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ORIGINAL ARTICLE

Clinical and microbiological characteristics of peritoneal dialysis-related peritonitis caused by *Klebsiella pneumoniae* in southern Taiwan

Wei-Hung Lin [a,b], Chin-Chung Tseng [a], An-Bang Wu [a], Deng-Chi Yang [a], Shian-Wen Cheng [c], Ming-Cheng Wang [a,d,], Jiunn-Jong Wu [b,c,e,*]**

[a] *Department of Internal Medicine, National Cheng Kung University Hospital, Tainan, Taiwan*
[b] *Institute of Clinical Medicine, College of Medicine, National Cheng Kung University, Tainan, Taiwan*
[c] *Department of Medical Laboratory Science and Biotechnology, College of Medicine, National Cheng Kung University, Tainan, Taiwan*
[d] *Institute of Clinical Pharmacy and Pharmaceutical Sciences, College of Medicine, National Cheng Kung University, Tainan, Taiwan*
[e] *Center of Infectious Disease and Signaling Research, National Cheng Kung University, Tainan, Taiwan*

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Background/Purpose(s): Gram-negative peritonitis is a frequent and serious complication of peritoneal dialysis (PD). No previous reports have focused on *Klebsiella pneumoniae* infection. The aim of this study was to investigate the host and bacterial factors associated with *K. pneumoniae* PD-related peritonitis.
Methods: We retrospectively studied *K. pneumoniae* PD-peritonitis cases treated at a university hospital in southern Taiwan during 1990–2011, and analyzed the clinical features and outcomes and bacterial characteristics of serotypes, hypermucoviscosity (HV), and virulence-associated genes such as *wabG*, *uge*, and *rmpA* in *K. pneumoniae* PD-related peritonitis. Fifty-four isolates of *K. pneumoniae*-related community-acquired urinary tract infection (UTI) and 76 morphologically different nonpathogenic *K. pneumoniae* isolates from healthy adults were used as controls.

* Corresponding author. Department of Medical Laboratory Science and Biotechnology, Infectious Disease and Signaling Research Center, College of Medicine, National Cheng Kung University, Number 1 University Road, Tainan 70101, Taiwan.
** Corresponding author. Division of Nephrology, Department of Internal Medicine, National Cheng Kung University Hospital, 138 Sheng-Li Road, 70428 Tainan, Taiwan.
E-mail addresses: wangmc@mail.ncku.edu.tw (M.-C. Wang), jjwu@mail.ncku.edu.tw (J.-J. Wu).

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Results: *K. pneumoniae* was the second most common monomicrobial pathogen causing Gram-negative PD-related peritonitis ($n = 13$, 2.7%), and the most common pathogen involved in polymicrobial peritonitis (16/43, 37.2%) and associated with high catheter removal rate (7/16, 43.8%). Compared with *Escherichia coli* peritonitis cases, patients with monomicrobial *K. pneumoniae* peritonitis also had insignificantly higher incidence of sepsis/bacteremia [$n = 5$ (38%), $p = 0.11$] and a higher mortality rate [$n = 3$ (23%), $p = 0.36$]. The prevalence of K1/K2 ($n = 1$, 7.7%) serotypes was low, but there was a higher prevalence of serotype K20 ($n = 3$, 23.1%) in *K. pneumoniae* isolates derived from monomicrobial PD-related peritonitis compared with control groups. HV phenotype ($p < 0.001$) and *rmpA* genotype ($p = 0.007$) were absent in the peritonitis group.

Conclusion: This is the first study focused on clinical and microbiological characteristics of *K. pneumoniae* PD-related peritonitis. *K. pneumoniae* was a common Gram-negative pathogen causing monomicrobial and polymicrobial PD-related peritonitis in southern Taiwan. The bacterial characteristics with low percentage of capsular serotype K1/K2, no significant HV, and absence of *rmpA* suggest a different pathogenesis in *K. pneumoniae* PD-related peritonitis compared with that in UTI and liver abscess.

