     |
| Cefepime             | 50                       |
| Ciprofloxacin        | 60.8                     |
| Ceftazidime          | 63.1                     |
| Aztreonam            | 73.9                     |
| Cotrimoxazole        | 80.7                     |
| Ampicillin-sulbactam | 90.3                     |
| Ceftriazone          | 99.4                     |
| Ampicillin           | 100                      |

Table 14: Analysis of multiple drug resistance rates of CRE-KPN in 2017.

| Drugs                | Drug resistance rate (%) |
|----------------------|--------------------------|
| CRE-KPN              |                          |
| Cotrimoxazole        | 52.7                     |
| Fosfomycin           | 60                       |
| Amikacin             | 72.8                     |
| Tobramycin           | 79                       |
| Gentamicin           | 82.1                     |
| Nitrofurantoin       | 96.3                     |
| Ciprofloxacin        | 98.3                     |
| Levofloxacin         | 98.3                     |
| Aztreonam            | 98.6                     |
| Cefepime             | 98.9                     |
| Piperacillin-tazobactam | 99.4                 |
| Ampicillin           | 100                      |
| Cefoperazone-sulbactam | 100                  |
| Ampicillin-sulbactam | 100                      |
| Cefazidime           | 100                      |
| Aztreonam            | 100                      |
| Ertapenem            | 100                      |
| Imipenem             | 100                      |

nitrofurantoin, and cefepime were all greater than 60%, with no strains being resistant to ertapenem, piperacillin-tazobactam, or imipenem (Table 15). A total of 263 strains of Acinetobacter were isolated, including 150 strains of MDRO, accounting for 57%, and no XDR and PDR strains were found (Figure 1(b)). The resistance rate of MDR-Acinetobacter baumannii (MDR-AB) to levofloxacin, moxifloxacin, and ampicillin was up to 100%, and the drug resistance to cotrimoxazole, amikacin, and other drugs was also more than 70% (Table 16). Of the 395 strains of Pseudomonas aeruginosa isolated, 90 strains of MDRO accounted for 22.8%, and 21 strains of XDR accounted for 5.3%. No PDR strain was found (Figure 1(c)). MDR-Pseudomonas aeruginosa (MDR-PAE) showed more than 97% resistance to ciprofloxacin, piperacillin, and amtronam, among which the resistance rate for ceftazidime, imipenem, and levofloxacin...
was 100%. While sensitivity to polymyxin B and tobramycin had a sensitivity of 98.7% (Table 17). A total of 732 strains of Staphylococcus were isolated, of which 316 were MDRO strains, accounting for 43.2%, and no XDR and PDR strains were found (Figure 1(d)). Methicillin-resistant Staphylococcus aureus (MRSA) was 100% resistant to benzacillin, 60% resistant to erythromycin, 50% resistant to ciprofloxacin, clindamycin, and tetracycline, but 100% sensitive to linezolid and vancomycin (Table 18).

In 2018, a total of 1293 strains of multidrug-resistant bacteria such as Enterobacteriaceae were isolated, of which 574 strains were isolated by MDR, accounting for 44.4%, and no XDR and PDR strains were found. A total of 270 strains of Acinetobacter were isolated, including 145 strains of MDRO, accounting for 53.7%, and no XDR and PDR strains were found (Figure 2(b)). A total of 406 strains of Pseudomonas aeruginosa were isolated, among which 107 strains of MDRO accounted for 26.4%, while 26 strains of XDR accounted for 6.4%, and no PDR strains were found (Figure 2(c)). A total of 704 strains of Staphylococcus bacteria were isolated, including 300 strains (42.6%) of MDRO, with no XDR and PDR strains being found (Figure 2(d)).

As shown in Figure 3(a), in 2019, a total of 1166 strains of Enterobacteriaceae were isolated, of which 484 strains were isolated by MDR, accounting for 41.5%, and no XDR and PDR strains were found. The high resistance of ESBLs-producing Enterobacteriaceae to ceftriaxone and amoxicillin-sulbactam was observed, both more than 95%. Its drug resistance to cephalosporin, tobramycin, and furantoin was less than 40%, among which the drug resistance rate for tigecycline, imipenem, and amikacin was less than 5% (Table 20). Carbapenem-resistant (CRE) Enterobacteriaceae bacteria showed the highest resistance to amoxicillin-sulbactam (97.1%), and the resistance rate to most drugs ranged from 70% to 90%, but they were sensitive to tigecycline and amikacin (Table 21). A total of 325 strains of Acinetobacter were isolated, of which 213 strains were isolated from MDR, accounting for 65.5%, and no XDR and PDR strains were

