Journal of Clinical and Nursing Research, 2022, Volume 6, Issue 6
http://ojs.bbwpublisher.com/index.php/JCNR
ISSN Online: 2208-3693
ISSN Print: 2208-3685

Analysis on Distribution and Drug Resistance of Pathogenic Bacteria in ICU Patients with Nosocomial Infection from 2019 to 2021

Yamei Wang, Xinwen Zhang*

Affiliated Hospital of Hebei University, Baoding 071000, Hebei Province, China

***Corresponding author:** Xinwen Zhang, 83096418@qq.com

Abstract: *Objective:* To understand the pathogenic bacteria isolated from patients and their drug resistance changes in general ICU of the Affiliated Hospital of Hebei University, so as to provide reference for appropriate selection of antibiotics in clinical practice. *Methods:* A retrospective investigation was conducted to analyze the bacteriological distribution and drug resistance of nosocomial pathogens isolated from the specimens of hospitalized patients in the comprehensive ICU of the hospital from 2019 to 2021. The US technology BD Phoenix 100 automatic bacterial identification analyzer was used for bacterial identification of the pathogen samples, disk diffusion method was used for drug susceptibility test, and SPSS 22.0 software was used to analyze the trend of drug resistance. *Results:* A total of 970 strains of nosocomial pathogens were detected in the three years. The main pathogens were *Acinetobacter baumannii* (133 strains, 13.71%), *Klebsiella pneumoniae* (106 strains, 10.93%), *Pseudomonas aeruginosa* (83 strains, 8.56%), *Escherichia coli* (76 strains, 7.84%) and *Enterococcus faecium* (69 strains, 7.11%). The resistance rate of *Acinetobacter baumannii* to antibiotics was high. *Klebsiella pneumoniae*, *Pseudomonas aeruginosa* and *Escherichia coli* had low resistance rates to carbapenems. The situation of bacterial drug resistance is still serious. *Conclusion:* The drug resistance of pathogenic bacteria collected from Class III Grade A Hospital's patients to antibiotics was generally high. Therefore, clinical departments should strengthen the inspection of specimens of infection and drug sensitivity test in order to grasp the resistance mechanisms and drug resistance of pathogenic bacteria changes, and select appropriate antimicrobial agents according to the test results. Besides, the formation of drug-resistant strains also needs to be prevented, and the treatment of patients with severe infection needs to be improved.

Keywords: Intensive care unit; Hospital infection; Pathogenic bacteria; Distribution; Drug resistance

Online publication: November 30, 2022

1. Introduction

Patients admitted to intensive care unit (ICU) are critically ill and need careful monitoring and precise treatment [1]. Due to more invasive operations, complex underlying diseases, low immune function, and long-term bed rest, patients admitted to ICU are prone to nosocomial infection [2]. The main part of hospital infection in ICU patients is lower respiratory tract infection, followed by urinary tract infection, and abdominal and pelvic tissue infection. The main pathogens of hospital infection are *Acinetobacter baumannii*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, *Escherichia coli*, *Candida albicans*, *Enterococcus faecium*, *Stenotrophomonas maltophilia*, *Staphylococcus aureus*, and many more [3-9]. The excessive application of antimicrobial agents in recent years has resulted in high bacterial resistance, which poses great difficulties to clinical treatment. The study of the distribution and drug resistance of pathogenic

bacteria in patients with nosocomial infection in intensive care unit is crucial for the selection of antibiotics for patients [10]. In this study, the distribution of pathogenic bacteria and drug-resistant bacteria in ICU patients with nosocomial infection from 2019 to 2021 in the Department of Intensive Care Medicine of the Affiliated Hospital of Hebei University were analyzed as follows.

2. Materials and methods

2.1. Clinical data

Among 1963 ICU patients admitted from January 2019 to December 2021, there were 1198 males and 765 females, and 475 cases of nosocomial infection.

2.2. Source of strain

From January 2019 to December 2021, the bacterial strains detected in all clinical specimens (blood, urine, sputum, feces, wound secretions, drainage fluid, and so on) cultured from patients with nosocomial infection, excluding the same bacteria repeatedly isolated from the same part of the same patient.