Introduction

Peritonitis is the most important cause of treatment failure in peritoneal dialysis (PD) patients.[1] The incidence of PD-related peritonitis has decreased markedly during the past decades because of advances in connection technique and *Staphylococcus* decolonization protocols.[2,3–5] These improvements have primarily had an effect on the incidence of Gram-positive peritonitis, so that the proportion of Gram-negative peritonitis has consequently increased.[2,3,6] However, the morbidity and outcomes of PD-related peritonitis caused by different organisms are not the same. Peritonitis caused by *Pseudomonas aeruginosa* and fungi is associated with increased catheter loss and transfer to hemodialysis.[7–10] Peritonitis caused by *Staphylococcus epidermidis* has a higher resolution rate than peritonitis caused by other pathogens.[11–13]

In the community setting, *Klebsiella pneumoniae* is a potential pathogen with various clinical manifestations, including septicemia, pneumonia, urinary tract infection (UTI), meningitis, and purulent abscesses at various sites. In particular, a distinctive clinical syndrome characterized by community-acquired *K. pneumoniae* bacteremia with primary liver abscess, metastatic meningitis, and endophthalmitis has been recognized in Taiwan.[14,15] Thus far, research on monomicrobial *K. pneumoniae* PD-related peritonitis or polymicrobial infection involving *K. pneumoniae* has been extremely limited.[2,7,16–19] Although a number of virulence factors have been identified in invasive strains of *K. pneumoniae*, including hypermucoviscosity (HV), capsular serotypes including K1, K2, K5, K20, K54, and K57[20–23] and virulence-associated genes such as *wabG*, *uge*, and *rmpA*,[24–28] it is not clear how these genes and phenotypes are associated with PD-related peritonitis.

The aim of this study was to investigate the microbiological characteristics and host factors in *K. pneumoniae* PD-related peritonitis. We also describe the changes in the distribution of causative organisms in PD-related peritonitis during a 22-year period in a university hospital in southern Taiwan.

Materials and methods

Diagnostic criteria, patient selection, and bacterial identification

From January 1990 to December 2011, all episodes of PD-related peritonitis in the renal unit of National Cheng Kung University Hospital, Tainan, Taiwan were collected and reviewed. A total of 479 episodes of PD-related peritonitis were identified. A diagnosis of PD-related peritonitis was based on at least two of the following criteria: (1) abdominal pain or cloudy peritoneal dialysis effluent (PDE); (2) leukocytosis in PDE (white blood cells $>100/\mu L$ with at least 50% polymorphonuclear neutrophils); and (3) positive Gram stain or culture from PDE. In our study, the monomicrobial *K. pneumoniae* peritonitis was demonstrated by isolation of single bacteria from ascites culture. The polymicrobial *K. pneumoniae* peritonitis was demonstrated by isolation of more than two pathogens, including *K. pneumoniae*, from ascites culture. Episodes with peritoneal eosinophilia but with a negative bacterial culture were excluded. *K. pneumoniae* isolates were collected from PDE samples of the 13 patients with monomicrobial *K. pneumoniae* peritonitis. Twenty-eight isolates of the 54 *E. coli* strains in monomicrobial peritonitis had been collected for future analysis (26 isolates were missed).

Bacterial culture of PDE was performed according to the recommendations of the International Society of Peritoneal Dialysis (ISPD).[29] All strains were stored at $-80^{\circ}C$ before use.

Medical records of identified patients were reviewed. Demographic data and information related to the underlying diseases, infection acquisition sites, clinical manifestations, and outcomes were collected.

Fifty-four isolates of *K. pneumoniae*-related community-acquired UTI from our previous study[18] and 76 morphologically different nonpathogenic *K. pneumoniae* isolates from 60 healthy adults collected from stool culture were used as controls. This study protocol has been approved by the Institutional Review Board of National Cheng Kung University Hospital, Tainan, Taiwan.

Modified string test for hypermucoviscosity

The string test was used to evaluate the HV phenotype.[15,22] The bacterial strains were inoculated on 5% sheep blood agar plates and incubated at 37°C overnight. Colonies were touched with a loop. The loop was then lifted vertically from the surface of the agar plate. The formation of a viscous string of at least 10 mm in length was considered as a positive modified string test.

