Prevalence of *pks* gene cluster and characteristics of *Klebsiella pneumoniae*-induced bloodstream infections

You Lan | Mao Zhou | Zijuan Jian | Qun Yan | Siyi Wang | Wenen Liu

**Background:** The emerging *pks*-positive (*pks*⁺) strains have aroused great public concern recently. Colibactin, encoded by *pks* gene cluster, has been reported to be involved in DNA damage and increased virulence. Little is known about its prevalence among *Klebsiella pneumoniae*-induced bloodstream infections (BSIs). Therefore, the aim of this study was to investigate the prevalence of *pks* gene cluster, and molecular and clinical characteristics of *K pneumoniae*-induced BSIs.

**Methods:** A total of 190 non-duplicate *K pneumoniae* bloodstream isolates were collected at a university hospital in China from March 2016 to March 2018. Molecular characteristics including capsular types, virulence, and *pks* genes were detected by polymerase chain reaction (PCR). Clinical characteristics and antimicrobial susceptibility were also investigated.

**Results:** Overall, 21.6% (41/190) of *K pneumoniae* bloodstream isolates were hypervirulent *K pneumoniae* (hvKP). The prevalence of *pks* gene cluster was 26.8% (51/190). The positive rates of K1, K57, and genes associated with hypervirulence, that is, *rmpA*, *wcaG*, *mrkD*, *allS*, *ybtS*, *kfu*, and *iucA*, were significantly higher in the *pks*⁺ isolates than the *pks*⁻ isolates (*P* < 0.05), while the *pks*⁺ isolates were significantly less resistant to 11 antimicrobial agents than the *pks*⁻ isolates. Multivariate analysis showed diabetes mellitus, and K1 and K20 capsular types as independent risk factors for *pks*⁺ *K pneumoniae* bloodstream infections.

**Conclusions:** The *pks*⁺ *K pneumoniae* was prevalent in individuals with bloodstream infections in mainland China. The high rates of hypervirulent determinants among *pks*⁺ *K pneumoniae* revealed the potential pathogenicity of this emerging gene cluster. Diabetes mellitus, and K1 and K20 capsular types were identified as independent risk factors associated with *pks*⁺ *K pneumoniae* bloodstream infections. This study highlights the significance of clinical awareness and epidemic surveillance of *pks*⁺ strains.

**KEYWORDS**

bloodstream infections, hypervirulent, *Klebsiella pneumoniae*, molecular characteristic, *pks* gene cluster

**1 | INTRODUCTION**

*Klebsiella pneumoniae* is one of the most important pathogens responsible for bloodstream infections, second only to *Escherichia coli*. Recently, a new variant termed hypervirulent *K pneumoniae* (hvKP) has been reported in Taiwan. Compared with classic *K pneumoniae* (cKP), hvKP is characterized by the hypermucoviscous phenotype and hypervirulent factors. Alarmingly, hvKP strains are...
capable of inducing severe, invasive, community-acquired infection in immunocompetent individuals with a propensity for causing metastatic spread to distant sites, which constitutes a serious threat to public health.

The pks gene cluster, originally identified in extraintestinal pathogenic E. coli, encodes enzymes responsible for the synthesis of colibactin, a genotoxin that has been shown to induce double-strand DNA breaks, cell cycle arrest, and cell death and contribute to increased virulence. It was shown that the presence of the pks genes is strongly correlated with bacteremia in E. coli. In a mouse model of septicemia, the colibactin-producing E. coli strains were reported to be associated with significantly lower survival rate. Several studies showed that inactivation of pks genes reduce the ability of E. coli strains to colonize the intestinal tract and consequently to translocate to the blood. Recently, the pks gene cluster was also found in K. pneumoniae. It was reported that pks-encoding colibactin was related to the K. pneumoniae hypervirulence in meningitis model. On the basis of these researches, we speculated that there may be a potential correlation between the pks gene cluster, virulence, and K. pneumoniae-induced bloodstream infections (BSIs). However, little reports are available regarding the characteristics of K. pneumoniae bloodstream strains caused by hvKP, and even less focused on colibactin-producing K. pneumoniae. Thus, the aim of this study was to investigate the prevalence of the pks gene cluster, and clinical and molecular characteristics of K. pneumoniae-induced BSIs.

