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Growth Situation of Drug-Resistant Strain in Cardiovascular Diseases upon Analyzing Gram-Negative (G -) Bacilli and Gram Positive (G +) Bacteria etc

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Upon analyzing the living state of pathogenic bacteria and antimicrobial resistance in cardiovascular disease, this paper is mainly to conclude that gram-negative (G -) bacilli, gram positive (G +) bacteria, fungi etc have all played an important role in the high morbility of heart cerebrovascular disease. Meanwhile bacteria resistance has also caused too much difficulty in its curing, and the proper monitoring of tiology and drug susceptibility would help rationally clinical selection and the right use of antimicrobial agents. The method is through making an identification and drug resistance analysis for 8705 samples of sputum, urine, blood that come from patients with cardiovascular disease in three years. Among 804 strains of bacteria separation, gram-negative bacteria and gram-positive bacteria have taken account for 87.69% and 12.31% respectively. In gram negative bacteria *Pseudomonas aeruginosa*, *Acinetobacter baumannii* is primary; *Staphylococcus aureus* is primary in gram-positive bacteria and enterococcus is secondary; white candida is primary in 547 strains of separation fungi; pseudomonas aeruginosa and acinetobacter is drug resistant to part of cephalosporins of antimicrobial agents, such as ampicillin, furadantin and cefotetan. It is sensitive to amikacin and polymyxin B, which have different drug resistance to other antimicrobial agents. *Staphylococcus aureus* and dung enterococcus are quite sensitive to rina thiazole amine, teicoplainin and vancomycin, and they have different drug resistance to other antimicrobial agents. The result is that a gram negative bacterium is the leading cause of cardiovascular disease's infection pathogens. The fungal infection is on the rise and drug resistance of pathogenic fungi is serious. Attaching great importance to pathogen monitoring and analysis of drug resistance is significant in guiding clinically rational use of antimicrobial agents, as well as controlling the spreading and hospital infection of drug resistance strains. Various clinical microbiology rooms should give tight and close monitoring, explore the changes and laws in the transformation of pathogen resistance, strictly control the laboratory quality and send accurate report to clinic, thus guide rational drug use clinically, all those are the important task of contemporary clinical microbiology.

Key words: Cardiovascular disease, pathogen bacteria, drug resistance, microbiology.

Cardiovascular disease is one of the main disease that modern people suffer from. With the change of living style and dietary structure, the incidence rate and mortality is increasing higher. As the wide use of antimicrobial agents, distribution and drug resistance of pathogen bacteria in cardiovascular system disease change. Even multiple drug-resistant strains appear. It increases the difficulty of clinic treatment. Therefore, it is necessary to monitor distribution

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and drug resistance of infecting pathogenic bacteria in cardiovascular system disease. This paper makes a retrospective analysis of distribution and drug resistance of 8705 straits of pathogenic bacteria, which provides a necessary foundation for clinical rational use of antimicrobial agents, and formulation of reasonable cardiovascular system infection diagnosis and treatment plan.

MATERIALS AND METHODS

Specimen Source

Collect 4375 cases of common bacteria cultivation specimens and 4330 fungal cultivation specimens such as sputum, urine, blood, secretion and catheter from the patients suffer from cardiovascular disease. Positive specimens of bacteria that are detected come from 2473 patients.

Bacteria Identification and Drug Sensitive Test

Adopt automatic identification and drug sensitive system VITEK-2 Compact from French BioMerieux on the detected 804 strains of bacteria. Adopt combination of handwork and VITEK-2 Compact detection on 547 straits of Fungi specimens.

Quality Control of Bacterial Strain

Select different antimicrobial agents to do drug sensitive experiment on staphylococcus aureus ATCC 25923, escherichia coli ATCC 25922, pseudomonas aeruginosa ATCC27853 and dung enterococcus ATCC 29212 according to NCCLS standard.

Table 1. Main source and composition ratio of detected bacteria (%)

