Distribution of Common Pathogens and Bacterial Resistance in A Tertiary Hospital in China

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We aimed to explore the distribution of common pathogens and bacterial resistance in our hospital from 2017 to 2020, and to standardize clinical medication guidance. The pathogens isolated from the submitted specimens were identified, and drug susceptibility results were interpreted according to the Clinical and Laboratory Standards Institute guidelines (2017-2020). A total of 43,588 specimens were collected from patients treatedfrom 2017 to 2020, and 6,285 strains of pathogens were isolated. The most common pathogens were Escherichia coli, Haemophilus influenzae and Klebsiella pneumoniae.Methicillin-resistant Staphylococcus aureus (MRSA) accounted for 32.85%, and methicillin-resistant coagulase-negative Staphylococcus (MRCNS) accounted for 78.79%. The resistance rates of MRSA and MRCNS to ciprofloxacin, levofloxacin, erythromycin, clindamycin and trimethoprim-sulfamethoxazole were significantly higher than those of methicillin-sensitive S. aureus and methicillin-sensitive coagulase-negative Staphylococcus. The resistance rate of Streptococcus pneumoniae to erythromycin, tetracycline and clindamycin was higher than 80%. The detection rates of E. coli and K. pneumoniae producing ESBL strains were 62.2% and 25.6%, respectively. Totally, 769 carbapenem-resistant strains were detected, of which carbapenem-resistant Acinetobacter baumannii (CRAB) accounted for 66.6%, followed by carbapenem-resistant K. pneumoniae (CRKP) and carbapenem-resistant Pseudomonas aeruginosa (CRPA). A total of 202 CRE strains were detected, which were mainly isolated from respiratory tract and urine specimens. CRAB, CRKP and CRPA had higher resistance rates to antibacterial drugs. Gram-negative bacilli are the most common pathogens from 2017 to 2020. Considering that pathogens have high drug resistance, it is recommended to strengthen clinical management and rational application of antibiotics, thus reducing the risk of nosocomial infections.

Key words: drug susceptibility; carbapenem resistance; resistance; monitoring
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In recent years, antibiotics have been frequently utilized in various anti-infective treatments, greatly affecting the safety of clinical medication, including most drug administration based on experience by physicians, lower submitting rate of pathogens, inaccurate medication, unreasonable course and compatibility, and unsuitable combination of drugs [1, 2]. Bacterial resistance is not only a difficult problem in clinical anti-infective treatments in China, but also an extensively concerned issue worldwide, and the development of new antibacterial drugs often fails to keep up with the changes and spread of drug-resistant bacteria [3]. The drug resistance of bacteria is different due to multiple factors, and drug-resistant bacteria tend to invade such low-immunity people as those with tumors [4, 5]. According to EU survey statistics, infections caused by multi-drug resistant bacteria lead to more than 25,000 deaths each year, resulting in economic losses of up to 1.5 billion euros in medical care and social productivity [6]. Besides, there are more than 2 million cases suffering from bacterial infections in the United States alone, and these bacteria have developed resistance to at least first-line antibiotics, which needs more than 20 billion dollars for medical and healthcare institutions to solve the drug resistance [6, 7]. Recently, the World Bank and the Food and Agriculture Organization of the United Nations reported that if antibiotic resistance continues until 2050, the global annual GDP will reduce by 1.1-3.8%, which is equivalent to the impact of the financial crisis in 2008 [8]. Therefore, bacterial resistance surveillance is of great significance to understand the changes of resistant bacteria and to stop the spread of drug-resistant bacteria. Clinical surveys have indicated that Gram-negative bacilli account for the majority of pathogens in the intensive care unit (ICU), mainly including *Pseudomonas aeruginosa*, *Acinetobacter baumannii* and *Escherichia coli*, while Gram-positive bacteria are relatively few, and the distribution of non-ICU pathogens is also dominated by Gram-negative bacteria [9, 10]. However, a previous study revealed that bacterial resistance has prominent regional differences due to different choices of antibacterial drugs in different regions and hospitals [11]. Hence, strengthening bacterial resistance surveillance in regional hospitals and understanding bacterial distribution and resistance are essential to standardize the application of antibacterial, thus improving clinical effects and reduce medical costs.