Detection of hypermucoviscosity-associated loci, other virulence genes, and capsular polysaccharides genotyping

Genomic DNA of *K. pneumoniae* was extracted and polymerase chain reaction (PCR) was performed to amplify the *rmpA*, *magA* (serotype K1), *uge*, and *wabG* genes, as previously described.[22] Specific primers used to detect the target gene sequences are shown in Table 1.[16,19–21] The first strain in which DNA sequencing of the PCR product showed a sequence identical to the published sequence was selected as a positive control strain for the subsequent PCR experiments. One clinical isolate of *E. coli* was selected as the negative control.

Primers and PCR conditions for detection of K1, K2, K5, K20, K54, and K57 serotypes have been described previously.[22,23] Reference strains of serotypes K1, K2, K5, K20, K54, and K57 were kindly provided by Dr Jin-Town Wang, National Taiwan University, Taipei, Taiwan, and served as positive controls.

Table 1 Primers used in this study

Target gene	Primer	Ref
magA (K1)		
Forward	5′-GGTGCTCTTTACATCATTGC-3′	16
Reverse	5′-GCAATGGCCATTTGCGTTAG-3′	
rmpA		
Forward	5′-ACTGGGCTACCTCTGCTTCA-3′	19
Reverse	5′-CTTGCATGAGCCATCTTTCA-3′	
wabG		
Forward	5′-ACCATCGGCCATTTGATAGA-3′	20
Reverse	5′-CGGACTGGCAGATCCATATC-3′	
uge		
Forward	5′-TCTTCACGCCTTCCTTCACT-3′	21
Reverse	5′-GATCATCCGGTCTCCCTGTA-3′	
K1		
wzx_K1-F	5′-GTAGGTATTGCAAGCCATGC-3′	19
wzx_K1-R	5′-GCCCAGGTTAATGAATCCGT-3′	
K2		
wzx_K2-F	5′-GGAGCCATTTGAATTCGGTG-3′	19
wzx_K2-R	5′-TCCCTAGCACTGGCTTAAGT-3′	
K5		
wzx_K5-F	5′-GCCACCTCTAAGCATATAGC-3′	19
wzx_K5-R	5′-CGCACCAGTAATTCCAACAG-3′	
K20		
wzx_K20-F	5′-CCGATTCGGTCAACTAGCTT-3′	19
wzx_K20-R	5′-GCACCTCTATGAACTTTCAG-3′	
K54		
wzx_K54-F	5′-CATTAGCTCAGTGGTTGGCT-3′	19
wzx_K54-R	5′-GCTTGACAAACACCATAGCAG-3′	
K57		
wzx_K57-F	5′-CGACAAATCTCTCCTGACGA-3′	19
wzx_K57-R	5′-CGCGACAAACATAACACTCG-3′	

Statistical analysis

For univariate analysis, Chi-square test or Fisher's exact test were used for categorical variables, whereas the Wilcoxon–Mann–Whitney test was used for continuous variables. A p value <0.05 was considered statistically significant for univariate analysis. The statistical software used was SPSS for Windows, version 15.0.1 (SPSS Inc., Chicago, IL, USA).

Results

Bacteria cultured from PD-related peritonitis during the 22-year period

A total of 479 PD-related peritonitis cases were identified from 1990 to 2011, of which 211 (44.1%) were monomicrobial Gram-positive, 125 (26.1%) were monomicrobial Gram-negative, 43 (9.0%) were polymicrobial, and 84 (17.5%) were culture negative. The most common pathogens causing monomicrobial PD-related peritonitis were coagulase-negative staphylococcus ($n = 106$, 22.1%) and *E. coli* ($n = 54$, 11.3%; Table 2). Monomicrobial *K. pneumoniae* PD-related peritonitis accounted for 2.7% of the peritonitis cases and was the second most common pathogen in Gram-negative PD-related peritonitis.