2 MATERIALS AND METHODS

2.1 Isolates

A total of 190 non-repetitive K. pneumoniae bloodstream isolates were collected from March 2016 to March 2018. Relevant clinical data were also retrieved. The detection of K. pneumoniae in blood cultures within 48 hours after admission was defined as community-acquired BSIs. Correspondingly, the development of bacteremia over 48 hours into inpatient admission was defined as hospital-acquired BSIs. The primary site of BSIs was identified if a localized infection was present before or coincident with the detection of bacteremia. Laboratory data were obtained on the day of the first positive episode isolated from blood.

2.2 Detection of the pks gene cluster, capsular types, and virulence genes

The presence of pks gene cluster, capsular types, and virulence genes were detected by polymerase chain reaction (PCR) as previously described. Genomic DNA of K. pneumoniae was extracted by boiling method. Briefly, 3-5 colonies from an overnight culture of K. pneumoniae was suspended in 200 μL of sterile distilled water and boiled at 95°C for 10 minutes and then centrifuged at 13,000 g for 10 minutes to remove cellular debris. The supernatant was used as template for amplifications. The PCR products were visualized by 1% agarose gel electrophoresis. Strains positive for p-rmpA and iucA were designated as hvKP. For pks-positive strains that were negative for K1, K2, K5, K20, K54, and K57, their capsular types were identified by PCR amplification and sequencing of wzi gene as previously described.

The prs gene cluster, originally identified in extraintestinal pathogenic E. coli, encodes enzymes responsible for the synthesis of colibactin, a genotoxin that has been shown to induce double-strand DNA breaks, cell cycle arrest, and cell death and contribute to increased virulence. It was shown that the presence of the pks genes is strongly correlated with bacteremia in E. coli. In a mouse model of septicemia, the colibactin-producing E. coli strains were reported to be associated with significantly lower survival rate. Several studies showed that inactivation of pks genes reduce the ability of E. coli strains to colonize the intestinal tract and consequently to translocate to the blood. Recently, the pks gene cluster was also found in K. pneumoniae. It was reported that pks-encoding colibactin was related to the K. pneumoniae hypervirulence in meningitis model. On the basis of these researches, we speculated that there may be a potential correlation between the pks gene cluster, virulence, and K. pneumoniae-induced bloodstream infections (BSIs). However, little reports are available regarding the characteristics of K. pneumoniae bloodstream strains caused by hvKP, and even less focused on colibactin-producing K. pneumoniae. Thus, the aim of this study was to investigate the prevalence of the pks gene cluster, and clinical and molecular characteristics of K. pneumoniae-induced BSIs.

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Logistic regression was employed to identify risk factors for pks+ K. pneumoniae-induced BSIs. All variables with P values<0.1 were incorporated into a multivariate model using a backward approach. All data analysis was performed by SPSS software (version 25.0). A P value < 0.05 was considered statistically significant.

2.5 Ethics statement

Permission for collecting the information in the medical records of the patients and the K. pneumoniae isolates for research purposes was approved by the Ethics Committee of Xiangya Hospital Central South University.

3 RESULTS

3.1 Prevalence of pks gene cluster, capsular types, and virulence gene distribution

In this study, the colibactin system markers clbB and clbN were simultaneously detected in 26.8% (51/190) isolates, which were considered as pks+ K. pneumoniae. The results of two additional colibactin genes clbA and clbQ were consistent with those for clbB and clbN. A total of 43 isolates tested positive for K1, K2, K5, K20, K54, and K57 capsular types. Capsular types K1, K2, K5, K20, K54, and K57 comprised 4.7% (9/190), 11.6% (22/190), 0.5% (1/190), 1.0% (2/190), 1.0% (2/190), and 3.7% (7/190) of all K. pneumoniae strains, respectively. Statistical analysis indicated that the positive
rates of K1 and K57 capsular types in pks+ strains were significantly higher than the pks− strains \((P < 0.05)\). The capsular type of remaining 25 pks+ isolates was further determined by wz amplification and sequencing. One isolate was PCR-negative, and the other 24 isolates were identified as K14, K23, K24, K25, K27, K80, and 17 distinct wz allelic types, respectively. The wz sequences are provided in Supplemental Material 1.

Seven virulence genes were detected including p-rmpA, wcaG, mrkD, allS, ybtS, kfu, and iucA. Compared with the pks− strains, the pks+ strains had significantly higher positive rates of all the tested virulence genes \((P < 0.05)\). As determined by positive p-rmpA and iucA, 21.6% (41/190) of K pneumoniae bloodstream isolates were hvKP. The pks-positive rate was significantly higher than pks-negative rate among hvKP isolates. More details regarding virulence factors are shown in Table 2.