EXPERIMENTAL

Materials and Methods

The data of patients admitted to our hospital from July 2017 to June 2020 were collected, and those diagnosed with infections were strictly screened. Patients with community-acquired infections according to the definition of nosocomial infections were excluded, and patients enrolled in this study were counted. The strain data of multi-site culture were collected, and the repeated strains isolated from the same site of the same object were removed. The annual antibacterial drug use data were obtained from Department of Pharmacy in our hospital, and the annual antibacterial drug consumption and antibacterial drug use rate were calculated.

The drug resistance and sensitivity of clinical isolates to antibacterial drugs were determined by automated instruments. The instruments included bacterial identification and drug susceptibility analyzer MicroScanWalkAway NA80 provided by Siemens and Sensititre ARIS automatic bacterial identification and drug susceptibility analyzer purchased from Trek Diagnostic Systems Ltd. (England).The NC50 bacterial identification/drug susceptibility testing composite board and additives were compatible with MicroScanWalkAway NA80 automatic microbial identification/drug sensitivity tester (Siemens), and the identification card, drug susceptibility card and blood agar medium were all bought from Siemens and Trek Diagnostic Systems Ltd[24].

The drug susceptibility results were interpreted according to paper diffusion method or automated instrument method recommended by the internationally recognized American Clinical and Laboratory Standards Institute (CLSI) guidelines (Clinical and laboratory standards institute 2015-2020) with the current year's standard.The quality-control strains were Staphylococcus aureus ATCC29213, S. aureus ATCC25923, E. coli ATCC25922, and P. aeruginosa ATCC27853. Those without CLSI breakpoint were determined in accordance with FDA recommendation. The cefoperazone/sulbactam of A. baumannii was interpreted accordingto the CLSI breakpoint for Enterobacteriaceae.

For K. pneumoniae, E. coli, Klebsiella oxytoca and Proteus mirabilis, according to paper diffusion method recommended by CLSI for any drug in the two groups, ≥5 mm increase in zone of inhibition with and without clavulanic acid was determined to produce ESBL.

Whonet 5.6 software was employed for data analysis, including bacteria source, composition, type and department distribution, as well as the drug susceptibility results of clinical common antibacterial drugs.

RESULTS

A total of 43,588 submitted specimens were collected from 2017 to 2020, including 13,189 sputum specimens (30.26%), followed by 7,628 urine specimens (17.50%), 4,189 secretions (9.61%), 3,487 whole blood (8.00%), 3,374 drainage fluid (7.74%), 2,589 pus (5.94%), 1,717 bile (3.94%), 1,569 ascites (3.6%), 1,491 other specimens (3.42%), 1,177 lavage fluid (2.70%), 1,042 cerebrospinal fluid (2.39%), 963 peritoneal dialysis fluid (2.21%), 628 pleural fluid (1.44%), and 545 dialysate (1.25%).

A total of 6,285 strains of pathogens were isolated, including 2,773 strains from sputum, 1,119 strains from urine, 762 strains from secretions, 666 strains from whole blood, 324 strains from draining fluid, 149 strains from pus, 140 strains from bile, 105 strains from ascites, 98 strains from others, 47 strains from lavage fluid, 45 strains from cerebrospinal fluid, 28 strains from peritoneal dialysis fluid, 18 strains from pleural fluid, and 11 strains from dialysate (Table I).