2.3. Detection methods

Specimen collection: In this study, disposable sterile sputum collectors or fiberoptic bronchoscopes were used to collect sputum samples from patients. Nursing staff extracted respiratory secretions from the patient under an artificial airway or endotracheal intubation or tracheotomy. When a fiberoptic bronchoscope was used, the patient's deep sputum could be directly extracted. When a indwelling catheter was used to collect the urine specimen, the catheter was temporarily closed for 30 min and sterilized. After that, the catheter was directly connected with a sterile syringe and the corresponding urine specimen was extracted. 3-5 ml of blood specimen was collected from the patient's central vein or peripheral vein, which is directly drawn by the nursing staff through a needle and injected into the blood culture bottle. During the collection of surgical incision secretions, nurses should strictly disinfect the skin at the incision of patients, and then perform small incision puncture again and extract the corresponding secretions from the incision. In cases where pleural and abdominal effusion samples are needed, the nursing staff will directly perform pleural and abdominal puncture under sterile conditions to complete sample extraction and retention. The bacterial strains secreted from the tip of the venous catheter were directly obtained by placing them in bacterial culture bottles. Strain testing: Bacterial isolation and culture in accordance to the requirements of the National Clinical Laboratory Practice (3rd edition) [11]; BD PhoenixTM100 automatic bacterial identification analyzer was used for cell identification; the susceptibility test was performed by disk agar diffusion method (Kirby-Bauer method), which was provided by Oxoid (UK), and the results were determined according to Clinical & Laboratory Standards Institute (CLSI) 2013 standards. The quality control strains were *Staphylococcus aureus* ATCC 29213, *Escherichia coli* ATCC 25922 and *Pseudomonas aeruginosa* ATCC 27853, and the standard strains were purchased from the Clinical Inspection Center of the National Health Commission.

2.4. Statistical methods

SPSS 22.0 software was used for data analysis, and the rates were compared by using the χ^2 test. $P \leq 0.05$ was considered statistically significant.

3. Results

3.1. Pathogen distribution

A total of 970 pathogenic strains were isolated, and the top 5 bacteria (excluding fungi) were *Acinetobacter baumannii* (133 strains, 13.71%), *Klebsiella pneumoniae* (106 strains, 10.93%), *Escherichia coli* (76 strains,

7.84%), *Pseudomonas aeruginosa* (83 strains, 8.56%), and *Enterococcus faecalis* (69 strains, 7.11%). Among them, there were 599 gram-negative bacilli, accounting for 61.75%; there were 204 gram-positive bacteria, accounting for 21.03%; and there were 167 fungal strains, accounting for 17.22%, as shown **Table 1**.

Table 1. Pathogenic bacteria distribution component ratio of ICU patients with nosocomial infection (%)

Type of pathogen	Number of strains (n)	Constituent ratio (%)
Gram-negative bacteria	599	61.75
Acinetobacter baumann	133	13.71
Klebsiella pneumoniae	106	10.93
Pseudomonas aeruginosa	83	8.56
Escherichia coli	76	7.84
Stenotrophomonas maltophilia	60	6.19
Dung enterococcus	21	2.16
Burkholderia cepacia	19	3.17
Others	51	8.51
Gram-positive bacteria	204	21.03
Excrement enterococcus	69	7.11
Staphylococcus aureus	31	3.20
Corynebacterium striatum	33	3.40
Dung enterococcus	21	2.16
Others	50	5.15
Fungus	167	17.22
Total	970	100.00

3.2. Nosocomial infection rate and site of infection

There were 475 cases of nosocomial infection among 1963 patients, the incidence of nosocomial infection was 24.20%, including 705 nosocomial infection sites. The top five hospital infection sites were as follows: 455 cases of lower respiratory tract infection, accounting for 64.54%; 66 cases of urinary tract infection, accounting for 9.36%; 56 cases of abdominopelvic tissue infection, accounting for 7.94%; 23 cases of ventilator-associated pneumonia, accounting for 3.26%; and 18 cases of sepsis, accounting for 2.55%, as shown in **Table 2**. The top three sources of hospital-acquired specimens were 565 strains from sputum, accounting for 58.98%; 147 strains from drainage fluid, accounting for 15.34%; and 79 strains from blood, accounting for 8.25%.