### Table 15: Analysis of multiple drug resistance rate of ESBLs-ECO in 2017.

| Drugs                  | Drug resistance rate (%) |
|------------------------|--------------------------|
| ESBLs-ECO              |                          |
| Ertapenem              | 0                        |
| Piperacillin-tazobactam| 0                        |
| Imipenem               | 0                        |
| ASmikacin              | 2.2                      |
| Nitrofurantoin         | 3                        |
| Cefoperazone-sulbactam | 6.4                      |
| Fosfomycin             | 12.3                     |
| Tobramycin             | 17.5                     |
| Cefepime               | 32.9                     |
| Gentamicin             | 41.1                     |
| Ceftazidime            | 43.4                     |
| Cotrimoxazole          | 53.9                     |
| Aztreonam              | 66.3                     |
| Ampicillin-sulbactam   | 66.8                     |
| Levofloxacin           | 71.6                     |
| Ciprofloxacin          | 75.8                     |
| Ampicillin             | 99.3                     |
| Ceftriaxone            | 99.5                     |

### Table 16: Analysis of multiple drug resistance rate of MDR-AB in 2017.

| Drugs                  | Drug resistance rate (%) |
|------------------------|--------------------------|
| MDR-AB                 |                          |
| Cotrimoxazole          | 74.7                     |
| Amikacin               | 78.1                     |
| Tobramycin             | 81.1                     |
| Gentamicin             | 82.2                     |
| Minocycline            | 84.3                     |
| Ampicillin             | 100                      |
| Piperacillin           | 100                      |
| Piperacillin-tazobactam| 100                      |
| Ceftazidime            | 100                      |
| Ceftriaxone            | 100                      |
| Cefotaxime             | 100                      |
| Cefepime               | 100                      |
| Aztreonam              | 100                      |

### Table 17: Analysis of multiple drug resistance rate of MDR-PAE in 2017.

| Drugs                  | Drug resistance rate (%) |
|------------------------|--------------------------|
| MDR-PAE                |                          |
| Polymyxin B            | 1.3                      |
| Tobramycin             | 19.4                     |
| Amikacin               | 46.6                     |
| Gentamicin             | 69.2                     |
| Cefoperazone-sulbactam | 81                       |
| Piperacillin-tazobactam| 93.3                     |
| Ciprofloxacin          | 97.7                     |
| Piperacillin           | 99.3                     |
| Aztreonam              | 99.3                     |
| Cefepime               | 99.7                     |
| Ceftazidime            | 100                      |
| Imipenem               | 100                      |
| Levofloxacin           | 100                      |

### Table 18: Analysis of multiple drug resistance rate of MRSA in 2017.

| Drugs                  | Drug resistance rate (%) |
|------------------------|--------------------------|
| MRSA                   |                          |
| Linezolid              | 0                        |
| Vancomycin             | 0                        |
| Nitrofurantoin         | 4.5                      |
| Cotrimoxazole          | 10                       |
| Rifampicin             | 28.9                     |
| Gentamicin             | 39.1                     |
| Levofloxacin           | 46.9                     |
| Moxifloxacin           | 48.6                     |
| Ciprofloxacin          | 51.1                     |
| Clindamycin            | 51.7                     |
| Tetracycline           | 52.5                     |
| Erythromycin           | 61.1                     |
| Oxacillin              | 100                      |

was 100%. While sensitivity to polymyxin B and tobramycin had a sensitivity of 98.7% (Table 17). A total of 732 strains of Staphylococcus were isolated, of which 316 were MDRO strains, accounting for 43.2%, and no XDR and PDR strains were found (Figure 1(d)). Methicillin-resistant Staphylococcus aureus (MRSA) was 100% resistant to benzacillin, 60% resistant to erythromycin, 50% resistant to ciprofloxacin, clindamycin, and tetracycline, but 100% sensitive to linezolid and vancomycin (Table 18).
XDR

PDR

Resistance situation Number of strains (n = 270)

Statistical bacteria: Acinetobacter

Resistance situation Number of strains (n = 704)

Statistical bacteria: Staphylococcus aureus

Resistance situation Number of strains (n = 406)

Statistical bacteria: Enterobacteriaceae bacteria

Figure 2: Analysis of multiple drug resistance for the main pathogenic bacteria in our hospital in 2018. (a) The analysis of multiple drug resistance of Enterobacteriaceae bacteria. (b) The analysis of multiple drug resistance of Acinetobacter bacteria. (c) The analysis of multiple drug resistance of Pseudomonas aeruginosa. (d) The analysis of multiple drug resistance of Staphylococcus aureus.

