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Brief Original Article

Dissemination of extensively drug-resistant and KPC-2 producing *Klebsiella pneumoniae* isolated from bloodstream infections

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Abstract

Introduction: Bloodstream infections (BSIs) are serious diseases associated with high mortality, especially when caused by extensively drug-resistant (XDR) *Klebsiella pneumoniae.* The prevalence and pandemic strains of extended-spectrum beta-lactamase (ESBL)-producing *K. pneumoniae* isolated from blood cultures of patients with BSIs were determined at Sir Run Run Shaw Hospital, China.

Methodology: A total of 24 XDR *K. pneumoniae* were isolated from blood cultures, and the clinical data of the patients were analyzed retrospectively. Bacterial species identification and antimicrobial susceptibility testing were performed using VITEK2 and E-test methods, respectively. Common ESBL-resistant genes were amplified and sequenced after the validation of a modified Hodge test. Strain homology was also analyzed by pulsed-field gel electrophoresis (PFGE).

Results: All of the isolates were resistant to 10 antimicrobial agents. Several strains showed partial sensitivity to aminoglycosides, but all showed sensitivity to polymyxin and tigecycline. All strains were *Klebsiella pneumoniae* carbapenemase (KPC-2) producing, and carried two or three ESBL-resistant genes, which belonged to 13 PFGE clones (A–M). The overall mortality rate in patients was as high as 29.2%.

Conclusions: KPC-2-producing *K. pneumoniae* BSIs are associated with high mortality rates. Our observations suggest that KPC-2 and ESBL-producing *K. pneumoniae* might be responsible for the clonal dissemination of extensively drug-resistant isolates in our hospital.

Key words: bloodstream infection; extensively drug-resistant; *Klebsiella pneumoniae*; ESBLs; clonal dissemination.

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Introduction

Bloodstream infections (BSIs) caused by *Klebsiella pneumoniae* carbapenemases (KPC)-producing *K. pneumoniae* are associated with high mortality rates. [1]. The isolation rate of resistant bacteria in BSIs has increased significantly with the rampant use of beta-lactams and aminoglycoside antibiotics, as well as the development of more invasive procedures and treatments [2]. The Chinese Ministry of Health National Antimicrobial Resistance Investigation Net annual reports of 2010 and 2011 estimated that the isolation rate of *K. pneumoniae*, which has become one of the most common pathogenic bacteria in BSIs, was 7.7% and 8.3%, respectively [3,4]. In this study, a total of 252 *K. pneumoniae* isolates were recovered from the blood of patients at Sir Run Run Shaw Hospital, a tertiary hospital, over the past two years; of the isolates, 24 were extensively drug-resistant strains. We investigated the prevalent characteristics of extensively drug-resistant (XDR) *K. pneumoniae* isolates in BSIs, which were resistant to almost all 15 antimicrobial agents tested. We also tested the β-lactamase genotypes, examined the clonal relatedness of the strains, and analyzed the clinical data of patients to provide evidence for nosocomial infection.

Methodology

Bacterial strains

From August 2010 to December 2012, clinical non-duplicate, consecutive *K. pneumoniae* isolates were recovered from BSIs of inpatients at Sir Run Run Shaw Hospital, School of Medicine, Zhejiang University. Bacterial species identification was performed using the VITEK2 system (BioMérieux, Marcy l'Etoile, France), and the identified XDR strains were included in this analysis [5]. The clinical data of these patients were also collected and analyzed.

Instruments and reagents

Both the VITEK2 system and the E-test method (AB bioMérieux, Solna, Sweden) were used to investigate the antimicrobial susceptibility profile.

CHEF pulsed field gel electrophoresis (PFGE), polymerase chain reaction (PCR), and gel image analysis systems were applied (all from Bio-Rad, Hercules, USA). A PCR amplification kit and the endonucleases *Apa*I and *Xba*I (TAKARA Bio Inc., Kusatsu, Japan,) were used to amplify common β-lactamase genes for the modified Hodge test (MHT)-positive strains.

Susceptibility test

The minimum inhibitory concentrations (MICs) of ceftazidime (CAZ), cefepime (FEP), cefotetan (CTT), aztreonam (ATM), ampicillin/sulbactam (SAM), piperacillin/tazobactam (TZP), ertapenem (ETP), imipenem (IPM), gentamycin (GEN), tobramycin (TOB), amikacin (AMK), and levofloxacin hydrochloride (LVX) were determined with an automated microbiology analyzer (VITEK2). The MICs of polymyxin (CST), tigecycline (TGC), and meropenem (MEM) were determined using the E-test. Quality control strains for the susceptibility test included *E. coli* ATCC 25922, following the Clinical and Laboratory Standards Institute (CLSI)'s 2013 guidelines. A modified Hodge test (MHT) was performed to detect carbapenemases in accordance with the guidelines recommended by CLSI 2013.

