

Clinical and Genomic Characteristics of Carbapenem-Resistant *Klebsiella pneumoniae* Bloodstream Infections in Older Adults: A Single-Center Study from Changsha, China

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Background: Bloodstream infections (BSIs) caused by carbapenem-resistant *Klebsiella pneumoniae* (CRKP) pose a huge threat to global public health. The mortality rates are particularly high among older adults. However, few studies have focused on CRKP BSIs in older adults. This study aims to investigate the clinical and genomic characteristics of CRKP-BSIs in older adults.

Methods: This study collected all eligible older patients (age ≥ 65 years) with CRKP-BSIs from a national regional medical center in Changsha, China from 2020 to 2023. The identification of CRKP strains was performed using MALDI-TOF mass. The antimicrobial susceptibility testing was evaluated by VITEK 2 Compact system. Clinical data of the patients were collected and a binary logistic regression model was used to analyze the risk factors associated with 30-day mortality. The genomic characteristics of CRKP were characterized by whole-genome sequencing (WGS).

Results: A total of 77 older adults with CRKP-BSIs were ultimately included in this study, with an all-cause mortality rate as high as 64.9% (50/77). Mechanical ventilation (OR=8.851; 95% CI 1.503–52.127; $p=0.016$) is a risk factor for 30-day mortality. 97.4% (75/77) of the strains carried carbapenemase genes, with *bla*_{KPC-2} alone (92.2%, 71/77) being the most common, followed by *bla*_{KPC-2} + *bla*_{NDM-1} (2.6%, 2/77). Up to 72.7% (56/77) of the isolates were identified as hypervirulent CRKP (Hv-CRKP). MLST revealed ST11 (96.1%, 74/77) dominated absolutely. Five different capsular serotypes were detected, with KL64 (81.8%, 63/77) being the most common. Through phylogenetic relationship analysis, we speculated that there might have been 10 clonal transmission events of CRKP within the hospital.

Conclusion: CRKP-BSIs in older adults are primarily driven by a limited genetic lineage, ST11, in Changsha, China. Therefore, it is urgently necessary to strengthen the active screening and continuous monitoring of high-risk clone ST11 CRKP among older adults.

Keywords: older adults, bloodstream infection, CRKP, genomic characteristics, mortality, risk factors

Introduction

Bloodstream infections (BSIs), due to their high incidence and mortality rates, pose a significant threat to public health. *Klebsiella pneumoniae* (*K. pneumoniae*, *KP*) is a Gram-negative opportunistic pathogen, and one of the most common pathogens causing BSIs. It usually colonizes the nasopharynx and intestines of healthy humans and animals, and can also be stored in the natural environment.¹ *K. pneumoniae* usually attacks hosts with weakened immune systems, causing both community-acquired and hospital-acquired infections, leading to pneumonia, urinary tract infections, and hepatobiliary infections.^{2–4} *K. pneumoniae* can also cause invasive infections in healthy individuals, such as liver abscesses and

bacteremia, when it possesses high virulence characteristics.⁵ According to relevant research, the 30-day mortality rate among patients with KP-BSIs ranges from 10% to 26%.^{6–8}

In recent years, with the extensive use of antibacterial drugs, the problem of resistance in *K. pneumoniae* has become increasingly serious. Carbapenems are usually the last line antibiotics for the treatment of *K. pneumoniae*, and when *K. pneumoniae* is resistant to them, the treatment options are extremely limited. Unfortunately, the resistance rate of *K. pneumoniae* to carbapenems is on the rise. According to CHINET (China Antimicrobial Surveillance Network), the resistance rates of *K. pneumoniae* to imipenem and meropenem have risen from 11.0% and 14.1% in 2014 to 22.6% and 23.4% in 2024, respectively (<https://www.chinets.com>). Relevant studies have shown that the mortality rate of patients with CRKP-BSIs is as high as 34–55%, which is much higher than that of patients with KP-BSIs.^{9–12}

Current studies mainly focus on the risk factors and prognostic influencing factors of CRKP-BSIs, as well as the molecular epidemiology of CRKP.^{9–14} These studies reveal that there are certain differences in the conclusions among different regions and different groups of people. Wang et al's research shows that age ≥ 55 years is an independent risk factor for mortality associated with BSIs caused by CRKP.¹⁵ Due to their weakened immune function and multiple underlying diseases, older adults (age ≥ 65 years) may be an important host-related reason for their poorer prognosis. However, there are few studies on CRKP-BSIs in older adults. To the best of our knowledge, studies on systematically evaluating the genetic characteristics of CRKP-BSIs in older adults based on whole-genome sequencing data have not been reported so far.