Table 19: Analysis of multiple drug resistance rate of MRSA in 2018.

| Drugs         | Drug resistance rate (%) |
|---------------|--------------------------|
| MRSA          |                          |
| Penicillin    | 100                      |
| Oxacillin     | 100                      |
| Erythromycin  | 74.3                     |
| Clindamycin   | 69.1                     |
| Tetracycline  | 38.4                     |
| Ciprofloxacin | 31.8                     |
| Moxifloxacin  | 30.3                     |
| Levofloxacin  | 28.3                     |
| Cotrimoxazole | 23.8                     |
| Gentamicin    | 20.5                     |
| Rifampicin    | 9.9                      |
| Nitrofurantoin| 1.3                      |
| Linezolid     | 0                        |
| Vancomycin    | 0                        |
| Teicoplanin   | 0                        |
| Tigecycline   | 0                        |

found (Figure 3(b)). A total of 409 strains of Pseudomonas aeruginosa were isolated, of which 86 strains were isolated by MDR, accounting for 21.0%, and 23 strains were isolated by XDR, accounting for 5.6%, with no PDR strain being found (Figure 3(c)). A total of 768 strains of Staphylococcus were isolated, of which 356 strains were isolated by MDRO, accounting for 46.4%, and no XDR and PDR strains were found (Figure 3(d)). Similar to 2018, MRSA showed 100% resistance to penicillin and benzacillin, and the sensitivity to tetracycline, ciprofloxacin, and other drugs was more than 60%, and no strains resistant to linezolid, vancomycin, and other four drugs were found (Table 22).

3.5. The Trend of Isolate Major Multidrug-Resistant Bacteria in Our Hospital in the Past Four Years. As shown in Figure 4, the isolation rate of MDR-AB, which remained at the top for three years, declined in 2018 but increased again in 2019. ESBLs-ranked second in the three-year average separation rate, while MDR-PAB showed a continuous downward trend, whereas MRSA was the opposite, with a continuous increase being observed and CRE also exhibited a rise.

4. Discussion

The discovery of antibiotics in the last century is considered one of the most important achievements in the history of medicine, and its use has greatly reduced morbidity and mortality associated with bacterial infections [2]. However, the evolution of new bacterial strains, as well as the excessive use and reckless consumption of antibiotics, has led to the development of antibiotic resistance. Multidrug resistance is a potential threat worldwide and is escalating at an extremely high rate [9]. Poor public health conditions, lack of awareness concerning drug-resistant bacteria among the public, high incidences of disease, ease of access, and their misuse are the major factors exacerbating the problem [5]. In the context of antibiotic resistance, due to the emergence and increased prevalence of multidrug-resistant (MDR) superbugs such as Staphylococcus aureus, Escherichia coli,
and *Klebsiella pneumoniae*, human health is being treated as a priority for the health of interdependent animals and related environments and is estimated to impose a significant health burden on the global population [10]. Therefore, we identified the clinical isolates obtained in the hospital from 2017 to 2019, carried out drug susceptibility tests and epidemiological infection analysis, obtained information about the pathogens for the whole hospital, and conducted a summary analysis, hoping to promote the rational use of antibiotics and play an active role in reducing the emergence of resistant bacteria in hospitals and controlling the spread of multidrug-resistant strains.

From 2017 to 2019, the isolation of pathogenic bacteria in the three departments of the hospital showed that the top five pathogens remained unchanged. These included *Escherichia coli*, *Staphylococcus aureus*, *Pseudomonas aeruginosa*, *Klebsiella pneumoniae*, and *Acinetobacter baumannii*, which, together with *Enterobacter faecium* as the...
most problematic clinical pathogens, were summarized as “ESKAPE” bugs by Louis Rice [11]. ESKAPEE pathogens have developed resistance mechanisms against most antibiotic treatments, including those that are the last line of defense, such as carbapenems and polymyxins [12]. According to the results of pathogen isolation in three ICU departments in the past three years, the five pathogens mentioned above always ranked among the top eight. The total number of isolates from central ICUs was always higher than that from specialized ICUs, namely RICUs and ICUs. The isolation rates of *Pseudomonas aeruginosa*, *Klebsiella pneumoniae*, and *Stenotrophomonas maltophilia* in the RICUs were the highest among the three ICU wards because they were all closely associated with lower respiratory tract infections [13]. In the last three years, the average proportion of *Pseudomonas aeruginosa* isolates was 17.5% in RICUs, similar to studies in the United States during the early years that found *P. aeruginosa* (17.0%) as a relatively common organism isolated in RICU with respiratory infections [14]. In EICUs, *Acinetobacter baumannii* occupies the highest isolation rate among the three ICU wards, and critically ill patients tend to be more susceptible to infection. Because *Acinetobacter baumannii* infection is associated with invasive surgery, the reason for hospitalization includes host factors, length of ICU stay, and prior use of broad-spectrum antibiotics [15].