PCR amplification of β-lactamase and DNA sequencing

PCR amplification of common β-lactamase genes was performed for MHT-positive strains. The amplified genes included bla_{KPC}, bla_{IPM}, bla_{VIM}, bla_{SPM-1}, bla_{GIM}, bla_{SIM-1}, bla_{NDM-1}, bla_{OXA-48}, bla_{TEM}, bla_{SHV}, bla_{CTX-M} ($bla_{CTX-M-1}$, $bla_{CTX-M-2}$, $bla_{CTX-M-8}$, $bla_{CTX-M-9}$), bla_{DHA}, bla_{MIR}, bla_{ACC}, and bla_{CIT}. Bacterial DNA template was extracted by the boiling method according to the previously reported protocol [6]. PCR reactions were designed as follows: pre-denaturation at 94°C for 5 minutes, followed by 35 cycles of denaturation at 95°C for 1 minute, annealing at 55°C for 30 seconds, and extension at 72°C for 40 seconds. PCR products were confirmed by 1% agarose gel electrophoresis, and images were acquired under a UV lamp. Positive PCR products were sent to Bo Shang Biotechnology Co. for DNA sequencing. The sequence analyses were performed using the BLAST program available on the National Center for Biotechnology Information server (http://blast.ncbi.nlm.nih.gov/).

Pulsed-field gel electrophoresis (PFGE)

The clonal relatedness of the isolates was determined with PFGE, as described previously [6]. A suspension of 0.5 McFarland bacteria was embedded in agarose and digested with XbaI for 4 hours at 37°C in advance. PFGE conditions were as follows: 6 V/cm^2 for 22 hours, with an initial pulse time of 5 seconds and a final pulse time of 25 seconds. PFGE patterns were read according to criteria defined by Tenover *et al*. [7] as follows: indistinguishable, variation in 1–3 bands; closely related, variation in 4–6 bands; and unrelated, variation in 7 or more bands. The phylogenetic tree was constructed by BioNumerics software version 7.0.

Results

Demographic and clinical characteristics of the patients

In total, 24 XDR *K. pneumoniae* isolates associated with BSIs were isolated from the following departments: intensive care unit (ICU) (n = 11), hematology (n = 4), gastroenterology (n = 3), infectious diseases (n = 1), general surgery (n = 3), and urology (n = 2). Nineteen patients were male, and five were female. Patients' ages ranged from 30 to 84 years (mean age, 61.3 ± 14.2 years), and 16 patients were 60 years of age or older. A total of 4 patients were diagnosed with malignant tumors; 4 with leukemia or other blood diseases; 8 with cholecystitis and other diseases of the digestive system; 2 were cases of trauma; and 6 had hypertension, diabetes, or other chronic diseases. A total of 19 patients received catheter intervention, and 24 patients received beta-lactamase antibiotics before the isolation of *K. pneumoniae*. Fourteen days after being infected, 17 patients were alive and 7 had died; the mortality rate was 29.2%. The clinical and demographic information of the patients are listed in Table 1.

Antimicrobial susceptibility results

Antimicrobial susceptibility tests for 15 antibiotics showed that all of the isolates were resistant to penicillin, cephalosporins, penicillin or penicillin enzyme inhibitors, aztreonam, and fluoroquinolones. Three strains were susceptible to aminoglycoside antibiotics, tobramycin, and amikacin. All 24 isolates were sensitive to polymyxin and tigecycline, and the results are listed in Table 2. The MICs were interpreted according to the 2013 CLSI guidelines.