A total of 6,285 strains of pathogens were isolated from the submitted specimens, including 1,794 strains of Gram-positive bacteria (28.54%), 4,314 strains of Gram-negative bacteria (68.64%) and 177 strains of fungi (2.82%). The mostly common pathogens wereE. coli, Haemophilus influenzae, Klebsiella pneumoniae, S. aureus, A. baumannii and P. aeruginosa. The top 5 Gram-positive bacteria were S. aureus, Streptococcus pneumoniae, Enterococcus faecium, Staphylococcus epidermidis, coagulase-negative Staphylococcus and Enterococcus faecalis, while the top 5 Gram-negative bacteria were E. coli, H. influenzae, K. pneumoniae, A. baumannii and P. aeruginosa. Among the 177 strains of fungi detected, Candida albicans was dominated (49.71%), followed by Candida tropicalis and Candida glabrata (Table II).

A total of 624 strains of S. aureus were detected in this study, in which methicillin-resistant S. aureus (MRSA) and methicillin-resistant coagulase-negative *Staphylococcus* (MRCNS) accounted for 32.85% and 78.79%, respectively. The resistance rates of MRSA and MRCNS to ciprofloxacin, levofloxacin, erythromycin, clindamycin and trimethoprim-sulfamethoxazole were significantly higher than those of methicillin-sensitive *S. aureus* (MSSA) and methicillin-sensitive coagulase-negative *Staphylococcus* (MSCNS). The resistance rate of MRSA and MRCNS to trimethoprim-sulfamethoxazole was 23.2% and 68.9%, respectively. No linezolid, nitrofurantoin-, tigecycline-, teicoplanin- and vancomycin-resistant Staphylococcus was observed, and its resistance rate to rifampicin was within 10% (Table III).

A total of 366 strains of *S. pneumoniae* were detected, which had resistance to vancomycin, linezolidand imipenem within 1%, penicillin G, moxifloxacin and levofloxacin within 5%, erythromycin, tetracycline and clindamycin higher than 80%, and no drug resistance to vancomycin and linezolid. Other streptococci were highly sensitive to chloramphenicol and levofloxacin, and no penicillin G-, vancomycin-. Linezolid- and ceftriaxone-resistant strains were observed (Table IV).

There were 196 strains of *E. faecium* and 61 strains of *E. faecalis*, with no tigecycline-, linezolid- and vancomycin-resistant strains, and none of them were sensitive to clindamycin. The resistance rate of E. faecium was higher to the tested drugs, and its resistance rate to moxifloxacin, ciprofloxacin, erythromycin, levofloxacin, gentamicin, ampicillin and penicillin was all >70%.*E. faecalis* had a significantly lower resistance rate to the tested antibacterial drugs than *E. faecium*, and the resistance rate of *E. faecalis* to other tested drugs was below 30%, except erythromycin (Table V).

ESBL-producing *E. coli* and *K. pneumoniae* detected accounted for 62.2% and 25.6%, respectively. There were 1,168 strains of *E. coli*, which had a resistance rate to amikacin and tigecycline within 5%, carbapenem antibiotics within 1.5%, cefotetan, piperacillin-tazobactam, amikacin, nitrofurantoin and cefoperazone-sulbactam within 10%, gentamicin, levofloxacin and ciprofloxacin within 48.6%, 52.9% and 56.0%, respectively, as well as highest resistance rate to ampicillin, reaching 86.3%. There were 632 strain of K. pneumoniae, which had a resistance rate of 5.1% to tigecycline, and a higher resistance rate to carbapenem antibiotics than E. coli, among which the resistance rate to imipenem and meropenem was 13.6% and 13.9% respectively, cefoperazone-sulbactam, piperacillin-tazobactam, amoxicillin-clavulanic acid, cefoxitin, cefepime, ceftazidime, levofloxacin, ciprofloxacin and gentamicin within 20-30%, as well as cefazolin and ceftriaxone, 55.2% and 52.1%, respectively. There were 632 strains of H. influenzae, which had a resistance rate of 78.6% to ampicillin, within 40-50% to amoxicillin-clavulanic acid and cefepime, less than 10% to levofloxacin, ciprofloxacin, piperacillin-tazobactam and meropenem, as well as 14.2% to ceftriaxone (Table VI).