### Table 1: Primers used in this study

| Primer name | DNA sequence (5′-3′) | Amplicon size (bp) |
|-------------|----------------------|--------------------|
| **Capsular serotypes** | | |
| K1 | F: GGTGCCTTTTACATCATTGC  
R: GCAATGGCCATTGGTGTTAG | 1283 |
| K2 | F: GACCCGGATATCCACTTGGAG  
R: CCTGAAATACCGTCATAG | 641 |
| K5 | F: GTGATGTGCTGGCGGA  
R: CCTGAAACCCACCAATC | 741 |
| K20 | F: CGGTGTCTGACATGTCATT  
R: GTTATACGATGTCATGTC | 811 |
| K54 | F: CATAGCCTATGTGGTTGGCT  
R: GCTTGACAAACACCATAGCAG | 280 |
| K57 | F: CTCAGGCGCTGAAATGTCAT  
R: CACTAACCAGAAAAGTCGAG | 1037 |
| **Wzi** | | |
| Wzi | F: GTGCGCGGGAGCGCTTTCTATTCCTGTA TTCC  
R: GAGAGCCCACTGTTCCAGAA(C/T)TT(C/G)ACCCG | 580 |
| **Virulence genes** | | |
| p-rmpA | F: CATAAGAGTATGGTTGACAG  
R: CTGATCAATGCCATCTTTCA | 461 |
| wcaG | F: GGTGGKTACGAAATCGTA  
R: ACTATCCGGCAACTCTTTGC | 169 |
| mrkD | F: AAAGCTATCGTGACTCTCCGGCA  
R: GCCGTTGCCGTCAGATAGG | 340 |
| allS | F: CATTAGCCACCTTTGTGC  
R: GAAGTGTGGGCGATCAGCTT | 764 |
| ybtS | F: GACGGAAAACAGCACCGGTA | 242 |
| kfu | F: GGGCTTTCAGGAGCTACG  
R: GAGCTTGGCCGACGATGAC | 638 |
| iucA | F: GCATAGGGCGATACGAACAT  
R: CAGAAGGCAATTGGCTTACCT | 556 |
| **Pks gene cluster** | | |
| clbA | F: CTAGATATCCGCGTTGACG  
R: CAGATACATACATCCATTCA | 1311 |
| clbB | F: GATTTGGATACTGGCGATAACCG  
R: CCAATTCCGCTTGGACGAC | 579 |
| clbN | F: GTTTGTGTCCGCGATAGCTTACAC  
R: CAGATCCGCTTGGTGGGCAAGG | 821 |
| clbQ | F: CTTGTATATTTCCACCACTATTTCC  
R: TTATCCGTTTAGCTTTCGTC | 333 |

More details regarding virulence factors are shown in Table 2.
Antimicrobial resistance of \( pks^+ \) and \( pks^- \) \( K \) pneumoniae bloodstream isolates

Overall, the \( pks^+ \) \( K \) pneumoniae isolates displayed lower resistance to all tested antimicrobial agents than the \( pks^- \) strains. In detail, the \( pks^+ \) \( K \) pneumoniae isolates were significantly more susceptible to piperacillin-tazobactam, cefoperazone-sulbactam, cefazolin, ceftazidime, ceftriaxone, aztreonam, ertapenem, meropenem, imipenem, levofloxacin, ciprofloxacin, and furantoin \( (P \ < \ 0.05) \). A summary of the results is shown in Table 3.

### Table 2: Capsular types and virulence gene distribution of \( pks^+ \)-positive and \( pks^- \)-negative \( K \) pneumoniae bloodstream isolates

| Virulence factors | \( pks^+ \)-positive isolates (\( n = 51 \)) | \( pks^- \)-negative isolates (\( n = 139 \)) | \( P \) value |
|-------------------|-------------------------------------|-------------------------------------|-------------|
| Capsular types    |                                     |                                     |             |
| K1                | 9 (17.6%)                           | 0                                   | 0.000*      |
| K2                | 7 (13.7%)                           | 15 (10.8%)                          | 0.575       |
| K5                | 0                                   | 1 (0.7%)                            | 1.000       |
| K20               | 2 (3.9%)                            | 0                                   | 0.071       |
| K54               | 2 (3.9%)                            | 0                                   | 0.071       |
| K57               | 6 (11.8%)                           | 1 (0.7%)                            | 0.000*      |
| Virulence genes   |                                     |                                     |             |
| \( p-rmpA \)      | 30 (58.8%)                          | 21 (15.1%)                          | 0.000*      |
| \( wcoG \)        | 20 (39.2%)                          | 4 (2.8%)                            | 0.000*      |
| \( mrkD \)        | 51 (100%)                           | 125 (89.9%)                         | 0.019*      |
| \( allS \)        | 38 (74.5%)                          | 52 (37.4%)                          | 0.000*      |
| \( ybtS \)        | 41 (80.4%)                          | 65 (47.0%)                          | 0.000*      |
| \( kfu \)         | 21 (41.2%)                          | 25 (18.0%)                          | 0.001*      |
| \( iucA \)        | 32 (62.7%)                          | 23 (16.5%)                          | 0.000*      |
| HvKP              | 28 (54.9%)                          | 13 (9.4%)                           | 0.000*      |