PCR amplification of β-lactamase and DNA sequencing

MHTs were positive for all strains. PCR demonstrated a high prevalence of β-lactamase genes. The sequencing results were compared with the GenBank database, and the corresponding genotypes were $bla_{\text{KPC-2}}$, $bla_{\text{TEM-1}}$, $bla_{\text{SHV-11}}$, $bla_{\text{SHV-12}}$, $bla_{\text{CTX-M-3}}$, $bla_{\text{CTX-M-16}}$, $bla_{\text{CTX-M-24}}$, and $bla_{\text{DHA-1}}$. The results of drug-resistance gene amplification are shown in Figure 1. Both of the $bla_{\text{KPC-2}}$ and $bla_{\text{TEM-1}}$ genes were identified in all the 24 strains. Twenty-one carried bla_{SHV}, 17 of which carried $bla_{\text{SHV-11}}$, and 4 of which carried $bla_{\text{SHV-12}}$. Twenty-two strains carried $bla_{\text{CTX-M}}$, 15 of which carried $bla_{\text{CTX-M-24}}$, 4 of which carried $bla_{\text{CTX-M-3}}$, and 3 of which carried $bla_{\text{CTX-M-16}}$. All of the strains co-carried two or three ESBL-resistant genes. Nine strains co-carried $bla_{\text{TEM-1}}$, $bla_{\text{SHV-11}}$ and $bla_{\text{CTX-M-24}}$. Four strains co-carried $bla_{\text{TEM-1}}$, $bla_{\text{SHV-12}}$, and $bla_{\text{CTX-M-24}}$. Three strains co-carried $bla_{\text{TEM-1}}$ and $bla_{\text{SHV-11}}$. Two strains co-carried $bla_{\text{TEM-1}}$, $bla_{\text{CTX-M-3}}$, and $bla_{\text{CTX-M-16}}$. In addition, three strains carried the *Amp*C gene ($bla_{\text{DHA-1}}$). The bla_{IPM}, bla_{VIM}, $bla_{\text{SPM-1}}$, bla_{GIM}, $bla_{\text{SIM-1}}$, $bla_{\text{NDM-1}}$, $bla_{\text{OXA-48}}$, bla_{ACC}, and bla_{CIT} gene tests were negative in all strains.

Figure 1. PFGE analysis and β-lactamase genes of the 24 *K. pneumoniae* strains of bloodstream infections

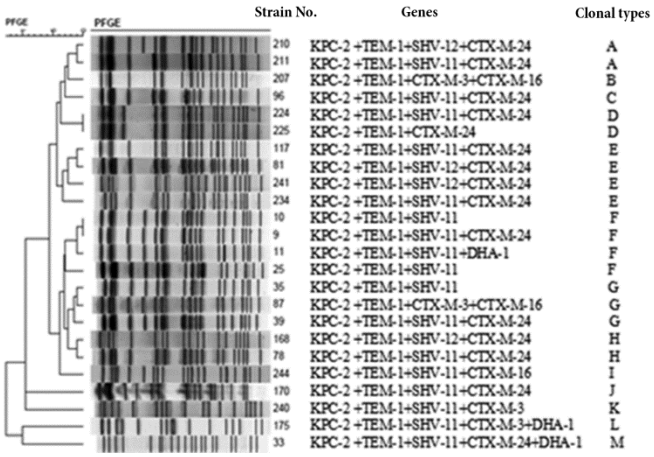

Table 1. Demographic and clinical characteristics of the 24 patients with extensively drug-resistant *K. pneumoniae* strains of bloodstream infections

Strain No.	Date	Department	Sex	Age	Clinical diagnosis	Alive or dead on day 14	History of stay in ICU	History of catheter treatment
9	2010-08-20	Urology	Male	79	Postoperative colorectal cancer, hypertension	Alive	No	No
10	2010-08-30	Urology	Female	53	Polycystic kidney, hypertension, diabetes	Alive	Yes	Left double-J catheter
11	2010-08-25	Hematology	Male	46	Acute leukemia	Alive	No	PICC
25	2010-11-14	Hematology	Male	47	Acute leukemia	Dead	No	Subclavian catheter
33	2010-12-07	ICU	Male	30	Multiple trauma of brain injury	Alive	Yes	Subclavian catheter
35	2010-12-12	ICU	Male	73	Coronary bypass, hypertension, diabetes	Alive	Yes	PICC
39	2010-12-30	Hematology	Male	54	Acute leukemia, hypertension	Dead	Yes	PICC
78	2011-06-07	ICU	Male	75	Left adrenal tumor	Alive	Yes	Intravenous catheter
81	2011-06-18	ICU	Male	67	Esophageal cancer	Dead	Yes	Abdominal drain
87	2012-07-22	ICU	Female	33	Hemolytic anemia	Dead	Yes	Intravenous catheter
96	2011-11-12	ICU	Male	74	Acute pancreatitis	Alive	Yes	Intravenous catheter
117	2012-02-02	ICU	Male	65	COPD, diabetes, hypertension	Alive	Yes	Intravenous catheter
168	2012-02-06	Gastroenterology	Female	80	Acute cholecystitis	Alive	No	No
170	2012-02-11	ICU	Male	74	Arteriosclerotic obliteration	Alive	Yes	Jugular vein catheter
175	2012-04-04	ICU	Male	84	Arterial embolism	Dead	Yes	Intravenous catheter
207	2012-11-21	Infectious disease	Male	52	Calculus of bile duct	Alive	No	T-tube drain
210	2012-05-04	ICU	Male	60	Septic shock, hypertension, diabetes	Dead	Yes	Femoral vein blood dialysis tube
211	2012-05-08	General surgery	Female	40	Liver tumor	Alive	No	Intravenous catheter
224	2012-05-26	General surgery	Male	68	Carcinoma of ampulla	Alive	No	No
225	2012-06-03	Gastroenterology	Female	62	Obstructive jaundice	Alive	No	No
234	2012-06-09	General surgery	Male	61	Cholecystitis	Alive	No	Intravenous catheter
240	2012-06-12	ICU	Male	64	Lung contusion	Alive	Yes	Intravenous catheter
241	2012-07-22	Gastroenterology	Male	66	Acute pancreatitis, hypertension	Alive	No	No
244	2012-11-21	Hematology	Male	64	Malignant lymphoma	Dead	Yes	Intravenous catheter