The resistance rate of 586 strains of *P. aeruginosa* to imipenem and meropenem was 18.8% and 16.2%, and it had a resistance rate of 0 and 1.7% to polymyxin B and amikacin, respectively, two tested enzyme inhibitor combination agents, gentamicin, ciprofloxacin, levofloxacin, cefepime and piperacillin <23%, and highest resistance rate to aztreonam, reaching 31.6%. The resistance rate of 674 strains of A. baumannii to tigecycline and minocycline was 4.3% and 14.4%, respectively, and it had a resistance rate to amikacin, gentamicin, piperacillin-tazobactam, cefoperazone-sulbactam, cefepime, ampicillin-sulbactam sodium, imipenem, meropenem, ciprofloxacin, levofloxacin and trimethoprim-sulfamethoxazole more than 60%. Besides, the resistance rate of all strains to polymyxin B was zero (Table VII).

Totally, 769 carbapenem-resistant strains were detected, accounting for 17.6% of all the Gram-negative bacilli, of which carbapenem-resistant A. baumannii (CRAB) accounted for 66.6% (512/769), followed by carbapenem-resistant K. pneumoniae (CRKP) and carbapenem-resistant P. aeruginosa (CRPA) accounting for 22.5% and 13.6%, respectively. The department with the highest CRAB detection rate was ICU (28%), followed by Neurosurgery Department (26.4%) and EICU (15.4%), the department with the highest CRKP detection rate was Neurosurgery Department (42.3%), followed by ICU (16.5%) and Emergency Department (7.8%), and the highest CRPA detection rate was observed in Neurosurgery Department, accounting for 40.6%, followed by Respiratory Department (35.6%) and Neurology Department (5.8%).In terms of specimen distribution, CRAB, CRKP and CRPA had the highest detection rate in respiratory tract specimens such as sputum, accounting for 88.6%, 84.3% and 91.2% of their respective strains.A total of 202 carbapenem-resistant Enterobacteriaceae (CRE) strains were detected, accounting for 7.6% of all Enterobacteriaceae. CRE strains were mainly distributed in Neurosurgery Department and ICU, accounting for 36.4% and 14.2%, respectively, and accounting for 20.8% of carbapenem-resistant strains. CRE had a higher rate of resistance to multiple tested antibacterial drugs. CRKP had a resistance rate of 31.8% to trimethoprim-sulfamethoxazole, 18.2% to minocycline, 0 to tigecycline and polymyxin, and >59% to the other tested antibacterial drugs. CRE was mainly isolated from respiratory tract specimens and urine specimens, accounting for 63.4% and 22.8% respectively. CRAB, CRKP and CRPA had a higher resistance rate to antibacterial drugs (Table IX).

DISCUSSION

At present, with the extensive application of broad-spectrum antibacterial drugs and the continuous increase of bacterial resistance, the difficulty of anti-infective treatment has increased significantly, reducing the clinical effects.Hence, it is of great significance to understand the distribution of main pathogens and to perform bacterial resistance surveillance. A total of 6,285 strains of pathogens were isolated from the submitted specimens of patients treated in our hospital from 2017 to 2020, with the highest positive rate in respiratory tract specimens, consistent with the reports of Yelin et al.[12], dominated by H. influenzae, P. aeruginosa and S. pneumoniae, and followed by urine specimens (with a positive rate of 17.8%), consistent with the study of Taye et al.[13]. The isolation rate of respiratory tract specimens is almost the same as the monitoring data of CHINET in 2017, and urine specimens have a significantly higher isolation rate than the monitoring data of CHINET. The reason may be due to the 4,314 strains of Gram-negative bacteria (68.64%) and 1,794 strains of Gram-positive bacteria (28.54%) with respect to the distribution of common pathogens in the Urology Department of our hospital, which somewhat differ from the proportions of Gram-negative bacteria and Gram-positive bacteria reported in the previous literature [14].Among the bacteria isolated in this study, E. coli accounted for the highest proportion of 18.58%, which are prone to cause urinary and respiratory system infections, followed by H. influenzae and K. pneumoniae. The latter was conditional pathogens, which are easy to colonize with the pharynx after infection and are difficult to remove. The submitting rate and quality of submitting should be ensured, the indications for submitting should be strictly grasped, and clean mid-stream urine should be collected before using antibiotics and submitted for inspection in time.

