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Original Article

Distribution and drug resistance analysis of multi-drug resistant bacteria in hospital

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Abstract: Objective: To retrospectively analyze the drug resistant characteristics and distribution of multi-drug resistant bacteria infection in our hospital, and to provide clinical reference for decreasing nosocomial infection rate of multi-drug resistant bacteria. Methods: A total of 120 cases treated in our hospital from October 2015 to June 2017 were selected as subjects. The automatic microorganism analyzer VITEK-2 was used for bacterial identification; Kirby-Bauer disk diffusion method was used for susceptibility test; WHONTE 5.6 software was used to analyze the distribution and drug sensitivity of isolated bacteria. Results: Among the 148 strains of multi-drug resistant bacteria, the proportion of Gram-negative bacteria was 62.16%, and the proportion of Gram-positive bacteria was 25.68%; other strains accounted for 12.16%. Multi-drug resistant bacteria mostly distributed in sputum, accounting for 47.97%; 50.00% multi-drug resistant strains were from intensive care unit. Resistant rates of staphylococcus aureus, staphylococcus epidermidis and staphylococcus haemolyticus to antibacterial agents (penicillins and cephalosporins) were close to or higher than 50%, and to both vancomycin and teicoplanin were 0. The antibacterial agents of low resistant rate for Escherichia coli, Klebsiella pneumoniae, Enterobacter cloacae, pseudomonas aeruginosa, acinetobacter baumannii were different. Conclusion: Gram-negative bacteria are the main multi-drug resistant bacteria of nosocomial infections in our hospital, mainly distributing in respiratory system and urinary system. They are highly resistant to most antibacterial agents, which provides a theoretical basis for the prevention and control of multi-drug resistant bacteria infection in hospital.

Keywords: Multi-drug resistant bacteria, nosocomial infection, antibacterial agents

Introduction

Multi-drug resistant bacterium refers to bacterium that is simultaneously resistant to 3 or more antibiotics currently used in clinic, and it has become a considerable pathogen of nosocomial infection [1]. With the worldwide abuse of antibiotics, multi-drug resistant bacteria have become a social problem, resulting in increasing difficulty of treatment for infectious diseases and higher mortality. According to a report, the top 5 multi-drug resistant bacteria were enterococcus faecalis, staphylococcus aureus, acinetobacter baumannii, Escherichia coli and pseudomonas aeruginosa [2]; the main kinds of drug resistant bacteria were consistent with the results of Yan's research [3]. However, it was reported that the main pathogens of nosocomial infection in a large hospital during 2011-2015 were Klebsiella pneumoniae, candida albicans, acinetobacter baumannii and Escherichia coli [4]. In summary, the bacteria spectrum and antibiotic use habits in different hospitals and departments are diverse, so the distribution of pathogenic bacteria and their drug susceptibility are also various. Therefore, we should understand the distribution and drug resistance of bacteria in our hospital, and provide basis and reference for the prevention and treatment of bacterial multi-drug resistance.

Materials and methods

Source of data

Data of 120 patients with nosocomial infection in Jining No.1 People's Hospital from October

Table 1. Distribution of 148 strains multi-drug resistant bacteria (n, %)

Bacteria	Number (strain)	Proportion (%)
G- bacteria	92	62.16
Escherichia coli	26	17.57
Acinetobacter baumannii	18	12.16
Pseudomonas aeruginosa	11	7.43
Klebsiella pneumoniae	10	6.76
Enterobacter cloacae	4	2.70
Stenotrophomonas maltophilia	4	2.70
Others	19	12.84
G+ bacteria	38	25.68
Staphylococcus epidermidis	6	4.05
Staphylococcus aureus	7	4.73
Staphylococcus haemolyticus	6	4.05
Enterococcus in urine	5	3.39
Enterococcus faecalis	4	2.70
Others	10	6.67
Fungus	16	10.8
Candida albicans	11	7.42
Candida tropicalis	2	1.35
Aspergillus	2	1.35
Others	1	0.68
Anaerobic bacteria	2	1.36
Bacteroides fragile	1	0.68
Others	1	0.68
Total	148	100.00

Table 2. Distribution of bacteria in 148 strains of multi-drug resistant bacteria

Specimen	Number (strain)	Proportion (%)
Sputum	71	47.97
Urine	23	15.54
Blood	22	14.86
Faeces	14	9.46
Pleural fluid and ascites	8	5.41
Pus	6	4.06
Others	4	2.70
Total	148	100.00

2015 to June 2017 were collected. The hospital infection cases were reported by the clinicians through real-time monitoring system of nosocomial infection, confirmed by the full-time staff of Hospital Infection Management Department, who were also responsible for regularly screening the missing reports of hospital infection. There were 62 males and 58 females, aged 19-89 years, with an average age of 47.88±2.91 years.

Source of bacterial strain

The bacterial strains were from 120 patients with nosocomial infection in our hospital; 148 clinical specimens were examined.