Clinical features of polymicrobial *K. pneumoniae* PD-related peritonitis

Analysis of the organisms from the 43 polymicrobial PD-related peritonitis episodes showed that PD catheter removal was indicated in 22 cases (51%). *K. pneumoniae* was the most common pathogen involved in polymicrobial peritonitis (16/43, 37.2%) and was associated with a high catheter removal rate (7/16, 43.8%), especially with concomitant fungal infection (4/4, 100%). No deaths were observed in the study cases with *K. pneumoniae*-associated polymicrobial PD-related peritonitis. *E. coli* was the second most common pathogen involved in polymicrobial PD-related peritonitis (10/43, 23.3%) and catheter removal was indicated in three cases (3/10, 30%). Five episodes of polymicrobial PD-related peritonitis involved both *K. pneumoniae* and *E. coli* with a catheter removal rate of 40%.

Clinical features of monomicrobial *K. pneumoniae* PD-related peritonitis

Table 3 lists the 13 cases of monomicrobial *K. pneumoniae* PD-related peritonitis. The duration of PD prior to peritonitis was from 1 year to 16 years. Three patients had diabetes mellitus, one patient had systemic lupus erythematosus, eight individuals had hypertension, and two individuals had malignancy. Five patients experienced sepsis or bacteremia with peritonitis and underwent PD

Table 2 Causative organisms of peritoneal dialysis-related peritonitis episodes during a 22-year period (the duration was divided to two parts for observation of the trend of the organisms)

Organisms	No. of episodes		
	1990—2001	2002—2011	Total
Gram-positive organisms	93 (43.3)	118 (44.7)	211 (44.1)
Coagulase-negative staphylococcus	49 (22.8)	57 (21.6)	106 (22.1)
Staphylococcus aureus	23 (10.7)	21 (8.0)	44 (9.2)
Streptococcus spp.	14 (6.5)	22 (8.3)	36 (7.5)
Enterococcus spp.	2 (0.9)	4 (1.5)	6 (1.3)
Others	5 (2.3)	14 (5.3)	19 (4.0)
Gram-negative organisms	58 (27)	67 (25.3)	125 (26.1)
Escherichia coli	23 (10.7)	31 (11.7)	54 (11.3)
Klebsiella pneumoniae	4 (1.9)	9 (3.4)	13 (2.7)
Pseudomonas spp.	6 (2.8)	1 (0.4)	7 (1.5)
Enterobacter spp.	2 (0.9)	1 (0.4)	3 (0.6)
Others	23 (10.7)	25 (9.5)	48 (10.0)
Fungi	9 (4.2)	4 (1.5)	13 (2.7)
Mycobacteria	1 (0.5)	2 (0.8)	3 (0.6)
Polymicrobial	11 (5.1)	32 (12.1)	43 (9.0)
Culture-negative	43 (20)	41 (15.5)	84 (17.5)
Total	215 (100)	264 (100)	479 (100)

Data are presented as *n* (%).

catheter removal. Of three patients (23%) who died of septic shock, two had diabetes mellitus (Table 3). We further reviewed the profile of antibiotic resistance in 13 isolates of monomicrobial *K. pneumoniae* PD-related peritonitis. One of the 13 isolates of *K. pneumoniae* showed resistance to cephalothin and gentamicin. Another tested positive for extended spectrum β-lactamase (ESBL). The other 11 isolates were sensitive to ampicillin/sulbactam, gentamicin, ertapenem, amikacin, cefazolin, cefuroxime, cefotaxime, levofloxacin, and cefixime.

Comparison with *E. coli* PD-related peritonitis

Compared with *E. coli* peritonitis cases, patients with *K. pneumoniae* peritonitis had insignificantly higher incidence

Table 3 Clinical characteristics and outcomes of 13 patients with monomicrobial *Klebsiella pneumoniae* peritoneal dialysis-related peritonitis

Case	Age (yr)/sex	PD duration (yr)	Comorbidity	PD catheter removal	Patient complication and outcome
1	35/M	3	HTN, CGN	No	Survived
2	43/F	4	Colon cancer, HCV	No	Survived
3	75/F	1	DM, CVA, tracheostomy, parkinsonism	Yes	Septic shock, expired
4	70/M	1	DM, HTN, CVA	No	Survived
5	59/M	3	HTN, HBV	No	Survived
6	50/F	6	Urothelial cancer	Yes	Septic shock, respiratory failure, survived
7	21/F	5	SLE	Yes	Septic shock, ARDS, bowel ischemia, expired
8	48/F	2	HTN, CGN	No	Survived
9	51/F	5	HTN	No	Survived
10	55/F	4	DM, HTN, CAD	Yes	Sepsis, expired
11	53/F	3	HTN, CGN	No	Survived
12	53/M	4	HTN	No	Survived
13	41/F	16	Vaginal peritoneal fistula, CGN	Yes	Septic shock, survived