* \( P \) value < 0.05 was considered to be statistically significant.

### Table 3: Antimicrobial resistance of \( pks^+ \)-positive and \( pks^- \)-negative \( K \) pneumoniae bloodstream isolates

| Antimicrobial agent | \( pks^+ \)-positive isolates (\( n = 51 \)) | \( pks^- \)-negative isolates (\( n = 139 \)) | \( P \) value |
|--------------------|-------------------------------------|-------------------------------------|-------------|
| Ampicillin-sulbactam | 20 (39.2%)                          | 71 (51.1%)                          | 0.097       |
| Piperacillin-tazobactam | 8 (15.7%)                           | 46 (33.1%)                          | 0.013*      |
| Cefoperazone-sulbactam | 10 (19.6%)                           | 51 (36.7%)                          | 0.017*      |
| Cefazolin          | 19 (37.3%)                           | 79 (56.8%)                          | 0.008*      |
| Cefuroxime         | 17 (33.3%)                           | 48 (34.5%)                          | 0.766       |
| Ceftazidime        | 14 (27.4%)                           | 52 (37.4%)                          | 0.196       |
| Ceftiraxone        | 18 (35.3%)                           | 71 (51.1%)                          | 0.032*      |
| Cefepime           | 20 (39.2%)                           | 59 (42.4%)                          | 0.508       |
| Cefotan            | 8 (15.7%)                            | 37 (26.6%)                          | 0.093       |
| Aztreonam          | 15 (29.4%)                           | 70 (50.4%)                          | 0.005*      |
| Ertapenem          | 8 (15.7%)                            | 49 (35.2%)                          | 0.006*      |
| Meropenem          | 7 (13.7%)                            | 45 (32.4%)                          | 0.007*      |
| Imipenem           | 9 (17.6%)                            | 47 (33.8%)                          | 0.022*      |
| Tobramycin         | 10 (19.6%)                           | 35 (25.2%)                          | 0.363       |
| Amikacin           | 7 (13.7%)                            | 33 (23.7%)                          | 0.110       |
| Gentamicin         | 13 (25.5%)                           | 48 (34.5%)                          | 0.186       |
| Levofloxacin       | 8 (15.7%)                            | 47 (33.8%)                          | 0.010*      |
| Ciprofloxacin      | 8 (15.7%)                            | 52 (37.4%)                          | 0.003*      |
| Trimethoprim-sulfamethoxazole | 11 (21.6%) | 48 (34.5%) | 0.065 |
| Furantoin          | 13 (26.0%)                           | 62 (47.0%)                          | 0.010*      |

* \( P \) value < 0.05 was considered to be statistically significant.
3.3 | Clinical characteristics of *pks*⁺ and *pks*⁻ *K pneumoniae* bloodstream isolates

The clinical characteristics of the *pks*⁺ and the *pks*⁻ isolates are shown in Table 4. There was no significant difference in age and sex between the two groups. More *pks*⁺ isolates (60.8%, 31/51) than *pks*⁻ isolates (42.4%, 59/139) were community-acquired. Individuals with diabetes mellitus and hypertension are more susceptible to the *pks*⁺ isolates than the *pks*⁻ isolates (*P* < 0.05). There was a trend of more *pks*⁺ bloodstream isolates originated from liver abscess, but the difference was not significant. Notably, the lymphocyte counts were significantly lower in the *pks*⁺ group than in the *pks*⁻ group (*P* < 0.05).

Multivariate regression analysis found that diabetes mellitus (OR 2.637, 95% CI: 1.001-6.948) and the carriage of K1 and K20 (OR 4.581, 95% CI: 1.271-16.521 and OR 11.716, 95% CI: 2.301-59.643) capsular types were independent risk factors for *pks*⁺ *K pneumoniae*-induced BSIs.