The composition of isolates from different sources from 2017 to 2019 was analyzed, and we found that the isolation rate of *Staphylococcus epidermidis* was higher in blood samples than in urine samples, but no isolates were found in sputum samples. *Staphylococcus hominis* isolates were only present in blood samples, and as previously reported, these two bacteria both produce biofilms that allow them to adhere to internal medical devices and are commonly isolated from bloodstream infections [16, 17]. Among the three sources, blood, urine, and sputum, *Escherichia coli* isolates accounted for the highest proportion in urine specimens. *Enterococcus faecium* and *Enterococcus faecalis* were distributed at higher levels in urine samples than in blood samples and were absent in sputum samples. As previously reported, the above three bacteria are the main pathogenic bacteria of urinary tract infections [18, 19]. The top five frequent isolates from sputum samples are *Pseudomonas aeruginosa*, *Klebsiella pneumoniae*, *Acinetobacter baumannii*, *Staphylococcus aureus*, and *Stenotrophomonas maltophilia*, and this is similar to previous findings [13].

**Figure 4:** The trend of separation rate (%) of main multidrug-resistant strains in our hospital in recent four years.

**Table 22:** Analysis of multiple drug resistance rate of MRSA in 2019.

| Drugs             | 2016 % | 2017 % | 2018 % | 2019 % |
|-------------------|--------|--------|--------|--------|
| MRSA              | 100    |        |        |        |
| Oxacillin         | 99.2   | 10     |        |        |
| Penicillin        | 99.2   | 10     |        |        |
| Erythromycin      | 79.5   | 31.4   | 31.7   | 31.4   |
| Clindamycin       | 76.5   | 31.7   | 31.4   | 31.4   |
| Tetracycline      | 51.6   | 31.4   | 31.4   | 31.4   |
| Ciprofloxacin     | 31.5   | 26.9   | 26.9   | 26.9   |
| Moxifloxacin      | 29.5   | 26.9   | 26.9   | 26.9   |
| Levofloxacin      | 28.2   | 26.9   | 26.9   | 26.9   |
| Gentamicin        | 20.3   | 26.9   | 26.9   | 26.9   |
| Rifampicin        | 10.6   | 26.9   | 26.9   | 26.9   |
| Cotrimoxazole     | 6.1    | 26.9   | 26.9   | 26.9   |
| Nitrofurantoin    | 2.3    | 26.9   | 26.9   | 26.9   |
| Linezolid         | 0      | 26.9   | 26.9   | 26.9   |
| Vancomycin        | 0      | 26.9   | 26.9   | 26.9   |
| Teicoplanin       | 0      | 26.9   | 26.9   | 26.9   |
| Tigecycline       | 0      | 26.9   | 26.9   | 26.9   |

Regarding antibiotic resistance, *Escherichia coli* showed low resistance to most third-generation cephalosporins and aminoglycoside antibiotics, the resistance rate is between 30% and 50%, which is similar to the study conducted by Miller et al. [20]. It is highly sensitive to imipenem, nitrofurantoin, piperacillin-tazobactam, and amikacin and is recommended for clinical use. *Klebsiella pneumoniae*, also belonging to the *Enterobacteriaceae* family, exhibited low
resistance to imipenem and cefoperazone-sulbactam. Similar antibiotic resistance rates have been reported by Liu et al. [21]. In 2018-2019, its resistance rate to amikacin, piperacillin-tazobactam, ertapenem, and other antibacterial drugs was less than 20%, indicating a wide range of drug choices that can be used as a good choice for current clinical treatment. *Pseudomonas aeruginosa* showed low to moderate rates of drug resistance to commonly used anti-pseudomonal drugs and most antibiotics such as carbapenems, amikacin, cefoperazone-sulbactam, piperacillin-tazobactam, and ceftazidime, were less than 30%, similar to the results of previous studies [22]. Thus, there are many options for medication. Especially in 2018 and 2019, no strains resistant to polymyxin B were found, and therefore, it is the recommended drug for clinical treatment. The drug resistance of *Acinetobacter baumannii* is relatively serious, and the resistance rate to most antibiotics is greater than 60%. Therefore, carbapenems are not recommended for single *Acinetobacter baumannii* infections, which can easily increase the risk of multidrug resistance. *Acinetobacter baumannii* has relatively high sensitivity to cefoperazone-sulbactam, which is the first choice for empirical medication in confirmed cases of infection to improve the curative effect. *Staphylococcus aureus* is resistant to penicillin by more than 85%, so the clinical application for these target bacteria should be suspended. No resistant strains were found to linezolid, vancomycin, teicarinon, and tigecycline. Hence they represent a good choice for empirical treatment.