Gram-negative bacteria (68.64%) accounted for the majority of pathogens isolated clinically in our hospital, mainly including Enterobacteriaceae and non-fermenting bacteria. The main resistance mechanism of E. coli and K. pneumoniae among Enterobacteriaceae was to produce ESBL carbapenemase. ESBL-producing strains are resistant to most third generation cephalosporins. The detection rate of ESBL-producing E. coli and K. pneumoniae was 62.2% and 25.6%, respectively. Considering that the isolation rate of ESBL strains in our hospital was higher than that of CHINET monitoring data in previous years, it is recommended to improve clinical attention (Ng et al. 2018). E. coli had a resistance rate of 48.6%, 52.9%, and 56.0% to gentamicin, levofloxacin and ciprofloxacin in our hospital, and the highest resistance rate to ampicillin, reaching 86.3%, approximately consistent with the reports by Salillaset al. [15].

According to drug susceptibility testing results, the results of ESBL confirmatory test for CRE strains were almost negative. A relevant study indicated that carbapenemase interferes with the detection of ESBL to a certain extent, and the results of detection of related β-lactamase resistance genes on CRE strains showed that more than 90% of the strains can produce carbapenemase and ESBL [16]. Hence, a previous related study suggested that laboratories do not need to report ESBL confirmatory test results of CRE strains [17]. The monitoring results in this study revealed that K. pneumoniae had a resistance rate of 13.6% and 13.9% to imipenem and meropenem, respectively, which as higher than the results of clinical drug resistance monitoring [18]. Among the non-fermenting Gram-negative bacilli, P. aeruginosa had a resistance rate of 18.8% and 16.2% to imipenem and meropenem, respectively, and A. baumannii had a resistance rate of more than 60% to imipenem and meropenem.

CRE strains have brought great difficulties to clinical anti-infective treatment. A previous study reported that the mortality rate of infections caused by CRKP is up to 23-75%, which should be paid more attention [19]. The clinically isolated CRE strains in our hospital were mainly in Neurosurgery Department and ICU, accounting for 36.4% and 14.2%, respectively. Clinical data indicated that [17], the distribution of CRE is slightly different, mainly in ICU and Respiratory Department, especially ICU. CRE in our hospital was mainly distributed in Neurosurgery Department, which may be because of the large number of patients admitted to the Neurosurgery Department of our hospital, and most of them are unconscious, lack of ability to cough with sputum spontaneously, and also have poor resistance, which are prone to infections. CRE is mainly isolated from respiratory tract and urine specimens, consistent with previous reports [20]. In addition, most patients in this ward have more serious underlying diseases and relatively more invasive operations. Therefore, it is essential to strengthen infection prevention and control of relevant departments. Producing carbapenemase is the main resistance mechanism of Enterobacteriaceae to carbapenemase antibacterial drugs, especially KPC-type carbapenemase[21]. Meanwhile, the plasmid containing carbapenemase may carry other drug-resistant genes, resulting in the increase and spread of CRE strains, and the study revealed that the main drug resistance mechanism of CRE is to produce carbapenemase[22]. Tigecycline and polymyxin are considered as most effective drugs for treating CRE infection, but the resistance to both drugs has been reported [23].

Although this study only focuses on the analysis of common pathogens and bacterial resistance in a tertiary hospital in Fuzhou, it is a large city playing a key role in central China. As a crucial transportation center, considerable people worldwide are traveling, studying and working in Fuzhou, so this study is representative and of global importance. Additionally, this study has a large sample size, so the findings can guide the rational use of antibacterialdrugs in clinical practice. Regardless, this study has limitations. The clonal relationship between isolates and resistance genes are not determined, which will be clarified in ongoing studies in our group.