### TABLE 4 Clinical characteristics of *pks*-positive and *pks*-negative *K pneumoniae*-induced bloodstream infections

| Characteristics                          | *pks*-positive isolates (n = 51) | *pks*-negative isolates (n = 139) | *P* value |
|------------------------------------------|----------------------------------|-----------------------------------|-----------|
| Age                                      | 54.3 ± 19.8                      | 37.7 ± 26.5                       | 0.099     |
| Female                                   | 14 (27.5%)                       | 22 (15.8%)                        | 0.841     |
| Acquisition                              |                                  |                                   |           |
| Community-acquired                       | 31 (60.8%)                       | 59 (42.4%)                        | 0.000 *   |
| Hospital-acquired                        | 20 (39.2%)                       | 80 (57.6%)                        | 0.000 *   |
| Underlying condition                     |                                  |                                   |           |
| Diabetes mellitus                        | 15 (29.4%)                       | 19 (13.6%)                        | 0.012 *   |
| Hypertension                             | 17 (33.3%)                       | 19 (13.7%)                        | 0.002 *   |
| Biliary tract disease                    | 3 (5.9%)                         | 17 (12.2%)                        | 0.206     |
| Liver cirrhosis                          | 4 (7.8%)                         | 4 (2.9%)                          | 0.131     |
| Pulmonary infection                      | 7 (13.7%)                        | 13 (9.3%)                         | 0.384     |
| Hematologic diseases                     | 7 (13.7%)                        | 17 (12.2%)                        | 0.783     |
| Cancer                                   | 8 (15.7%)                        | 23 (16.5%)                        | 0.846     |
| Surgery within 30 d                      | 19 (37.3%)                       | 44 (31.7%)                        | 0.467     |
| Chemotherapy within 7 d                  | 8 (15.7%)                        | 21 (15.1%)                        | 0.704     |
| Primary site                             |                                  |                                   |           |
| Biliary tract                            | 2 (3.9%)                         | 10 (7.2%)                         | 0.411     |
| Respiratory tract                        | 29 (56.9%)                       | 93 (65.5%)                        | 0.276     |
| Urinary tract                            | 5 (9.8%)                         | 10 (7.2%)                         | 0.554     |
| Intra-abdomen                            | 5 (9.8%)                         | 13 (9.4%)                         | 0.925     |
| Brain                                    | 2 (3.9%)                         | 3 (2.2%)                          | 0.182     |
| Liver abscess                            | 3 (5.9%)                         | 0                                 | 0.573     |
| Laboratory data (mean ± SD)              |                                  |                                   |           |
| WBC count, ×10⁹/L                        | 8.7 ± 6.6                        | 10.9 ± 8.9                        | 0.746     |
| RBC count, ×10¹²/L                       | 3.2 ± 0.9                        | 3.1 ± 0.8                         | 0.051     |
| HB, g/L                                  | 95.4 ± 28.5                      | 97.4 ± 26.2                       | 0.272     |
| PLT, ×10⁹/L                              | 119.4 ± 97.4                     | 105.0 ± 92.4                      | 0.876     |
| NEUT count, ×10⁹/L                       | 7.5 ± 6.3                        | 7.9 ± 7.6                         | 0.952     |
| LY count, ×10⁹/L                         | 0.6 ± 0.6                        | 1.6 ± 1.5                         | 0.016 *   |

HB, hemoglobin; LY, lymphocyte; NEUT, neutrophil granulocyte; PLT, platelet; RBC, red blood cell; WBC, white blood cell.

* A *P* value <0.05 was considered to be statistically significant.

4 | DISCUSSION

This retrospective study was conducted in 190 patients with *K pneumoniae*-induced BSIs during a 24-month period from March 2016 to March 2018. It was the first systematic study focusing on the *pks* prevalence of *K pneumoniae* bloodstream isolates. Meanwhile, the clinical and microbiological characteristics were also analyzed in this study.

Currently, there is no absolute definition of hvKP. But it is clear that hypermucoviscosity and iron acquisition systems contributed to the virulence of *K pneumoniae*. Hence, strains positive for *p-rmpA* and *iucA* were defined as hvKP in the present study. Our
investigation indicated that HvKP accounted for 21.6% of K pneumoniae-induced BSIs. In two previous studies conducted in China, the prevalence of hvKP among K pneumoniae bloodstream isolates was 31.4% and 36.8%, respectively. In this study, the prevalence of pks gene cluster among K pneumoniae bloodstream isolates was 26.8%. To date, there have been few epidemic reports on emerging pks K pneumoniae in mainland China. In two previous studies conducted in Taiwan, the positive rates of pks among K pneumoniae isolated from various body sites were reported 25.6% and 16.7%, respectively. In E coli, the prevalence of pks gene was high, ranging from 31.5% to 58%, and reported to be significantly associated with bacteremia. Our results revealed that the rates of pks among K pneumoniae isolates collected from blood were higher than the overall pks rate in Taiwan and lower than that in E coli.