Diagnostic criteria

Hospital infection was diagnosed according to the *Hospital Infection Diagnosis Standard (Trial)* laid down by National Health and Family Planning Commission of the People's Republic of China in 2001 [5]. Multi-drug resistant bacterium was judged on the basis of the *Expert Consensus on Multi-drug, Pan-drug and Extensively Drug Resistance* launched and established by the European Centre for Disease Prevention and Control and the U.S. Centre for Disease Prevention and Control in 2011 [6].

Methods

Strain identification: Specimen collection and test methods are in accordance with the operational approaches in *Clinical Laboratory Operating Instructions*. The samples taken from subjects included sputum, blood, cerebrospinal fluid, ascites, pleural fluid, throat swab and urine etc. Microbiological laboratory preliminarily classified the clinical specimens by conventional bacterial culture and Gram staining. Then, the VITEK2 Compact 3450 type automatic microbiological identification and analysis system (Merieux, France) was used to identify bacterial species.

Susceptibility test: Susceptibility test included piperacillin, ampicillin, ceftazidime, cefepime, cefoperazone, cefotaxime, cefalotin, cefuroxime, imipenem and teicoplanin, vancomycin, levofloxacin, ciprofloxacin, gentamicin, oxacillin, chloramphenicol, clindamycin, rifampicin, penicillin and clindamycin. Drug-sensitivity reagent strips (model ATB FUNGUS) was from BioMerieux, France. Quality control strains included staphylococcus aureus ATCC29213, Escherichia coli ATCC25922 and streptococcus pneumoniae ATCC49619.

Statistical methods

Pathogenic bacteria detected in the specimens of patients with nosocomial infection were cen-

Table 3. Departments distribution of 271 strains of candida

Department	Number (strain)	Proportion (%)
Intensive care unit	74	50.00
Infectious disease	18	12.16
Respiratory medicine	14	9.47
General surgery	7	4.73
Geriatrics	6	4.05
Oncology	6	4.05
Other surgical departments	5	3.38
Cardiology	4	2.70
Neurology	4	2.70
Internal medicine of hematology	4	2.70
Nephrology	3	2.03
Others	3	2.03
Total	148	100.00

Table 4. Drug resistance of main G^+ bacteria to common clinical drugs (%)

Antibacterial agent	Staphylococcus epidermidis	Staphylococcus epidermidis	Staphylococcus haemolyticus
Penicillin	100.0	100.0	100.0
Piperacillin	96.4	100.0	93.7
Cefotaxime	45.1	60.4	60.1
Cefepime	43.1	81.3	76.5
Cefalotin	71.2	65.1	65.4
Vancomycin	0	0	0
Levofloxacin	14.0	8.4	10.5
Ampicillin	0	0	100.0
Oxacillin	0	4.5	0
Teicoplanin	0	0	0
Gentamicin	59.5	33.0	65.1
Rifampicin	71.6	82.8	76.4
Clindamycin	65.9	66.3	81.5

sused by Xinglin nosocomial infection real-time monitoring system, and multiple detections of the same bacterium at the same part of the same patient were recorded as 1 time. The data were analyzed by SPSS17.0 software package. Rate was expressed as percentage. The distribution of bacteria, strains and departments were compared by X^2 test. The difference was statistically significant when $P<0.05$. WHONET 5.6 software recommended by Bacterial Resistance Monitoring Center of World Health Organization was used to analyze the drug resistance of pathogens.

Results

Distribution of bacteria

The proportion of Gram-negative (G-) bacteria in 148 strains of multi-drug resistant bacteria was as high as 62.16%, followed by Gram positive (G+) bacteria (25.68%); compared with the summational proportion of fungi and anaerobic bacteria, the difference was statistically significant ($X^2=10.35$, $X^2=13.69$, and $X^2=19.74$ respectively, $P<0.05$). The top 5 multi-drug resistant bacteria were Escherichia coli (26 strains), acinetobacter baumannii (18 strains), pseudomonas aeruginosa (11 strains), candida albicans (11 strains) and Klebsiella pneumoniae (10 strains). See **Table 1**.

Distribution of strains

In 148 strains of multi-drug resistant bacteria, there were as high as 47.97% from sputum; compared with the proportion from other samples (urine, blood, faeces, pleural fluid, ascites and pus), the difference was statistically significant ($P<0.05$). See **Table 2**.

Department distribution

Among the 148 strains of multi-drug resistant bacteria, intensive care unit accounted for 50.00%; compared with the proportion of other departments (infectious disease department, respiratory medicine department and department of general surgery), the difference was statistically significant ($P<0.05$). See **Table 3**.

Drug resistance analysis of common G+ bacteria

The resistant rates of staphylococcus aureus, staphylococcus epidermidis and staphylococcus haemolyticus to common antibacterial agents (penicillins and cephalosporin) were near or higher than 50%, to vancomycin and teicoplanin were 0. See **Table 4**.