From 2017 to 2019, the important multidrug-resistant bacteria in our hospital included extended-spectrum β-lactamases (ESBLs)-producing *Klebsiella pneumoniae* (ESBLs-KPN) and carbapenem-resistant *Klebsiella pneumoniae* (CRE-KPN), ESBLs-producing *Escherichia coli* (ESBLs-ECO) and carbapenem-resistant *Escherichia coli* (CRE-ECO), multidrug-resistant *Acinetobacter baumannii* (MDR-AB), multidrug-resistant *Pseudomonas aeruginosa* (MDR-PAE), and methicillin-resistant *Staphylococcus aureus* (MRSAs), which were mainly detected by Chinese Antimicrobial Resistance Surveillance System. *Acinetobacter baumannii*, Enterobacteriaceae, and *Pseudomonas aeruginosa* are the common clinical carbapenem-resistant Gram-negative bacteria. Several drugs that are active against carbapenem-resistant *Acinetobacter baumannii* have been approved for clinical use or have entered late-stage clinical development, including eravacycline, cefiderocol, and plazomicin [23]. For MDR-AB, carbapenems are not recommended for empirical use, not only because of their high resistance rate, but more importantly, they further increase the risk of multidrug resistance caused by high intensity antimicrobial use. For pan-resistant *Acinetobacter baumannii*, some clinical departments have chosen tigecycline for treatment, but CLSI (American Institute of Clinical and Laboratory Standards) lacks the criteria for determining the susceptibility of *Acinetobacter baumannii* to tigecycline, and its efficacy remains to be validated.

The detection rate of multidrug-resistant bacteria in the *Enterobacteriaceae* family was the highest and was mainly concentrated on the detection of ESBLs-ECO, ESBLs-KPN, CRE-KPN, and CRE-ECO. The number of ESBLs-KPN and CRE-KPN isolates ranked first in 2017, followed by MDR-AB, and these results are in agreement with those obtained by Talaat et al. [24], who showed that the most predominant Gram-rod in the hospital were *Klebsiella pneumoniae* (28.7%) and Acinetobacter sp. (13.7%). ESBLs-producing isolates showed resistance to β-lactam antibiotics, including third-generation cephalosporins; in addition, they often exhibit resistance to other classes of drugs such as aminoglycosides, cotrimoxazole, and fluoroquinolones [25]. Tigecycline and imipenem can be used as empirical drugs for ESBL-producing bacteria. It should be emphasized that ESBLs-ECO and ESBLs-KPN have high drug resistance rates to ceftriaxone and ampicillin-sulbactam, and the risk of induced drug resistance is also very high. Therefore, the drug sensitivity test results should be referred to for selection. The detection rate of CRE bacteria in 2019 was higher than the national average in 2018, and therefore, it is necessary to reduce the overuse of carbapenem antibiotics and prevent the spread of bacteria in hospitals and regions. The resistance rate of CRE bacteria to ampicillin-sulbactam exceeded 95%, and their clinical use should be suspended. No strains sensitive to ticarcillin have been found, and they can be used as clinically recommended drugs, usually in combination with other drugs. *Enterobacteriaceae* represents a key family of carbapenem-resistant bacteria. Colistin, tigecycline, ceftazidime-avibactam, plazomicin, eravacycline, and cefiderocol can all be used for their clinical treatment [23].