ICU: intensive care unit; PICC: peripherauy inserted central catheter; COPD: chronic obstructive pulmonary disease

Pulsed-field gel electrophoresis (PFGE)

The 24 isolates belonged to 13 PFGE clones (A–M): A clone (n = 2), B clone (n = 1), C clone (n = 1), D clone (n = 2), E clone (n = 4), F clone (n = 4), G clone (n = 3), H clone (n = 2), I clone (n = 1), J clone (n = 1), K clone (n = 1), and L clone (n = 1). The distribution according to department was as follows: ICU, 9 clones for 11 strains; gastroenterology, 3 clones for 3 strains; hematology, 3 clones for 4 strains; general surgery, 3 clones for 3 strains; urology, 1 clone for 2 strains; and infectious disease, 1 clone for 1 strain. The β-lactamase genotypes of the same clone were almost the same. PFGE clones and department distribution are shown in Figure 1.

Discussion

Previous studies have indicated that long-term use of catheters is the main cause of BSIs, and that the frequent use of antibiotics such as carbapenems is one of the main risk factors associated with antimicrobial resistance acquisition in *K. pneumoniae* [8]. The retrospective analysis in our study showed that among 24 cases, 9 cases had malignant disease; 6 cases had digestive disease; 7 cases had hypertension, diabetes and various types of chronic disease; and only 2 cases were of traumatic injury. Before the isolation of XDR *K. pneumoniae*, most of the patients had been exposed to invasive procedures, and all of the patients had received β-lactamase antibiotics. The elderly accounted for the majority of our patients, most of whom had chronic diseases. It is reasonable to postulate that due to their weakened immune systems, exposure to antimicrobial therapy, and invasive devices, these patients are likely to have significantly different risk factors compared to normal patients [8,9]. With these confounding variables, patients infected with multi-drug resistant bacteria also have an increased mortality risk [10]. The 14-day mortality for patients with drug-resistant *K. pneumoniae* BSIs has been reported to be up to 41.7% [11]. The overall mortality in our patients was high (29.2%), similar to that observed in other studies [10,11].

Carbapenems have been widely utilized as the treatment of choice for serious infections caused by

Table 2. Antimicrobial susceptibility profiles of the 24 extensively drug-resistant *K. pneumoniae* strains of bloodstream infections