ARDS = acute respiratory distress syndrome; CAD = coronary artery disease; CGN = chronic glomerulonephritis; CVA = cerebral vascular accident; DM = diabetes mellitus; ESRD = end-stage renal disease; F = female; HBV = chronic hepatitis B; HCV = chronic hepatitis C; HTN = hypertension; M = male; PD = peritoneal dialysis; SLE = systemic lupus erythematosus.

Table 4 Comparison of monomicrobial peritoneal dialysis-related peritonitis caused by *Klebsiella pneumoniae* and *Escherichia coli*

Characteristic and outcome	*K. pneumoniae* ($n = 13$)	*E. coli* ($n = 28$)	p
Age (yr)	50.3 ± 14.0	48.3 ± 15.2	0.67
Male sex	4 (31)	12 (43)	0.51
PD duration [months; median (IQR)]	48 (30–60)	35 (13–70)	0.04
Comorbidity			
Diabetes mellitus	3 (23)	2 (7)	0.30
SLE/RA	1 (8)	5 (18)	0.64
Malignancy	1 (8)	4 (14)	> 0.99
Sepsis/bacteremia	5 (38)	4 (14)	0.11
Outcome			
PD catheter removal	5 (38)	13 (46)	0.74
Patient death	3 (23)	3 (11)	0.36

Data are expressed as mean ± standard deviation or *n* (%), unless otherwise indicated.
ESRD = end-stage renal disease; IgAN = immunoglobulin A nephropathy; IQR = interquartile range; PD = peritoneal dialysis; RA = rheumatoid arthritis; SLE = systemic lupus erythematosus.

of sepsis/bacteremia (38% vs. 14%) and higher mortality rates (23% vs. 11%), and underwent PD therapy for a longer period (median, 48 vs. 35 months; $p = 0.04$). The patient age, sex, and PD catheter removal rate were similar between both groups (Table 4).

Bacterial characteristics in monomicrobial *K. pneumonia* peritonitis

Thirteen *K. pneumoniae* strains of PD-related peritonitis were tested for K serotypes by PCR. The prevalence of K2 and K20 serotype genes was 7.7% and 23.1%, respectively; no K1, K5, K54, and K57 serotype genes were found. The prevalence of K20 serotype was higher in peritonitis isolates compared with that in isolates derived from community-acquired UTI and healthy adults ($p = 0.05$). The prevalence of HV phenotype and genotype (*rmpA* gene) in peritonitis isolates was significantly lower than that in community-acquired UTI isolates [0/13 vs.15/54 (27.8%), $p = 0.03$ and 0/13 vs. 16/54 (29.6%), $p = 0.03$; respectively]. No significant difference was found in other virulence genes, including *magA*, *uge*, and *wabG* (Table 5).

Discussion

This is the first study focused on clinical and microbiological characteristics of *K. pneumoniae* PD-related peritonitis. In this study, *K. pneumoniae* was the second most common Gram-negative pathogen causing monomicrobial PD-related peritonitis and the most common pathogen involved in polymicrobial PD-related peritonitis in southern Taiwan. We demonstrated that *K. pneumoniae* could contribute to severe morbidity, PD catheter removal, and mortality in PD-related peritonitis. The bacterial characteristics with a

Table 5 Comparison of bacterial capsular serotypes, hypermucoviscosity, and genes of hypermucoviscosity and virulence in *Klebsiella pneumoniae* isolates derived from peritoneal dialysis-related peritonitis, urinary tract infection, and healthy adults