The average separation rate of MDR-PAE ranks third (31.7%), with no major fluctuations in recent years. It is also a common clinical carbapenem-resistant Gram-negative bacterium. Our results showed that MDR-PAE and XDR-PAE occupy 23.4% and 5.8% of the average proportion of *Pseudomonas aeruginosa* isolates, higher than the results from other studies. In 2015, the European Centers for Disease Prevention and Control stated that MDR-PAE and XDR-PAE isolates accounted for 13.7% and 5.5% [26]. The high prevalence of resistant species in developing countries could be due to noncompliance with infection control regulations and to the lack of or an imperfect antibiotic policy. Studies [26] have shown that multiple antibiotic combinations can be used as a clinical solution for MDR-PAE and XDR-PAE infections. Previous studies [27, 28] have reported that combinations of polymyxins with these anti-pseudomonas drugs (such as imipenem, piperacillin, aztreonam, ceftazidime, or ciprofloxacin) are more effective than polymyxins alone against MDR-PAE, providing a reference for the treatment of MDR-PAE infection. Yadav et al. [29] demonstrated substantially enhanced death in vivo against an MDR-PAE clinical isolate with an optimized imipenem-plus-tobramycin combination regimen, which was an alternative to colistin therapy, especially in patients with renal insufficiency. In addition, drugs such as cefiderocol and fosfomycin are potential treatment options in the near future [26]. The available clinical solution for MDR-PAE infections requires a precise diagnostic and combination antibiotic therapy based on diagnostics. Several infections which are recurrent need additional care to stop the proliferation of MDR-PAE contaminating the surrounding environment.
MRSA is a virulent and difficult-to-treat “superbug,” and our results show that MRSA accounted for 30% to 50% of *Staphylococcus aureus* infections in hospital settings over the three-year period, which was slightly higher than the 25% to 50% reported in previous studies [30]. As previously reported [31], the infection rates of resistant *Staphylococcus*, *Pseudomonas*, *Acinetobacter*, and *Klebsiella* vary by country and region, with Asia being higher than North America and Western Europe. This may be due to the apparent wide variations in health care systems, ICU facilities, and policies for infectious disease control in the different geographical regions. Drug resistance, however, is consistent with previous research results, where MRSA is resistant to beta-lactam antibiotics [32], and the resistance to penicillin was observed to be as high as 99.2%, and clinical use of this target bacterium should be suspended. Many drugs remain active against MRSA, including glycopeptides (vancomycin and teicoplanin), linezolid, and tigecycline, to which no resistant strains have been found and are, therefore, good choices for empirical treatment. Even some newer lactams, such as ceftazolin and cefdiopropanol, can be used as treatment options for MRSA [33].

With the promotion of rational applications for antibiotics, the isolation spectrum of pathogenic bacteria and the isolation rate of multidrug-resistant strains in our hospital have also changed accordingly, mainly reflected by the fact that although the isolation and drug resistance rates of MDR-AB always ranked first. After 2016, the separation rate of MDR-AB decreased significantly, which is probably due to the implementation of the Guiding Principles of Clinical Use of Antibiotics in 2015. The prevalence of CRE *Enterobacteriaceae* bacteria has increased in recent years, which is consistent with the national drug resistance monitoring information. The isolation rates of other bacteria did not fluctuate greatly, but the epidemiology of these bacteria still needs to be addressed.

The emergence of multidrug-resistant bacteria, or superbugs, poses a serious threat to public health and requires multilevel efforts to prevent them from overcoming antibiotic resistance. Governments must allocate sufficient funds to improve and develop new drug products, monitor the use of antibiotics, and establish strict policies and regulations. In addition, infection control measures must be strictly implemented in hospitals, but management practices must be considered for the use of antibiotics and microbicides and appropriate disposal or discharge of medical waste. Clinicians should avoid prescribing unnecessary and excessive antibiotics to patients with normal infections and advise patients to follow good hygiene practices such as hand washing and appropriate infection control measures. As an individual, we can take antibiotics that are prescribed only by our doctors, take them exactly as prescribed, and use them sensibly. Efforts to address the spread of antibiotic resistance include limiting the overuse of antibiotics in the food and animal sectors.

Nonantibiotic strategies for the treatment of antibiotic-resistant pathogens have been reported, such as gene editing techniques, immunotherapies, and vaccines, and antivirulence inhibitor bacteriophages [5, 10]. Antimicrobial adjuvants, fecal microbiota transplant (FMT), and competitive exclusion of pathogens through genetically modified probiotics and postbiotics are prospective alternative, unconventional strategies [5]. In addition, epidemiological and surveillance studies should be carried out and powerful tools should be used to deepen our understanding of antibiotic resistance and provide a timely and precise diagnosis of antibiotic use and consumption. Therefore, a multidisciplinary approach is needed to eliminate the serious threat of multidrug resistance.

However, this study also has some limitations. When analyzing multiple drug resistance, multiple bacteria in the same family and genus were not studied separately. In the future, a specific analysis should be carried out for important multidrug-resistant pathogens.

### 5. Conclusion

The distribution of pathogenic bacteria in different hospital departments and sample sources is variable. Therefore, targeted prevention and control of key pathogenic bacteria in different hospital departments must be carried out. Understanding the drug resistance and multiple drug resistance of the main pathogenic bacteria can provide guidance for the rational use of antibiotics in clinic.