Drug resistance analysis of common G- bacteria

Drug resistances of Escherichia coli to amikacin, gentamicin and imipenem were low (30.3%,

Table 5. Drug resistance of main G- bacteria to common clinical drugs (%)

Antibacterial agent	Escherichia coli	Klebsiella pneumoniae	Enterobacter cloacae	Pseudomonas aeruginosa	Acinetobacter baumannii
Ampicillin	96.3	98.2	91.1	77.2	100.0
Piperacillin	65.3	59.2	60.5	70.1	90.3
Cefoperazone	90.5	90.2	76.8	66.9	50.4
Cefuroxime	93.5	92.1	92.4	76.8	73.1
Cefotaxime	91.3	91.5	75.8	70.1	55.5
Ceftazidime	90.5	87.7	70.9	65.5	61.1
Cefepime	70.5	64.8	80.3	55.7	40.1
Imipenem	2.0	1.0	4.0	0	54.8
Ciprofloxacin	79.5	51.3	46.3	6.0	39.1
Gentamicin	39.1	42.2	45.1	36.1	50.1
Amikacin	30.3	25.6	30.2	30.4	50.0
Chloramphenicol	49.5	55.3	48.3	65.8	36.7

39.1% and 2.0% respectively); resistant rates of Klebsiella pneumoniae to amikacin and imipenem were 25.6% and 1.0% respectively; resistant rates of pseudomonas aeruginosa to ciprofloxacin and imipenem were 6.0% and 0% respectively; resistant rates of acinetobacter baumannii to ciprofloxacin, cefepime, chloramphenicol were 39.1%, 40.1% and 36.7%, respectively (**Table 5**).

Discussion

Our results showed that the proportions of G- bacteria and G+ bacteria in 148 strains of multi-drug resistant bacteria were 62.16% and 25.68% respectively. The top 5 multi-drug resistant bacteria were Escherichia coli, acinetobacter baumannii, pseudomonas aeruginosa, candida albicans and Klebsiella pneumoniae. The proportion of multi-drug resistant bacteria isolated from sputum was as high as 47.97%, which was consistent with other reports, suggesting that these strains may be the main pathogens causing nosocomial infections, especially pulmonary infections [7-9].

In G- bacteria, resistant rates of Escherichia coli to penicillins and cephalosporins were more than 50%, and to amikacin, gentamicin and imipenem were low. A related study showed that resistant rate of extended-spectrum β-lactamase-producing Escherichia coli to penicillins, cephalosporins, monobactams, fluoroquinolones and aminoglycosides was significantly higher than that of non-extended-spectrum β-lactamase-producing strains, which suggested that producing extended-spectrum β-lactamase was the main reason for the multi-drug resistance of Escherichia coli [10]. The resistant rates of Klebsiella pneumoniae to penicillins, cephalosporins and quinolones were relatively higher. With the widespread use of quinolones, drug resistance of fluoroquinolone and penicillin has attracted more and more attention. Acinetobacter baumannii is resistant to a variety of antimicrobial agents, and has limited sensitivity to imipenem, chloramphenicol and ciprofloxacin, which was similar to results of other reports [11-14]; it has resistance genes itself with complicated mechanism, and it can easily cause hospital acquired pneumonia and other diseases, so it is worthy of attention. Pseudomonas aeruginosa was highly resistant to penicillins and cephalosporins, and sensitive to imipenem and ciprofloxacin. The above results suggest that combined treatment of multiple antibacterial agents is needed for strongly pathogenic and difficultly removed G- bacilli based on timely and accurate drug sensitivity results.

In this study, the multi-drug resistant positive bacteria including staphylococcus aureus, staphylococcus epidermidis and staphylococcus haemolyticus were highly resistant to penicillins, cephalosporins and other antimicrobial agents, which was similar to other researches [15-18]; that may be related to the large use of penicillins and cephalosporins in recent years. At the same time, we found that staphylococcus aureus, staphylococcus epidermidis and staphylococcus haemolyticus were

sensitive to vancomycin, teicoplanin and oxacillin. Therefore, we recommend vancomycin as the first choice for these bacteria, and oxacillin as the first choice for patients with obvious renal damage. But in order to prevent the formation of drug-resistant strains, careful clinical selection is still needed, and abuse is forbidden.

Irrational use of antibiotics is the main cause of current antibiotic resistance [19]. So, we should always abide by the using principles of antibacterial agents and the classification management system of antimicrobial drugs; personalized use of antibiotics according to drug sensitivity and culture results is essential for the prevention of multi-drug resistant bacteria [20, 21].

To sum up, the multi-drug resistant pathogenic bacteria of nosocomial infection in our hospital are G- bacteria, mainly including Escherichia coli, acinetobacter baumannii, pseudomonas aeruginosa, candida albicans, Klebsiella pneumoniae, and they are highly resistant to cephalosporins and penicillins. Therefore, we should use antibiotics rationally according to the results of drug sensitivity test to control the formation of drug-resistant strains. However, the number of cases in this study is small with limited scope, and the cross infection has not been analyzed, so further research and improvement is needed.

Disclosure of conflict of interest

None.

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