CONCLUSIONS

In conclusion, Gram-negative bacilli are the most common pathogens in our hospital from 2017 to 2020. Considering that pathogens have high drug resistance, it is recommended to strengthen clinical department management and rational application of antibiotics, thus preventing the epidemic of drug-resistant strains and reducing the risk of nosocomial infections.

LIMITATION

This is a single-center study. In-depth multicenter studies should be performed to verify the conclusion of this study.

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CONFLICT OF INTEREST

No potential conflict of interest was reported by the authors.

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Table 1.
Types of strains isolated from submitted specimens.

Distribution of specimen	Number of submission (n)	Composition ratio (%)	Number of positive (n)	Positive composition ratio (%)
Sputum	13189	30.26	2773	44.12
Urine	7628	17.50	1119	17.8
Secretions	4189	9.61	762	12.12
Whole blood	3487	8.00	666	10.6
Draining fluid	3374	7.74	324	5.15
Pus	2589	5.94	149	2.37
Bile	1717	3.94	140	2.23
Ascites	1569	3.6	105	1.67
Others	1491	3.42	98	1.56
Lavage fluid	1177	2.70	47	0.75
Cerebrospinal fluid	1042	2.39	45	0.72
Peritoneal dialysis fluid	963	2.21	28	0.45
Pleural fluid	628	1.44	18	0.28
Dialysate	545	1.25	11	0.18
Total	43588	100	6285	100

Table 2.
Number and composition ratio of main pathogens detected in various specimens in 2020.

Bacteria	Number of strains (strain)	Composition ratio (%)
Gram-positive bacteria	1794	
Staphylococcus aureus	624	9.93
Streptococcus pneumoniae	366	5.82
Enterococcus faecium	196	3.12
Staphylococcus epidermidis	154	2.45
Coagulase-negative Staphylococcus	132	2.10
Enterococcus faecalis	76	1.21
Other positive bacteria	246	3.91
Gram-negative bacteria	4314	
Escherichia coli	1168	18.58
Haemophilus influenzae	758	12.06
Klebsiella pneumoniae	632	10.06
Acinetobacter baumannii	586	9.32
Pseudomonas aeruginosa	574	9.13
Other negative bacteria	596	9.48
Fungi	177	
Candida albicans	88	1.4
Candida tropicalis	48	0.76
Candida glabrata	19	0.3
Other fungi	22	0.35
Total	6285	100

Table 3.
Resistance rates of Staphylococcus to common antibacterial drugs (%).

Antibacterial drug	Staphylococcus aureus (n=624)				Coagulase-negative Staphylococcus (n=132)			
	MSSA(n=419)		MRSA(n=205)		MSCNS(n=28)		MRCNS(n=104)	
	R	S	R	S	R	S	R	S
Linezolid	0.0	100.0	0.0	100.0	0.0	100.0	0.0	100.0
Tetracycline	34.6	65.4	46.9	53.1	24.2	75.8	31.5	68.5
Levofloxacin	6.2	93.8	15.0	85.0	12.5	87.5	30.8	69.2
Ciprofloxacin	19.4	80.6	30.6	69.4	31.0	69.0	46.1	53.9
Clindamycin	24.8	75.2	41.7	58.3	32.5	66.3	68.6	31.4
Erythromycin	57.1	42.9	76.9	23.1	72.8	27.2	92.7	7.3
Nitrofurantoin	0.0	100.0	0.0	100.0	0.0	100.0	0.0	100.0
Moxifloxacin	11.6	88.4	13.9	86.1	12.0	80.0	14.3	85.7
Penicillin G	93.2	6.8	100.0	0.0	78.9	21.1	100.0	0.0
Rifampicin	7.8	92.2	4.0	80.0	0.0	100.0	8.8	91.2
Tigecycline	0.0	100.0	0.0	100.0	0.0	100.0	0.0	100.0
Oxacillin	0.0	100.0	0.0	100.0	0.0	100.0	0.0	100.0
Gentamycin	25.6	74.4	25.8	74.2	0.0	100.0	23.2	76.8
Vancomycin	0.0	100.0	0.0	100.0	0.0	100.0	0.0	100.0
Trimethoprim-sulfamethoxazole	15.3	84.7	23.2	76.8	28.4	71.6	68.9	31.1
Teicoplanin	0.0	100.0	0.0	100.0	0.0	100.0	0.0	100.0