### Data Availability

The data used to support the findings of this study are available from the corresponding author upon request.

### Ethical Approval

The study protocol was approved by the ethics committee of our hospital.

### Conflicts of Interest

The authors declare that there are no conflicts of interest.

### References

[1] N. A. Lerminiaux and A. D. S. Cameron, “Horizontal transfer of antibiotic resistance genes in clinical environments,” Canadian Journal of Microbiology, vol. 65, no. 1, pp. 34–44, 2019.

[2] B. Aslam, W. Wang, M. I. Arshad et al., “Antibiotic resistance: a rundown of a global crisis,” Infection and Drug Resistance, vol. 11, pp. 1645–1658, 2018.

[3] C. L. Ventola, “The antibiotic resistance crisis: part 1: causes and threats,” *P and T: A Peer-Reviewed Journal for Formulary Management*, vol. 40, no. 4, pp. 277–283, 2015.

[4] A. Mann, K. Nehra, J. S. Rana, and T. Dahiya, “Antibiotic resistance in agriculture: perspectives on upcoming strategies to overcome upsurge in resistance,” *Current research in microbial sciences*, vol. 2, Article ID 100030, 2021.

[5] M. Kumar, D. K. Sarma, S. Shubham et al., “Futuristic non-antibiotic therapies to combat antibiotic resistance: a review,” *Frontiers in Microbiology*, vol. 12, Article ID 609459, 2021.

[6] A. P. Magiorakos, A. Srinivasan, R. B. Carey et al., “Multidrug-resistant, extensively drug-resistant and pandrug-resistant bacteria: an international expert proposal for interim standard
definitions for acquired resistance,” Clinical Microbiology and Infections, vol. 18, no. 3, pp. 268–281, 2012.

[7] M. E. El Zowalaty, A. A. Al Thani, T. J. Webster et al., “Pseudomonas aeruginosa: arsenal of resistance mechanisms, decades of changing resistance profiles, and future antimicrobial therapies,” Future Microbiology, vol. 10, no. 10, pp. 1663–1706, 2015.

[8] H. H. Chang, T. Cohen, Y. H. Grad, W. P. Hanage, T. F. O’Brien, and M. Lipsitch, “Origin and proliferation of multiple-drug resistance in bacterial pathogens,” Microbiology and Molecular Biology Reviews, vol. 79, no. 1, pp. 101–115, 2015.

[9] M. Saha and A. Sarkar, “Review on multiple facets of drug resistance: a rising challenge in the 21st century,” Journal of Xenobiotics, vol. 11, no. 4, pp. 197–214, 2021.

[10] B. Aslam, M. Khurshid, M. I. Arshad et al., “Antibiotic resistance: one health one world outlook,” Frontiers in Cellular and Infection Microbiology, vol. 11, Article ID 771510, 2021.

[11] L. B. Rice, “Federal funding for the study of antimicrobial resistance in nosocomial pathogens: no ESKAPE,” Journal of Infectious Diseases, vol. 197, no. 8, pp. 1079–1081, 2008.

[12] Y. K. Schneider, “Bacterial natural product drug discovery for new antibiotics: strategies for tackling the problem of antibiotic resistance by efficient bioprospecting,” Antibiotics, vol. 10, no. 7, p. 842, 2021.

[13] N. Duan, J. Du, C. Huang, and H. Li, “Microbial distribution and antibiotic susceptibility of lower respiratory tract infections patients from pediatric ward, adult respiratory ward, and respiratory intensive care unit,” Frontiers in Microbiology, vol. 11, p. 1480, 2020.

[14] S. K. Fridkin, “Increasing prevalence of antimicrobial resistance in intensive care units,” Critical Care Medicine, vol. 29, pp. N64–N68, 2001.

[15] M. F. Lin and C. Y. Lan, “Antimicrobial resistance in Acinetobacter baumannii: from bench to bedside,” World Journal of Clinical Cases, vol. 2, no. 12, pp. 787–814, 2014.

[16] S. Mendoza-Olazaran, R. Morfin-Otero, L. Villarreal-Trevino et al., “Antibiotic susceptibility of biofilm cells and molecular characterisation of Staphylococcus hominis isolates from blood,” PLoS One, vol. 10, no. 12, Article ID e0144684, 2015.

[17] L. E. Cole, J. Zhang, A. Kesselly et al., “Limitations of murine models for assessment of antibody-mediated therapies or vaccine candidates against Staphylococcus epidermidis bloodstream infection,” Infection and Immunity, vol. 84, no. 4, pp. 1143–1149, 2016.