Characteristic	Peritonitis ($n = 13$)	UTI ($n = 54$)	Healthy adults ($n = 76$)	p
Serotype				
K1 (*magA*)	0	3 (5.6)	3 (3.9)	0.66
K2	1 (7.7)	5 (9.3)	6 (7.9)	0.96
K5	0	2 (3.7)	0 (0)	0.19
K20	3 (23.1)	6 (11.1)	3 (3.9)	0.05
K54	0	0 (0)	1 (1.3)	0.64
K57	0	2 (3.7)	0 (0)	0.19
Others	9 (69.2)	36 (66.7)	63 (82.9)	0.09
HV phenotype	0[a]	15 (27.8)[a]	2 (2.6)	<0.001
Gene				
rmpA	0[a]	16 (29.6)[a]	9 (11.8)	0.007
uge	12 (92.3)	47 (87)	67 (88.2)	0.87
wabG	13 (100)	54 (100)	76 (100)	>0.99

[a] PD-related peritonitis vs. UTI, $p = 0.03$.
Data are presented as *n* (%).
HV = hypermucoviscosity; PD = peritoneal dialysis; UTI = urinary tract infection.

low percentage of capsular serotype K1/K2, no significant HV, and absence of gene *rmpA* suggest a different pathogenesis in PD-related peritonitis from those in UTI and liver abscess caused by *K. pneumoniae*.

The current study found that the overall incidence of PD-related peritonitis decreased with similar decline in the incidence of both Gram-positive and Gram-negative peritonitis during the 22-year study period. The major causative pathogens in single-organism Gram-negative peritonitis were *E. coli*, *K. pneumoniae*, *Enterobacter*, *Serratia*, and *Pseudomonas* species.[2,6,19] The overall prevalence of Gram-negative PD-related peritonitis was from 14.8% to 23% (10.4% in our study),[6,19,30] and it was from 3.1% to 3.9% (2.7% in our study) in peritonitis caused by *Klebsiella* species.[2,31] Gram-negative bacteria—related peritonitis was the leading cause of temporary or permanent peritoneal catheter loss, and it was associated with a higher mortality rate in patients with ESRD undergoing continuous ambulatory peritoneal dialysis.[30] The catheter removal rate was 24% in a study of 837 cases with PD-associated non-*Pseudomonas* Gram-negative peritonitis (38% and 46% in our *K. pneumoniae* and *E. coli* groups, respectively) in monomicrobial infection;[19] their death rate was 4% (23% and 11% in our *K. pneumoniae* and *E. coli* groups, respectively). Compared with other organisms, non-*Pseudomonas* Gram-negative peritonitis was associated with significantly higher risks of hospitalization, catheter removal, permanent hemodialysis transfer, and death.[19] Our study suggested worse outcomes in PD-related peritonitis caused by *K. pneumoniae* and *E. coli*.

PD-related peritonitis caused by Enterobacteriaceae may result from touch contamination, exit site infection, or intra-abdominal source caused by constipation, colitis, or transmural migration of bacteria, or intra-abdominal infections; the exact etiology often remains unclear.[30–33] Polymicrobial peritonitis involving at least one non-*Pseudomonas* Gram-negative organism was associated with greatly increased risks of catheter removal (50%) and death (6%).[19] In cases of peritonitis of multiple enteric organisms, the ISPD guidelines recommend surgical evaluation, consideration of catheter removal, and treatment with metronidazole in combination with ampicillin and ceftazidime or an aminoglycoside.[29] Our data revealed an increased incidence of polymicrobial peritonitis associated with *K. pneumoniae* during the past 10 years following the advance in connection technique (data not shown). In this study, *K. pneumoniae* was the major pathogen responsible for polymicrobial PD-related peritonitis (37.2% vs. *E. coli* 23.3%) and resulted in higher PD catheter removal rate (43.8% vs. *E. coli* 30%).

