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ORIGINAL ARTICLE

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

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Peritonitis;
Virulence factor

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.

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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.

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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.

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