Our research focused on older adults with CRKP-BSIs in a large tertiary hospital in China from 2020 to 2023. We collected their clinical data and CRKP clinical isolates, and performed whole-genome sequencing on the collected CRKP strains. We systematically evaluated the clinical characteristics of patients and the risk factors related to 30-day mortality, as well as the genomic characteristics of CRKP, with the aim of providing suggestions for the precise prevention and control of CRKP-BSIs in older adults.

Methods and Materials

Data Collection

This retrospective study included all older adults (age ≥ 65 years) with CRKP-BSIs who were hospitalized in a national regional medical center with 3,500 beds in Hunan Province, China from January 2020 to December 2023. The inclusion criteria for patients are as follows: (1) Blood culture identification as *Klebsiella pneumoniae*, and drug sensitivity test shows resistance to carbapenem antibiotics; (2) Age ≥ 65 years; (3) Have symptoms of bloodstream infection such as fever and chills. The exclusion criteria are as follows: (1) Repeated infections in the same patient are excluded; (2) Blood cultures identifying multiple different bacteria are excluded; (3) Cases with missing clinical data or isolates are excluded. 85 eligible patients were identified, of which 6 patients had multiple bacterial bloodstream infections, 2 patients with strain loss were excluded, and 77 patients were ultimately included in the study (Figure 1). We collected the clinical data of patients, including demographic characteristics, invasive procedures, underlying diseases, 30-day survival outcomes, and nonduplicate CRKP isolates from bloodstream infections.

Bacterial Identification and Antimicrobial Susceptibility Test

Blood samples were collected aseptically before the patient developed fever or chills and before the administration of antibacterial drugs. The blood culture bottles were placed into the blood culture incubator (Becton, Dickinson and Company, USA) for cultivation after collection, and subsequent procedures were carried out after positivity was reported. The entire operation process complies with the standards of ISO15189. *K. pneumoniae* was identified by using MALDI-TOF (Bruker, Germany) mass spectrometry. The in vitro susceptibility to antibacterial drugs was evaluated using the VITEK 2 Compact system (BioMerieux, France). The in vitro susceptibility of tigecycline was evaluated by determining the minimum inhibitory concentration (MIC) using the broth microdilution method. All the results of the antimicrobial susceptibility tests in this study were interpreted according to the CLSI (Clinical and Laboratory Standards Institute) (2023) guidelines, except for tigecycline, which was interpreted based on the breakpoints recommended by the Food and