Strain No.	MIC (μg/mL)*														
	CAZ	FEP	CTT	ATM	SAM	TZP	ETP	IPM	MEM	GEN	TOB	AMK	LVX	TGC	CST
9	≥ 64	≥ 64	≥ 64	≥ 64	≥ 32	≥ 128	≥ 8	≥ 16	≥ 16	≥ 16	≥ 16	≥ 64	≥ 8	2	0.38
10	≥ 64	≥ 64	≥ 64	≥ 64	≥ 32	≥ 128	≥ 8	≥ 16	≥ 16	≥ 16	≥ 16	≥ 64	≥ 8	0.19	0.25
11	≥ 64	≥ 64	≥ 64	≥ 64	≥ 32	≥ 128	≥ 8	≥ 16	≥ 16	≥ 16	≥ 16	≥ 64	≥ 8	2	0.38
25	≥ 64	≥ 64	≥ 64	≥ 64	≥ 32	≥ 128	≥ 8	≥ 16	≥ 16	1	≤ 4	≤ 2	≥ 8	0.5	0.25
33	≥ 64	≥ 64	≥ 64	≥ 64	≥ 32	≥ 128	≥ 8	≥ 16	≥ 16	≥ 16	≤ 4	≤ 2	≥ 8	1	0.19
35	≥ 64	≥ 64	≥ 64	≥ 64	≥ 32	≥ 128	≥ 8	≥ 16	≥ 16	≥ 16	≥ 16	≥ 64	≥ 8	1	0.38
39	≥ 64	≥ 64	≥ 64	≥ 64	≥ 32	≥ 128	≥ 8	≥ 16	≥ 16	≥ 16	≥ 16	≥ 64	≥ 8	1	0.75
78	≥ 64	≥ 64	≥ 64	≥ 64	≥ 32	≥ 128	≥ 8	≥ 16	≥ 16	≥ 16	≥ 16	≥ 64	≥ 8	2	0.38
81	≥ 64	≥ 64	≥ 64	≥ 64	≥ 32	≥ 128	≥ 8	≥ 16	≥ 16	≥ 16	≥ 16	≥ 64	≥ 8	0.75	0.25
87	32	≥ 64	≥ 64	≥ 64	≥ 32	≥ 128	≥ 8	≥ 16	≥ 16	≥ 16	≥ 16	≥ 64	≥ 8	1.5	0.25
96	≥ 64	≥ 64	≥ 64	≥ 64	≥ 32	≥ 128	≥ 8	≥ 16	≥ 16	≥ 16	≥ 16	≥ 64	≥ 8	0.19	0.19
117	≥ 64	≥ 64	≥ 64	≥ 64	≥ 32	≥ 128	≥ 8	≥ 16	≥ 16	≥ 16	≥ 16	≥ 64	≥ 8	1	0.38
168	32	≥ 64	≥ 64	≥ 64	≥ 32	≥ 128	≥ 8	≥ 16	≥ 16	≥ 16	≥ 16	≥ 64	≥ 8	0.75	2
170	≥ 64	≥ 64	≥ 64	≥ 64	≥ 32	≥ 128	≥ 8	≥ 16	≥ 16	≥ 16	≥ 16	≤ 2	≥ 8	1.5	0.38
175	≥ 64	≥ 64	≥ 64	≥ 64	≥ 32	≥ 128	≥ 8	≥ 16	≥ 16	≥ 16	≥ 16	≥ 64	≥ 8	0.75	0.125
207	32	≥ 64	≥ 64	≥ 64	≥ 32	≥ 128	≥ 8	≥ 16	≥ 16	≥ 16	≥ 16	≥ 64	≥ 8	0.5	0.38
210	≥ 64	≥ 64	≥ 64	≥ 64	≥ 32	≥ 128	≥ 8	≥ 16	≥ 16	≥ 16	≥ 16	≥ 64	≥ 8	1.5	0.38
211	32	≥ 64	≥ 64	≥ 64	≥ 32	≥ 128	≥ 8	≥ 16	≥ 16	≥ 16	≥ 16	≥ 64	≥ 8	0.5	0.38
224	≥ 64	≥ 64	≥ 64	≥ 64	≥ 32	≥ 128	≥ 8	≥ 16	≥ 16	≥ 16	≥ 16	≥ 64	≥ 8	0.75	0.125
225	≥ 64	≥ 64	≥ 64	≥ 64	≥ 32	≥ 128	≥ 8	≥ 16	≥ 16	≥ 16	≥ 16	≥ 64	≥ 8	0.75	0.125
234	≥ 64	≥ 64	≥ 64	≥ 64	≥ 32	≥ 128	≥ 8	≥ 16	≥ 16	≥ 16	≥ 16	≥ 64	≥ 8	0.38	0.38
240	32	≥ 64	32	≥ 64	≥ 32	≥ 128	≥ 8	8	4	≤ 1	≤ 4	≤ 2	≥ 8	1	0.25
241	≥ 64	≥ 64	≥ 64	≥ 64	≥ 32	≥ 128	≥ 8	≥ 16	≥ 16	≥ 16	≥ 16	≥ 64	≥ 8	0.75	0.25
244	≥ 64	≥ 64	≥ 64	≥ 64	≥ 32	≥ 128	≥ 8	≥ 16	≥ 16	≥ 16	≤ 4	≤ 2	≥ 8	1.5	0.19