Fungus	Phlegm	Urine	Venous Blood	Secreta	Total Strains Composition	Total ratio
Gram negative bacteria	608	72	21	4	705	87.69
Pseudomonas aeruginosa	341	15	10	1	367	45.65
Acinetobacter baumannii	107	2	0	1	110	13.68
Klebsiella pneumoniae	45	5	0	0	50	6.22
Stenotrophomonas maltophilia	31	0	0	1	32	3.98
E. coli	18	21	8	0	47	5.85
Frictional Morgan frictional subspecies	2	16	0	0	18	2.24
Klebsiella bacteria	12	1	0	1	14	1.74
Onion burkholderia bacteria	10	0	3	0	13	1.62
Singular deformation bacteria	4	6	0	0	10	1.24
Serratia fade	9	0	0	0	9	1.12
Enterobacter cloacae	7	0	0	0	7	0.87
Achromobacter xylosoxidans	6	0	0	0	6	0.75
Citrobacter freundii	3	0	0	0	3	0.37
Stench pseudomonas	0	3	0	0	3	0.37
Other enteric bacilli	2	0	0	0	2	0.25
Ralstonia pickettii	2	0	0	0	2	0.25
Other gram negative bacteria	9	3	0	0	12	1.49
Gram positive bacteria	50	20	26	3	99	12.31
Staphylococcus aureus	47	0	2	0	49	6.09
Enterococcus faecalis(Group D)	0	13	0	0	13	1.62
Sraphylococcus epidermidis	0	2	4	1	7	0.87
Enterococcus faecalis	0	3	2	0	5	0.62
Enterococcus faecium)Group D)	1	0	3	0	4	0.50
People staphylococcus	0	0	2	2	4	0.50
Staphylococcus haemolyticus	0	0	4	0	4	0.50
Staphylococcus capitis	0	0	3	0	3	0.37
Streptococcus agalactiae	0	0	2	0	2	0.25
Staphylococcus aureus subspecies	0	0	2	0	2	0.25
Other gram positive bacteria	2	2	2	0	6	0.75
Total	658	92	47	7	804	100.00

Statistical Analysis

Apply East-top4.0 and Microsoft Excel software to make a statistical analysis of materials.

Result analysis

Category and Composition of Bacteria

Detect 804 straits of bacteria and 705 straits of gram negative bacteria in 4375 of common

Table 2. Main source and composition ratio of detected bacteria(%)

Fungus	Phlegm	Urine	Shit	Venous blood	Total	
					Strains Composition	ratio
Candida albicans	275	22	18	0	315	57.59
Candida tropicalis	66	17	4	0	87	15.90
Candida Parapsilosis	64	15	1	4	84	15.36
Candida glabrata	24	1	7	0	32	5.85
Filamentous fungi	15	1	0	0	16	2.92
Candida krusei	8	1	0	0	9	1.65
Aspergillus	4	0	0	0	0	0.73
Total	456	57	30	5	547	100.00

Table 3. Drug resistance rate of main gram negative bacilli to common antibacterial agents (%)

Antibacterial agents	*Pseudomonas aeruginosa* (n=367)		Acinetobacter baumannii (n=110)	
	Strains	Drug resistance rate	Strains	Drug resistance rate
Ampicillin anhydrous	367	100.00	110	100.00
Ampicillin anhydrous/ sulbactam	367	100.00	97	88.46
Amikacin	117	31.96	101	91.59
Aztreonam	283	76.99	109	99.07
Cefoperazone/ sulbactam	267	72.81	102	92.93
Ciprofloxacin	236	64.41	102	92.52
Cefotetan	367	100.00	110	100.00
Ceftriaxone	367	100.00	110	100.00
Cefazolin	367	100.00	110	100.00
Cefepime	265	72.27	102	92.52
Macrodantin	367	100.00	110	100.00
Gentamicin	270	73.53	105	95.19
Imipenem	334	90.88	102	92.45
Levofloxacin	259	70.59	97	87.85
Meropenem	291	79.18	102	92.93
Minocycline	364	99.08	103	93.88
Polymyxin B	20	5.56	64	58.59
Cefoperazone	311	84.72	110	100.00
Piperacillin	232	63.13	108	98.11
Cefuroxime sodium	...	...	110	100.00
Cefuroxime axetil	367	100.00	110	100.00
Sulfamethoxazole/Trimethoprim	365	99.33	...	...
Cafetaxime	367	100.00	110	100.00
Ceftazidime	207	56.30	104	94.39
Ticarcillin/ Clavulanic acid	273	74.40	99	90.00
Tetracycline	359	97.73	110	100.00
Tobramycin	188	51.18	101	91.67
Piperacillin/ Tazobactam	205	55.88	103	93.46

bacteria culture specimens, such as sputum, urine, blood, secretion and catheter of patients with cardiovascular disease. Pseudomonas aeruginosa and Bowman's acinetobacter is the primary among them. Detect 99 strains of gram-positive bacteria, among which staphylococcus aureus is primary and dung enterococcus is secondary. The source and composition is showed in Table1.

Category and Composition of Fungus

547 strains were detected fungus in 4330 of fungus cultivation sample. And candida albicans were primary. Table 2 shows its category and composition.

Detection of Drug Resistance Analysis

Make a drug sensitive test on 804 strains of isolated bacteria. Drug resistance analysis result of former two gram negative bacilli and gram positive coccus is showed in Table 3 and 4.