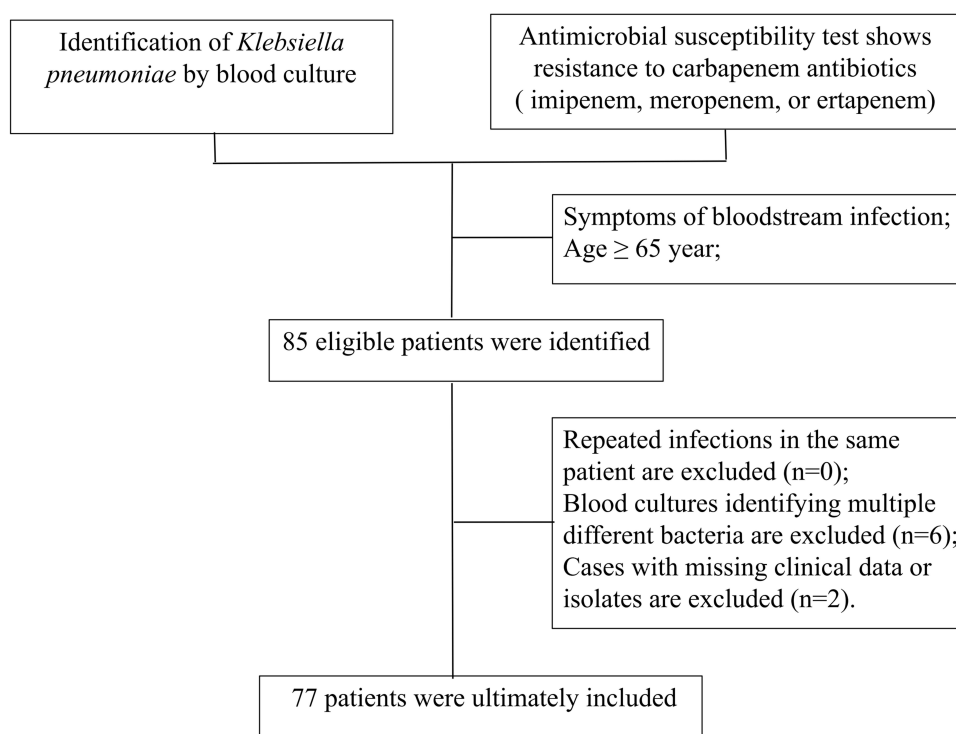


Figure 1 Case collection.

Drug Administration (FDA). *Escherichia coli* ATCC 25922 was used as the strain for quality control. According to previous studies, CRKP strains were classified as “MDR” and “XDR”.¹⁶

Whole-Genome Sequencing

Genomic DNA was extracted from fresh bacterial broth culture utilizing TIANamp Bacteria DNA Kit (Tiangen Biotech, Beijing, China), strictly following the operation steps in the instruction manual. The extracted DNA was sheared into fragments of 200–400bp and purified using magnetic beads. The qualified libraries were sequenced on the Illumina NovaSeq 6000 platform at Sangon Biotech (Shanghai, China). The raw reads were filtered using Trimmomatic (v0.36) to obtain clean reads. SPAdes (v3.15) was utilized for the assembly of whole-genome sequencing data.

Genomic Characteristics Analysis and Phylogenetic Tree

MLST, capsular serotype of CRKP were identified using Pathogen.watch (<https://pathogen.watch/>). Virulence genes and antibiotic resistance genes were predicted by using the virulence factors database(VFDB)(<https://www.mgc.ac.cn/VFs/>) and Resfinder (v4.6.0)(<http://genepi.food.dtu.dk/resfinder>). CRKP strains carrying both *iucA* and *rmpA/rmpA2* were defined as hypervirulent CRKP (hv-CRKP).¹⁷

The phylogenetic tree was constructed based on the SNP strategy, with *K.pneumoniae* HS11286 (No. CP003200) as the reference strain, and generated by the Neighbour-joining clustering method through the snippy 4.6.0 software. Visualization and annotation of the phylogenetic tree through the online tool iTOL (<https://itol.embl.de/itol.cgi>). 21 SNPs serve as the threshold for determining whether CRKP strains belong to the same clone.^{18–20}

Results

Clinical Characteristics

Demographic Characteristics

From January 2020 to December 2023, a total of 77 older adults with bloodstream infections of CRKP were ultimately included in the study. Detailed clinical characteristics are presented in Table 1. The median age of patients was 74 years,

Table 1 Clinical Characteristics in Older Adults with CRKP BSI

Variables	Patients No.(%) or Parameter Value (Median [IQR])			P-value
	Survivors (n=27)	Non-Survivors (n=50)	Overall (n=77)	
Age (years)	74.00(68.50–78.00)	73.00(68.25–82.75)	74.00 (68.00–81.50)	0.839
Male	23 (85.2%)	37 (74.0%)	60 (77.9%)	0.259
Departments				
ICU	19 (70.4%)	42 (84.0%)	61 (79.2%)	0.160
Infectious Diseases Department	1 (3.7%)	2 (4.0%)	3 (3.9%)	1.000
Epilepsy Department	1 (3.7%)	1 (2.0%)	2 (2.6%)	1.000
Burn surgery department	1 (3.7%)	1 (2.0%)	2 (2.6%)	1.000
Others	6 (22.2%)	5 (10.0%)	11 (14.3%)	0.262
Invasive operation				
Mechanical ventilation	13 (48.1%)	41 (82.0%)	54 (70.1%)	0.002
Bronchoscopy	9 (33.3%)	26 (52.0%)	35 (45.5%)	0.116
Central catheter	13 (48.1%)	34 (68.0%)	47 (61.0%)	0.088
Comorbidities				
Coronary heart disease	4 (14.8%)	20 (40.0%)	24 (31.2%)	0.023
Diabetes	9 (33.3%)	19 (38.0%)	28 (36.4%)	0.685
Hypertension	18 (66.7%)	24 (48.0%)	42 (54.5%)	0.116
Alimentary tract hemorrhage	4 (14.8%)	7 (14.0%)	11 (14.3%)	1.000
Cancer	3 (11.1%)	7 (14.0%)	10 (13.0%)	0.996
Cholecystitis	2 (7.4%)	9 (18.0%)	11 (14.3%)	0.354
Chronic kidney disease	6 (22.2%)	11 (22.0%)	17 (22.1%)	0.982