Table 2. Proportion of nosocomial infection sites in ICU patients (%)

Infection site	Number of infections	Composition ratio (%)
Lower respiratory tract infection	455	64.54
Urinary tract infection	66	14.51
Abdominal and pelvic tissue infection	56	12.31
Ventilator-associated infections	23	5.05
Sepsis	18	3.96
Blood vessel related	16	2.27
The urine tube related	12	1.70
Bacteremia	9	1.28
Soft tissue infection	7	0.99
Pleural cavity	6	0.85
Ascites	6	0.85
Other parts	6	0.85
Gastrointestinal tract infection	5	0.71
Superficial incision	4	0.57
Meningitis, ventriculitis	3	0.43
Organ lacuna	3	0.43
Upper respiratory tract infection (URTI)	2	0.28
Skin infections	2	0.28
Site of infection	2	0.28
Antibiotics associated diarrhea	2	0.28
Intracranial abscess	1	0.14
Genital tract infection	1	0.14
Oral infections	1	0.14
Total	705	100.00

Table 3. Type distribution and composition ratio of nosocomial infection specimens in ICU patients (%)

Specimen source	Number of strains (n)	Composition ratio (%)
Sputum	565	58.98
Drainage of fluid	147	15.34
Blood	79	13.98
Urine	70	7.31
Secretions	28	2.92
Ascites	22	2.30
Abdominal cavity drainage fluid	14	1.46
Catheter	7	0.73
Exudate	5	0.52
Pleural effusion	5	0.52
Bile	3	0.31
Cerebrospinal fluid	2	0.21
Puncture fluid	2	0.21
Pus	2	0.21

(Continued on next page)

(Continued from previous page)

Specimen source	Number of strains (n)	Composition ratio (%)
Dianeal	1	0.10
Effusion	1	0.10
Faeces	1	0.10
Others	3	0.31
Total	958	100.00

3.3. Resistance of major gram-negative bacteria to commonly used antibiotics

The drug susceptibility results showed that the resistance rates of the three major gram-negative bacteria to cefuroxime, cefazolin and ampicillin were high. Besides, the resistance rate of *Acinetobacter baumannii* to cefuroxime, cefazolin, cefotetan, aztreonam, ampicillin, amoxicillin and clavulanic acid was high. The resistance rate of *Klebsiella pneumoniae* to cefazolin, cefuroxime and ampicillin was high. Moreover, the resistance rate of *Pseudomonas aeruginosa* to amoxicillin clavulanic acid, compound sulfamethoxazole, cefuroxime, cefazolin, ampicillin, ampicillin sulbactam and ceftriaxone was high, as shown in **Table 4**.

Table 4. Resistance of major Gram-negative bacteria to common antimicrobial agents (%)

Antibacterial agents	*Acinetobacter baumannii* (n = 133)		*Klebsiella pneumoniae* (n = 106)		*Pseudomonas aeruginosa* (n = 83)	
	Drug-resistant strains	Drug resistance rate	Drug-resistant strains	Drug resistance rate	Drug-resistant strains	Drug resistance rate
Amoxicillin/clavulanic acid	133	100.00	32	30.19	83	100.00
Cefepime	101	75.90	33	31.13	6	7.23
Cefotaxime	100	75.18	46	43.40	83	100
Sulbactam and Cefopcrazone	102	76.80	35	33.02	5	6.02
Sulfamethoxazole and Trimethoprim	95	71.43	36	33.96	78	93.98
Gentamicin	100	75.18	20	18.87	2	1.20
Ciprofloxacin	107	80.45	33	31.13	-	-
Ampicillin	133	100.00	106	100.00	83	100.00
Ampicillin/sulbactam	100	75.18	33	31.13	77	92.77
Piperacillin	106	79.70	47	44.34	16	19.28
Piperacillin/tazobactam	111	83.1	27	25.47	8	9.64
Cefazolin	133	100.00	90	84.91	83	100.00
Cefuroxime	133	100.00	98	92.45	76	91.57
Ceftriaxone	113	85.71	38	35.85	76	91.57
Ceftazidime	103	77.44	32	30.19	10	12.05
Cefotetan	133	100.00	34	32.08	73	87.95
Aztreonam	133	100.00	32	30.19	22	26.51
Meropenem	105	78.94	22	21.75	15	18.07
Imipenem	102	76.69	27	25.47	16	19.28

(Continued on next page)

(Continued from previous page)

Antibacterial agents	*Acinetobacter baumannii* (n = 133)		*Klebsiella pneumoniae* (n = 106)		*Pseudomonas aeruginosa* (n = 83)	
	Drug-resistant strains	Drug resistance rate	Drug-resistant strains	Drug resistance rate	Drug-resistant strains	Drug resistance rate
Tobramycin	96	72.18	13	11.32	1	1.20
Levofloxacin	105	78.95	27	25.47	3	3.61

Note: "-" indicates that this drug sensitivity test has not been performed

3.4. Resistance of major gram-positive bacteria to commonly used antibacterial drugs

The resistance rate of *Enterococcus faecium* to common antibiotics was high. The drug resistance rate of *Staphylococcus aureus* to penicillin G and ampicillin was high, as shown in **Table 5**.