[18] S. S. Magill, J. R. Edwards, W. Bamberg et al., “Multistate point-prevalence survey of health care-associated infections,” New England Journal of Medicine, vol. 370, no. 13, pp. 1198–1208, 2014.

[19] K. A. Kline and A. L. Lewis, “Gram-positive uropathogens, polymicrobial urinary tract infection, and the emerging microbiota of the urinary tract,” Microbiology Spectrum, vol. 4, no. 2, 2016.

[20] E. A. Miller, T. J. Johnson, G. Omondi et al., “Assessing transmission of antimicrobial-resistant Escherichia coli in wild giraffe contact networks,” Applied and Environmental Microbiology, vol. 85, no. 1, Article ID e02136-18, 2019.

[21] C. Liu, E. J. Yoon, D. Kim et al., “Antimicrobial resistance in South Korea: a report from the Korean global antimicrobial resistance surveillance system (Kor-GLASS) for 2017,” Journal of Infection and Chemotherapy, vol. 25, no. 11, pp. 845–859, 2019.

[22] M. A. Khan and A. Faiz, “Antimicrobial resistance patterns of Pseudomonas aeruginosa in tertiary care hospitals of Makkah and Jeddah,” Annals of Saudi Medicine, vol. 36, no. 1, pp. 23–28, 2016.

[23] Y. Doi, “Treatment options for carbapenem-resistant gram-negative bacterial infections,” Clinical Infectious Diseases, vol. 69, pp. S565–S575, 2019.

[24] M. Talaat, M. El-Shokry, J. El-Kholy et al., “National surveillance of health care-associated infections in Egypt: developing a sustainable program in a resource-limited country,” American Journal of Infection Control, vol. 44, no. 11, pp. 1296–1301, 2016.

[25] S. V. Gajul, S. T. Mohite, S. S. Mangalali, S. M. Wavare, and S. V. Kakade, “Klebsiella pneumoniae in septicemic neonates with special reference to extended spectrum beta-lactamase, AmpC, metallo beta-lactamase production and multiple drug resistance in tertiary care hospital,” Journal of Laboratory Physicians, vol. 7, pp. 032–037, 2015.

[26] J. P. Horcajada, M. Montero, A. Oliver et al., “Epidemiology and treatment of multidrug-resistant and extensively drug-resistant Pseudomonas aeruginosa infections,” Clinical Microbiology Reviews, vol. 32, no. 4, Article ID e00313-19, 2019.

[27] S. I. Ahmad, “Treatment of post-burns bacterial infections by bacteriophages, specifically ubiquitous Pseudomonas spp. notoriusly resistant to antibiotics,” Medical Hypotheses, vol. 58, no. 4, pp. 327–331, 2002.

[28] P. Pachori, R. Gothalwal, and P. Gandhi, “Emergence of antibiotic resistance Pseudomonas aeruginosa in intensive care unit; a critical review,” Genes & Diseases, vol. 6, no. 2, pp. 109–119, 2019.

[29] R. Yadav, J. B. Bulitta, J. Wang, R. L. Nation, and C. B. Landersdorfer, “Evaluation of pharmacokinetic/pharmacodynamic model-based optimized combination regimens against multidrug-resistant Pseudomonas aeruginosa in a murine thigh infection model by using humanized dosing schemes,” Antimicrobial Agents and Chemotherapy, vol. 61, no. 12, Article ID e01268-17, 2017.

[30] D. J. Diekema, M. A. Pfaller, F. J. Schmitz et al., “Survey of infections due to Staphylococcus species: frequency of occurrence and antimicrobial susceptibility of isolates collected in the United States, Canada, Latin America, Europe, and the Western Pacific region for the SENTRY Antimicrobial Surveillance Program, 1997-1999,” Clinical Infectious Diseases, vol. 32, 2001.

[31] J. L. Vincent, J. Rello, J. Marshall et al., “International study of the prevalence and outcomes of infection in intensive care units,” JAMA, vol. 302, no. 21, pp. 2323–2329, 2009.

[32] S. Lakhundi and K. Zhang, “Methicillin-resistant Staphylococcus aureus: molecular characterization, evolution, and epidemiology,” Clinical Microbiology Reviews, vol. 31, no. 4, Article ID e00020-18, 2018.

[33] G. M. Rossolini, F. Arena, P. Pecile, and S. Pollini, “Update on the antibiotic resistance crisis,” Current Opinion in Pharmacology, vol. 18, pp. 56–60, 2014.