Notes: Bold font indicates statistical significance.

77.9% (60/77) of them were male. The most common department for patient admission was the ICU (79.2%, 61/77), followed by the Infectious Diseases Department (3.9%, 3/77). Patients frequently presented with multiple comorbidities, the most prevalent of which was hypertension (54.5%, 42/77), followed by diabetes (36.4%, 28/77) and coronary heart disease (31.2%, 24/77). Mechanical ventilation was performed in 36 (80.0%) patients. The majority of patients underwent invasive procedures, with 70.1% undergoing mechanical ventilation and 61.0% undergoing central venous catheters.

Risk Factors Associated with 30-Day Mortality

The 30-day all-cause mortality rate of patients with CRKP-BSIs was 64.9% (50/77). To identify risk factors associated with 30-day death, patients were divided into survival and non-survival groups based on their 30-day survival status. Univariate analysis of the clinical characteristics of the patients revealed that the proportion of patients with coronary heart disease ($p=0.023$) and those receiving mechanical ventilation ($p=0.002$) was significantly higher in the non-survival group than in the survival group (Table 1). To further explore the independent risk factors for 30-day mortality, all variables were included in a binary Logistic regression model to eliminate the influence of confounding factors. The results showed that mechanical ventilation (OR = 8.851; 95% CI 1.503–52.127; $p=0.016$) was an independent risk factor for patient mortality (Table 2).

Antimicrobial Susceptibility Test

As shown in Figure 2, all the strains in this study were subjected to antimicrobial susceptibility test against 18 antimicrobial agents. The results indicated that all the CRKP strains were resistant to cephalosporins (ceftazidime, ceftriaxone and cefepime), monobactams (aztreonam), β -lactam/ β -lactamase inhibitors (piperacillin/tazobactam and amoxicillin/clavulanic acid), and carbapenems (imipenem, meropenem and ertapenem).

Table 2 Binary Logistic Regression Model

Variables	OR (95%)	OR 95% CI	P-value
Age	1.027	0.942–1.120	0.546
Male	0.239	0.043–1.323	0.101
ICU	1.054	0.219–5.083	0.948
Mechanical ventilation	8.851	1.503–52.127	0.016
Bronchoscopy	1.032	0.258–4.132	0.965
Central catheter	2.551	0.613–10.607	0.198
Coronary heart disease	3.138	0.705–13.972	0.133
Diabetes	1.209	0.302–4.829	0.789
Hypertension	0.251	0.060–1.046	0.058
Alimentary tract hemorrhage	0.547	0.092–3.237	0.506
Cancer	2.906	0.345–24.459	0.326
Cholecystitis	4.704	0.594–37.276	0.143
Chronic kidney disease	0.757	0.173–3.309	0.712

Notes: Bold font indicates statistical significance.

Furthermore, these isolates also exhibited high resistance rates to other kinds of antimicrobial agents. The resistance rate to levofloxacin was 100% (n = 77), to ciprofloxacin was 98.7% (n = 76), to tobramycin was 85.7% (n = 66), to amikacin was 85.7% (n = 66), and to trimethoprim/sulfamethoxazole was 68.8% (n=53). Notably, strains with an extensively drug resistant(XDR) phenotype accounted for as high as 94.8% (73/77), while only 5.2% (4/77) of the strains were multidrug resistant(MDR).