Serotypes K1 and K2 are generally considered to be the predominant virulent strains of *K. pneumoniae*, and are highly resistant to phagocytosis.[34–36] Serotype K1 is frequently associated with community-acquired *K. pneumoniae* bacteremia and liver abscesses in Taiwan.[37,38] Our previous study showing a low prevalence of the K1 or K2 serotype in UTI suggested that capsular serotype K1 or K2 is not a major virulence determinant in community-acquired UTI. Expression of HV and presence of *rmpA* in *K. pneumoniae* were strongly correlated in UTI strains.[22] Fang et al[20] reported a higher prevalence of the HV phenotype in invasive strains of liver abscess than that in noninvasive strains without liver abscess (98% vs. 17%) in Taiwan. Expression of the HV phenotype and the presence of *rmpA* and *magA* genes were generally predominant in cases of secondary bacteremia and purulent disease.[15] In this study, the prevalence of K1/K2 serotypes was low in *K. pneumoniae* PD-related peritonitis. There was a higher prevalence of K20 serotype in PD-related peritonitis compared with those in the UTI and healthy control groups ($p = 0.05$). The three cases infected with capsular type K20 were Cases 4, 6, and 12, and the patient infected with capsular type K2 was Case 8 (Table 3). One of the three isolates of *K. pneumoniae* with capsular type K20 underwent PD catheter removal and septic shock. Others had good treatment response without PD catheter removal. In addition, one of the three isolates of *K. pneumoniae* with capsular type K20 was positive for ESBL. The other three isolates with capsular type K2 or K20 were sensitive to all antibiotics. There was no distinctive pattern in capsular serotype of *K. pneumoniae* isolates in PD-related peritonitis, which is different from the primary *Klebsiella* liver abscess predominantly comprising the K1 and K2 serotypes. Further study is necessary to clarify the role of K20 serotype in the pathogenesis of *K. pneumoniae* PD-related peritonitis. In this study, HV and *rmpA* were absent in the peritonitis group, which was significantly different from those in the UTI group (0 vs. 27.8% and 0 vs. 29.6%, respectively). *rmpA* (regulator of mucoid phenotype) is encoded on a 180-kb plasmid. Its expression appears to control the mucoid phenotype and allows the overproduction of capsular polysaccharide, which enhances antiphagocytic activity *in vitro* and *in vivo*.[15,39] The clinical syndrome whereby *K. pneumoniae* strains have the ability to invade tissue may not be limited to liver abscess only.[15]

Information is scarce about the outcomes of peritonitis caused by *K. pneumoniae*, with or without *rmpA*, in patients undergoing continuous ambulatory peritoneal dialysis. We investigated the association of *rmpA* between peritonitis, urinary tract infection, and healthy adults. In our monomicrobial *K. pneumoniae* PD-related peritonitis cases, however, HV phenotype and genotype were absent and not associated with poor outcome or mortality. The unique bacterial characteristics in serotypes and virulence suggest that the mechanism of *K. pneumoniae* PD-related peritonitis is different from the common *K. pneumoniae* infections (UTI, liver abscess, and bacteremia). *K. pneumoniae* isolates causing PD-related peritonitis and UTI or liver abscess were genetically diverse and exhibited varying virulence profiles. To our knowledge, this is the first study investigating the bacterial characteristics of serotypes, HV phenotype and genotype, and virulence factors in *K. pneumoniae* PD-related peritonitis. Further study to investigate novel virulence gene for peritonitis is needed.

Considering the relatively increased incidence of *K. pneumoniae* PD-related peritonitis following advance in connection technique, unobvious bacterial HV, and high participation of *K. pneumoniae* in polymicrobial infection, we suggest that the *K. pneumoniae* isolates causing PD-related peritonitis in this study were possibly associated with the bowel disorders.

The strengths of this study included its long follow-up period (22 years). To our knowledge, this is the first study investigating the bacterial characteristics of *K. pneumoniae*

PD-related peritonitis. In addition, we demonstrated a unique pattern of *K. pneumoniae* isolates in serotypes, HV phenotype and genotype, and virulence factors. Our limitations included a retrospective study with limited sample size in a single center.

In conclusion, patients with monomicrobial *K. pneumoniae* PD-related peritonitis were associated with a high rate of PD catheter removal and mortality, although the causative organisms possess low bacterial HV and virulence. In polymicrobial peritonitis, *K. pneumoniae* was the most common pathogen and was associated with a high PD catheter removal rate. These findings highlight the importance of increasing awareness and improving the management of patients with *K. pneumoniae* PD-related peritonitis, especially in regions where *K. pneumoniae* is more prevalent. Further studies are needed to increase the understanding of the bacterial virulence factors and pathogenesis in *K. pneumoniae* PD-related peritonitis.

Conflicts of interest

All authors declare no conflicts of interest.

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