The capsule is an important virulence factor of K pneumoniae. Some capsular serotypes, especially K1, K2, K5, K20, K54, and K57, are recognized as hypervirulent variants of K pneumoniae. The above six capsular serotypes were detected by the PCR, and K2 was the most frequently identified serotypes of K pneumoniae bloodstream isolates in this study. The analysis of distribution showed that K1, K2, K5, K20, K54, and K57 were all present among pks isolates while the serotypes of pks isolates were less diverse. Statistical analysis revealed that compared with pks strains, the rates of K1 and K57 in pks strains were significantly higher. In addition, the K1 strains appeared to be associated with the pks genes, as all the K1 strains were positive for pks. In a word, these results suggested the diverse serotype distribution and potential pathogenicity of pks isolates.

Multiple studies emphasized a positive correlation between the presence of virulence genes and pks E coli. Similar results were found in our study. The analysis of virulence factors associated with hvKP showed that the proportion of all these virulence genes in pks isolates was significantly higher than that in pks isolates. The mrkD gene was carried by all pks isolates. Besides, rmpA, allS, ybtS, and iucA, the genes involved in hyphromucoviscosity, allantoin metabolism, yersiniabactin, and aerobactin production, were identified in more than half of pks isolates. These findings further supported the notion that pks genotype may have a relationship with hypervirulent strains. Relevant experiments are needed to figure out whether pks gene cluster contributes to virulence directly or serve as a marker for something else involved in pathogenesis.

It is found that pks isolates are associated with low antimicrobial resistance. Statistical analysis revealed that pks isolates were significantly less resistant to 11 of 20 tested antimicrobial agents than pks isolates. This circumstance was possibly owing to the fact that pks isolates possessed high percentages of hypervirulent serotypes and virulence genes as the acquisition of virulence is usually accompanied by reduced drug resistance. Currently, the emergence of multidrug-, extremely drug-, or pan-drug-resistant cKP has already become a tough situation in clinical studies. Nonetheless, multidrug-resistant hvKP strains producing extended spectrum β-lactamase (ESBL) or carbapenemase have also been described. It is noteworthy that the confluence of genotoxicity and drug resistance is also a disturbing situation in future. Epidemiologic surveillance, effective infection control measures, and novel therapeutic measures targeting the virulence factors are needed to prevent surmountable K pneumoniae infections.

The analysis of clinical characteristics showed that pks isolates were more frequently encountered in community-acquired infection. This implied that pks isolates may play an important part in community-acquired infection like hvKP, which is commonly reported as the cause of community-acquired infections in young people, particularly pyogenic liver abscesses (PLA). The crucial information obtained from laboratory data was a remarkable decrease in lymphocytes among pks isolates. In comparison with pks isolates, the lymphocyte count of pks isolates was significantly lower. A similar discovery that production of colibactin by E coli induced profound lymphopenia in a mouse model of sepsis was noted by Ingrid et al. We thus speculated that the colibactin generated from pks K pneumoniae may harbor the same genotoxicity to lymphocytes as E coli. More data are needed to clarify the mechanism, which may enlighten the invention of therapeutic targets since the prevention of lymphopenia improved survival in sepsis. In accordance with other studies, underlying disease including diabetes mellitus, and K1 and K20 capsular types were significant risk factors for pks K pneumoniae infections. It is noticeable that all the strains originated from PLA were positive for pks, even though there were only three PLA cases in our study. Large number researches are required to corroborate the association between pks K pneumoniae and PLA.

In conclusion, the pks K pneumoniae was prevalent in individuals with bloodstream infections in mainland China. The high rates of hypervirulent determinants among pks K pneumoniae revealed potential pathogenicity of this emerging gene cluster. Diabetes mellitus, and K1 and K20 capsular types were identified as independent risk factors associated with pks K pneumoniae bloodstream infections. This study highlights the significance of clinical awareness and epidemic surveillance of pks strains.

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DISCLOSURE

This work was original research that has not been published previously and not under consideration for publication elsewhere, in whole or in part.

CONFLICT OF INTEREST

None declared.

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