MRSA: Methicillin-resistant Staphylococcus aureus; MSSA: methicillin-sensitive S. aureus; MRCNS: methicillin-resistant coagulase-negative Staphylococcus; MSCNS: methicillin-sensitive coagulase-negative Staphylococcus.

Table 4.
Resistance rates of major streptococci to common antibacterial drugs (%).

	Streptococcus pneumoniae (n=366)		Other streptococci (n=182)	
	R	S	R	S
Erythromycin	89.6	10.4	86.4	10.6
Tetracycline	84.7	15.3	59.3	32.6
Imipenem	0.8	99.2	NA	NA
Amoxicillin	30.6	69.4	NA	NA

Ceftriaxone	11.5	88.5	0	100
Vancomycin	0	100	0	100
Penicillin G	1.4	98.6	0	100
Moxifloxacin	1.1	98.9	NA	NA
Clindamycin	88.5	11.5	82.4	15.2
Chloramphenicol	7.1	92.9	2.2	97.8
Linezolid	0	100	0	100
Meropenem	25.7	74.3	NA	NA
Levofloxacin	1.4	98.6	6	94

Table 5.
Resistance rates of Enterococcus to common antibacterial drugs (%).

	Enterococcus faecium (n=196)		Enterococcus faecalis (n=76)	
	R	S	R	S
Moxifloxacin	82.2	16.3	12.3	81.6
Ciprofloxacin	85.6	14.4	15.8	84.2
Streptomycin	38.4	61.6	4.8	93.4
Erythromycin	91.1	8.9	31.6	68.4
Tetracycline	58.9	41.1	34.2	61.8
Vancomycin	0.0	100.0	0.0	100.0
Clindamycin	100.0	0.0	100.0	0.0
Tigecycline	0.0	100.0	0.0	100.0
Levofloxacin	78.8	21.2	13.7	85.5
Nitrofurantoin	39.7	55.1	0.7	99.3
Linezolid	0.7	99.3	2.7	92.1
Dafopristin/Quinupstin	1.4	98.6	NA	NA
Teicoplanin	0.0	100.0	0.0	100.0
Gentamicin	71.4	28.6	21.2	78.8
Ampicillin	89.7	10.3	2.7	97.3
Penicillin G	91.1	8.9	4.1	95.9

Table 7.
Resistance rates of major Gram-negative bacteria to common antibacterial drugs (%).

	Escherichia coli (n=1168)		Klebsiella pneumoniae (n=632)		Haemophilus influenzae (n=758)	
	R	S	R	S	R	S
Ampicillin	86.3	13.7	NA	NA	78.6	21.4
Polymyxin B	0	100	0	100	100	100
Aztreonam	42.8	57.2	38.3	61.7	NA	NA
Piperacillin-tazobactam	4.2	95.8	20.1	79.9	2.8	97.2
Meropenem	1.2	98.8	13.6	86.4	8.6	91.4
Imipenem	0.6	99.4	13.9	86.1	NA	NA
Cefazolin	69.3	30.7	55.2	44.8	NA	NA
Cefotetan	3.2	96.8	14.2	85.8	NA	NA
Cefoxitin	15.1	84.9	21.4	78.6	NA	NA
Ceftriaxone	61.7	38.3	52.1	47.9	14.2	85.8
Ceftazidime	25.8	74.2	30.7	69.3	NA	NA
Cefepime	20.3	79.7	24.7	75.3	47.5	52.5
Cefoperazone-sulbactam	7.4	92.6	20.6	79.4	NA	NA
Gentamycin	47.2	52.8	25.9	74.1	NA	NA
Tobramycin	20.7	79.3	13.9	86.1	NA	NA
Amikacin	4.9	95.1	9.2	90.8	NA	NA
Ciprofloxacin	54.3	45.7	29.7	68.3	2.8	97.2
Levofloxacin	51.3	48.7	26.7	73.3	0.3	99.7
Nitrofurantoin	5.1	94.9	NA	NA	NA	NA
Tigecycline	2.5	97.5	5.1	94.9	NA	NA