CAZ: ceftazidime; FEP: cefepime; CTT: cefotetan; ATM: aztreonam; SAM: ampicillin/sulbactam; TZP: piperacillin/tazobactam; ETP: ertapenem; IPM: imipenem; MEM: meropenem; GEN: gentamycin; TOB: tobramycin; AMK: amikacin; LVX: levofloxacin hydrochloride; TGC: tigecycline; CST: polymyxin; *MICs were interpreted according to the CLSI 2013 guidelines

ESBL producers, exerting selection pressure for carbapenem resistance acquisition [5]. Carbapenem-resistant *K. pneumoniae*, especially KPC-2-producing isolates, have been therefore disseminated globally and pose remarkable clinical and therapeutic challenges [12]. The increasing prevalence of severe infections with high mortality rates underlines the need for effective treatment. In our study, antimicrobial susceptibility tests showed that all of the 24 KPC-2 positive isolates were extensively drug-resistant and completely resistant to penicillin, cephalosporins, penicillin/penicillin enzyme inhibitors, aztreonam, and fluoroquinolones. These strains were highly resistant to carbapenems, but only susceptible to polymyxin and tigecycline, which have been ultimately considered as the last-resort treatment for such infections. Previous research demonstrated that antimicrobial-resistant *K. pneumoniae* isolates could carry multiple resistance genes simultaneously [13,14]. In our study, a high prevalence of β-lactamase genes was observed. All of the strains carried $bla_{\text{TEM-1}}$, 21 carried $bla_{\text{SHV-11}}$ or $bla_{\text{SHV-12}}$, and 21 carried $bla_{\text{CTX-M}}$. Among $bla_{\text{CTX-M}}$ carriers, 15 strains carried $bla_{\text{CTX-M-24}}$, indicating that $bla_{\text{CTX-M-24}}$ was the major epidemic type of $bla_{\text{CTX-M}}$, and 3 strains carried $bla_{\text{DHA-1}}$. All of the strains carried multiple resistance determinants in various combinations, especially the combination of $bla_{\text{TEM-1}}$, $bla_{\text{SHV-11}}$, and $bla_{\text{CTX-M-24}}$. According to previous studies both in China and the United States of America (USA), the most commonly identified $bla_{\text{CTX-M}}$ type was $bla_{\text{CTX-M-15}}$ in *K. pneumoniae* [15,16]. However, this study reports, for the first time, that in our hospital, $bla_{\text{CTX-M-24}}$ is the major type of $bla_{\text{CTX-M}}$ and should be monitored with care.

PFGE analysis showed that 24 XDR *K. pneumoniae* BSIs in our hospital had 13 clonal clusters (A–M). Eleven isolates in the ICU were from 9 clusters; only 2 strains were type E, 2 were type G, and the remaining 7 strains had different spectral types. Moreover, J, K, L, and M types appeared only in the ICU, and the other 5 types were detected in other departments. This distribution could be primarily due to the high frequency of transfer of critically ill patients in the ICU ward. Patients are transferred to the ICU when they are critically ill, and they are transferred back to their designated ward when they are in stable condition. Therefore, the ICU has become an important route of transmission by which bacterial strains are embedded and then disseminated to other patients. Strains are then carried to other departments with the patients as they recover and leave, or as they are transferred between units for specialized procedures or treatment. In our study, the clonal spread existed not only between the ICU and other departments, but also among other departments. For example, strain No. 224 was isolated from a patient with ampullary carcinoma in the department of general surgery, and strain No. 225 was collected from a patient with obstructive jaundice in the gastroenterology department. Patient No. 224 had an endoscopic retrograde cholangiopancreatography (ERCP), and patient No. 225 also received the same procedure. Interestingly, D clonal type XDR *K. pneumoniae* could also have been isolated from both departments. Thus, it is reasonable to speculate that the use of medical devices is another risk factor that causes XDR *K. pneumoniae* transmission among different departments. Therefore, we concluded that simultaneous sporadic and clonal dissemination were responsible for the wide distribution of XDR *K. pneumoniae* isolated in multiple departments of our hospital.

Conclusions

It is evident that most of the BSI patients with XDR *K. pneumoniae* had malignant and chronic diseases with high mortality. The XDR *K. pneumoniae* isolates harbouring $bla_{\text{KPC-2}}$ also carried several ESBL-resistant genes, and the strain spread between the ICU and other departments in both was both sporadic and clonal. Screening and surveillance of XDR *K. pneumoniae* is urgently needed in our hospital to control and prevent the further spread of these resistance genes and resistant organisms.

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