Table 4. Drug resistance rate of main gram positive coccus to common antibacterial agents(%)

Antibacterial agents	*Staphylococcus aureus* (n=49)		*Enterococcus faecalis* (n=13)	
	Strains	Drug resistance rate	Strains	Drug resistance rate
Ampicillin anhydrous	49	100.00	0	0.00
Clindamycin	16	33.33	13	100.00
Ciprofloxacin	41	82.98	4	33.33
Erythrocin	16	33.33	4	33.33
Linezolid	0	0.00	0	0.00
Quinupristin/Dalfopristin	0	0.00	13	100.00
Tetracycline	41	83.33	0	0.00
Teicoplanin	0	0.00	0	0.00
Vancomycin	0	0.00	0	0.00
Gentamicin with high concentration	-	-	0	0.00
Furadantin	0	0.00	-	-
Gentamicin	40	81.25	-	-
Cefoxitin	49	100.00	-	-
Cefazolin	49	100.00	-	-

DISCUSSION

Cardiovascular disease is one of main diseases of modern people. Incidence infection rate of cardiovascular disease is high for its delay of disease course that lead to long time of illness and recession of immune. It will hurt patients' mind and body and affect their living quality. With the wide application of broad spectrum of antimicrobial agents, drug resistance of bacteria is increasingly growing, which have drawn the worldwide attention. Master bacteria drug resistance situation in time and apply antibacterial agents rationally, which is of great significance to delay spread and popular of drug resistance strains, improve prognosis and reduce hospitalization costs.

Distribution of bacteria

The analysis result of this research show that pathogenic bacteria of cardiovascular disease mainly come from phlegm and secondary is urine. It illustrate that nosocomial infection mainly appear in respiratory tract and urinary tract, which is related with weak immunity, respiratory recession and variety of diseases of patients.

Pathogenic bacteria can be divided into gram negative bacteria and fungus,and partial gram positive bacteria. Pseudomonas aeruginosa is primary in gram negative bacteria and then acinetobacter baumannii, klebsiella pneumoniae and stenotrophomonas maltophilia. Pseudomonas aeruginosa is widely distributed in natural world, normal skin, respiratory tract, intestinal tract, hospital ward and medical apparatus and instruments. It is the important pathogenic bacteria of nosocomial infection and also the common pathogenic bacteria of concurrent infection of old

and weak and patients with chronic disease and weak immunity. Gram positive bacteria are mainly staphylococcus aureus and enterococcus faecalis and staphyloccus epidermidis is also included. They can be pathogenic bacteria under some situations. The detection rate of fungus is high. Therefore, it is an important pathogenic bacteria, among which canidia albicans is most common and candida tropicalis and candida parapsilosis account for a certain proportion.

Patients with cardiovascular disease always merge several diseases. Adopt interventional therapy in clinic treatment while using antimicrobial agents. Or adopt relative therapeutic measures because merging other disease, such as urine tube and intravenous cannula, which will imbalance flora and damage immune system. Surface of skin mucous membrane and anic normal flora are likely to be pathogenic bacteria, which is the main reason of infection.

Analysis of Drug Resistance

Detection of drug resistance found that pseudomonas aeruginosa and acinetobacter baumannii are completely resistant to some cephalosporin antibiotic drugs, such as ampicillin anhydrous, furadantin and cefotetan. And they are sensitive to amikacin and polymyxin B and have different degree of drug resistance to other antibacterial agents. However, stenotrophomonas maltophilia is completely resistant to imipenem and meropenem and is sensitive to minocycline.

It can be seen from the number of isolated bacterial strains that pseudomonas aeruginosa and acinetobacter baumannii are main pathogenic bacteria, therefore, make a further analysis of drug resistance mechanism. The drug resistance mechanism is very complex and mainly consists of β-lactamase, active efflux system expression of epicyte, permeability decline caused by change of outer membrane protein, penicillin combined with protein change and drug resistance caused by biological membrane. Penicillium carbon alkene antimicrobial agents are one of the effective drugs of resisting pseudomonas aeruginosa, which is characterized by unique chemical construction, stable antimicrobial activity and broad-spectrum antibacteria. However, in this research, pseudomonas aeruginosa show drug resistance to imipenem and meropenem. So we should apply it rationally to control its drug resistance. Acinetobacter baumannii mainly cause respiratory tract infection which can induce Septicaemia, urinary tract infection, secondary meningitis. It distributed widely in hospital and can survive for long time, which is a big risk for critical patients and elder patients. Acinetobacter baumannii that resist to penicillium carbon alkene in China develop quickly and recently acinetobacter baumannii of complete drug resistance become an obvious sign. Drug resistance of isolated acinetobacter baumannii to cephalosporin antibiotic drugs, aminoglycosides and even imipenem and meropenem is higher than 90%. And it is sensitive to polymyxin B. So we should pay attention to it in order to prevent acinetobacter baumannii with complete drug resistance.

CONCLUSION

Cardiovascular system disease is one of the common clinic infectious diseases. In recent years, the wide application and pharmacy reasonability appear problems. It lead to transition of drug-resistance spectrum of clinical pathogenic bacteria, drug resistance level become more and more serious and multi-drug resistance situation stand out. Clinic should combine the individual situation of infectors with result of drug sensitive test to use drug, which can control the spread and infection of drug resistance strains.

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