Trimethoprim-sulfamethoxazole	NA	NA	66.3	33.7	NA	NA

Table 8.
Resistance rates of non-fermenting Gram-negative bacteria to common antibacterial drugs (%).

	Pseudomonas aeruginosa (n=586)		**Acinetobacter baumannii (n=674)**	
	R	S	R	S
Piperacillin	22.2	77	NA	NA
Amikacin	1.7	98.3	71.7	28.3
Gentamycin	8.9	91.1	73.6	26.4
Piperacillin-tazobactam	12.3	87.7	74.2	23.6
Cefoperazone-sulbactam	19.1	80.4	68.8	31.2
Cefepime	8.9	91.1	73.6	26.4
Ampicillin-sulbactam sodium	NA	NA	73.9	26.1
Aztreonam	31.6	68.4	NA	NA
Imipenem	18.8	81.2	74.6	25.4
Meropenem	16.2	83.4	74.6	25.4
Ciprofloxacin	18.1	81.9	75.1	24.7
Levofloxacin	20.5	79.5	74.9	25.1
Trimethoprim-sulfamethoxazole	NA	NA	64.2	35.8
Polymyxin B	0	100	0	100
Tigecycline	NA	NA	4.3	95.7
Minocycline	NA	NA	14.4	85.6

Table 9.
Resistance and sensitivity rates of carbapenem antibiotic-resistant strains to various antibacterial drugs (%).

	CRKP (n=22)		**CRPAE (n=235)**		**CRAB (n=512)**	
	R	S	R	S	R	S
Ampicillin-sulbactam	100.0	0.0	NA	NA	95.1	4.9
Piperacillin-tazobactam	100.0	0.0	43.8	56.2	97.1	2.9
Cefazolin	100.0	0.0	NA	NA	NA	NA
Imipenem	100.0	0.0	97	3	97.1	2.9
Meropenem	90.9	9.1	79.6	20.4	96.3	3.7
Cefepime	100.0	0.0	37.9	62.1	95.1	4.9
Ceftazidime	100.0	0.0	34.9	65.1	97.1	2.9
Ceftriaxone	100.0	0.0	NA	NA	97.1	2.9
Amikacin	59.1	40.9	1.7	98.3	92.4	7.6
Gentamycin	86.4	13.6	26.4	73.6	95.1	4.9
Ciprofloxacin	86.4	13.6	47.7	52.3	97.1	2.9
Levofloxacin	86.4	13.6	57	43	97.1	2.9
Minocycline	18.2	81.8	NA	NA	17.8	82.2
Tigecycline	0.0	100.0	NA	NA	5.5	90
Polymyxin B	0.0	100.0	0.0	100.0	0.0	100.0
Cefoperazone-sulbactam	100.0	0.0	59.1	40.9	88.1	11.9
Trimethoprim-sulfamethoxazole	31.8	68.2	NA	NA	81.6	18.4
Aztreonam	68.2	31.8	50.6	49.4	NA	NA

CRKP: Carbapenem-resistant *Klebsiella pneumoniae*; CRAB: carbapenem-resistant *Acinetobacter baumannii*; CRPA: carbapenem-resistant *Pseudomonas aeruginosa*; NA: not available.