Table 5. Resistance rate of major Gram-positive bacteria to common antibiotics (%)

Antibacterial agents	*Enterococcus faecium* (n = 69)		*Staphylococcus aureus* (n=31)	
	Drug-resistant strains	Drug resistance rate	Drug-resistant strains	Drug resistance rate
Erythromycin	69	100.00	12	41.94
Penicillin G	62	89.86	31	100.00
Clindamycin	65	94.21	10	35.48
Tetracycline	33	46.38	4	12.90
Moxifloxacin	62	89.86	5	16.13
Gentamicin	31	44.93	4	12
Ciprofloxacin	66	95.65	-	-
Levofloxacin	60	86.96	-	-
Ampicillin	62	89.86	31	100.00

4. Discussion

Patients in ICU are critically ill and are prone to nosocomial infection. Nosocomial infection will lead to prolonged hospital stay, increased risk of death, and bring economic burden to the families of patients [12]. This investigation showed that sputum, drainage fluid and urine samples were the main specimens sent for examination. Gram-negative bacteria (599 strains, 61.75%) were the most common pathogens, followed by Gram-positive bacteria (204 strains, 21.03%) and fungi (167 strains, 17.22%). Among the bacterial species collected from the samples, *Acinetobacter baumannii*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, *Escherichia coli* were the most common. Among the 1963 patients, there were 475 cases of nosocomial infection, and the incidence of nosocomial infection was 24.20%. Among them, 455 cases had lower respiratory tract infection, accounting for 64.54%. Studies have shown that the incidence of lower respiratory tract infection is closely related to the severity of the patient's condition. For example, severe disturbance of consciousness or diabetes will increase the infection rate of lower respiratory tract [13].

The results of drug sensitivity test showed that the resistance rates of *Acinetobacter baumannii* to meropenem and imipenem were 78.94% and 76.69%, respectively, which were similar to those reported in the literature [3]. The increasing drug resistance rate of *Acinetobacter baumannii* is greatly related to the irrational use or abuse of new broad-spectrum and ultra-broad-spectrum antimicrobial agents [14]. The drug

resistance rates of *Klebsiella pneumoniae* to cefuroxime, ampicillin, cefuroxime and cefazolin were very high, and the drug resistance rates to imipenem and meropenem were 25.47% and 21.75%, respectively, which were similar to the results reported in other literatures [15-18]. *Pseudomonas aeruginosa* was highly resistant to ampicillin, cefazolin and ceftriaxone. *Enterococcus faecalis* was highly resistant to moxifloxacin, ciprofloxacin and clindamycin. Staphylococcus aureus was highly resistant to penicillin and ampicillin.

5. Conclusion

In conclusion, the main pathogenic bacteria of nosocomial infection in ICU patients in our hospital aare gram-negative bacteria. The main pathogens are *Acinetobacter baumannii*, *Klebsiella pneumoniae* and *Pseudomonas aeruginosa*. The level drug resistance of those bacteria is highly concerning. However, the drug resistance of these pathogenic bacteria to Carbapenems and vancomycin are low. Clinical departments should increase the collection of infection specimens and improve drug sensitivity tests to grasp the drug resistance mechanism and changes in drug resistance of pathogenic bacteria, reasonably select antibacterial drugs according to the drug sensitivity results, prevent the generation of drug-resistant strains, and improve the level of treatment for patients with severe infections.

Funding

In-Hospital Fund Project of Affiliated Hospital of Hebei University: Analysis of Nosocomial Infection in Intensive Care Unit (2019Q030)

Disclosure statement

The authors declare no conflict of interest.

References

[1] Zhou X, Du G, Li Y, et al., 2018, Detection and Drug Resistance Differences of Multidrug-Resistant Bacteria in ICU and non-ICU Wards. Chin J Control, 17(3): 219–223.

[2] Li L, Liu J, 2020, Distribution and Drug Resistance of Pathogenic Bacteria in Patients with Nosocomial Infection in Intensive Care Unit. Journal of Practical Medicine, 27(4) :478-479.

[3] Li H, Qiu G, 2015, Analysis of bacterial flora distribution and drug resistance in 3391 patients with Icu infection. International Journal of Lab Medicine, 36(17): 2595–2597.

[4] Sun J, Zhang X, Xing M, et al., 2016, Analysis of Multi-Drug Resistant Bacteria in Multi-Center Intensive Care Unit in Shandong Province. Chin J Nosocomiology, 26(11): 2465–2467 + 2616.

[5] Zhang H, Qiu G, Zhai R, 2015, Analysis on the Distribution and Drug Resistance of Pathogenic Bacteria in Patients with Comprehensive ICU Infection. Journal of Clinical Military Medicine, 43(2): 182–185.

[6] Yang YS, Lee YT, Huang Tw, et a1., 2013, Acinetobacter Baumannii Nosocomial Pneumonia: Is the Outcome More Favorable in Non-Ventilated than Ventilated Patients． BMC Infect_Dis, 13: 142.

[7] Shi J, Guo Y, Weng J, et al., 2016, Distribution and Drug Resistance of Non-Fermentative Bacteria in Patients with ICU Infection. Chin J Nosocomiology, 26(17): 3866–3868.

[8] Wang Yi, Xu E, Ji P, et al., 2015, Analysis on the Distribution and Drug Resistance of Pathogenic Bacteria in ICU Patients. Chin J Nosocomiology, 25(15): 3402–3404.

[9] Chong J, Quach C, Blanchard AC, et a1., 2016, Molecular Epidemiology of a Vancomycin-

Intermediate Heteroresistant Staphylococcus Epidermidis Outbreak in a Neonatal Intensive Care Unit. Antimicrob Agents Ch, 60(10): 5673–5681. https://www.doi.org/10.1128/AAC.00726-16

[10] Yu J, Pathogen distribution and drug resistance analysis of nosocomial infection in intensive care unit. Practical Journal of Heart, Brain, Lung and Vascular Diseases, 21(9):99.

[11] Ye Y, Wang Y, Shen Z, 2006, National Clinical Laboratory Procedure (Version 3), Southeast University Press, Nanjing, 736–753.

[12] Xu J, 2011, Analysis of Risk Factors and Prognosis of Hospital Acquired Pneumonia After Acute Intracerebral Hemorrhage. Chin J Nosocomiology, 24(21): 5183–5185.

[13] Kohlenberg A, Schwab F, Ruden H, 2012, Wide Dissemination of Extended-Spectrum β-Lactamase (ESBL)-Producing Escherichia Coliand Klebsiella Spp in Acute Care and Rehabilitation Hospitals. Epidemiol Infect, 140(3): 528–534.

[14] Ge L, Yang W, Luo Y, et al., 2017, Distribution and Drug Resistance of Pathogenic Bacteria in ICU Patients from 2011 to 2015. Foreign Medical Antibiotics, 38(2): 67–71.

[15] Sharma M, Pathak S, Srivastava P, 2013, Prevalence and Antimicrobial Spectrum of Ultra-Broad Spectrum β-Lactamase (ESBL)-Producing Gram-Negative Bacilli and Molecular Characteristics of ESBL-Producing Escherichia Coli and Klebsiella. L Clin Diagn Res, 7(10): 2173–2177.

[16] Bao L, Peng R, RenX, et al., 2013, Analysis of Several Common Pathogens and their resistance to Antibiotics. Pak JMED Sci, 29(1):135–139.

[17] Lalzampuia H, Dutta TK, Warjri I, et al., 2013, PCR-Based Detection of Ultra Broad-Spectrum β-Lactams (blaCTX-M-1 and blaTEM) in Escherichia Coli, Salmonella and Klebsiella Pneumoniae Isolates from Pigs in Northeast India (Mizoram). Indian J Microbiol, 53(3): 291–296.

[18] Hu Z, Pan X, Zhou D, et al., 2014, Clinical Distribution and Drug Resistance Monitoring of Klebsiella Pneumoniae Infection. Chinese Journal of Nosocomiology, 24(12): 2865–2866.