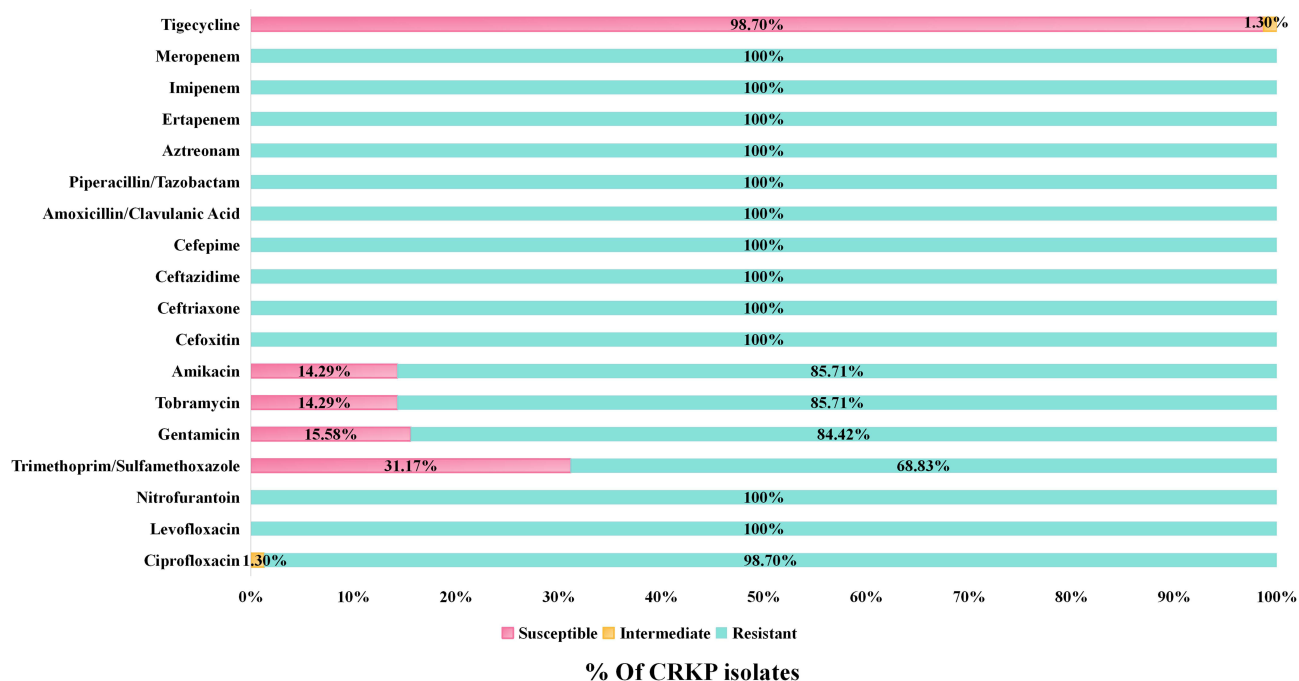


Figure 2 Results of in vitro antimicrobial susceptibility test for CRKP isolates.

Genomic Characteristics

Antimicrobial Resistance Genes

The antimicrobial resistance genes of CRKP were detected by whole genome sequencing. More than 60 kinds of antimicrobial resistance genes were detected in CRKP strains. Among all the isolated CRKP, 75 strains (97.4%) carried carbapenemase genes, with *bla*_{KPC-2} alone accounting for 92.2% (71/77), *bla*_{KPC-2}+*bla*_{NDM-1} accounting for 2.6% (2/77), *bla*_{KPC-3} accounting for 1.3% (1/77), and *bla*_{NDM-1} alone accounting for 1.3% (1/77). Notably, two CRKP strains lacking carbapenemase genes carried *bla*_{SHV-1}, while no mutations were observed in *OmpK35* or *OmpK36*. The gene *bla*_{CTX-M-65} encoding extended-spectrum β-lactamase was detected in 68.8% (53/77) of the isolated bacteria. Other β-lactamase genes *bla*_{TEM-1B}, *bla*_{LAP-2}, and *bla*_{SHV-12} were detected in 76.6% (59/77), 59.7% (46/77), and 28.6% (22/77) of the isolated bacteria, respectively. Genes related to aminoglycoside resistance, *rmtB*, *aadA2b*, were detected in 77.9% (60/77), 59.7% (46/77) of the isolated bacteria, respectively. Genes related to quinolone resistance, *qnrS1*, *qnrB52*, *OqxA*, and *OqxB*, were detected in 55 isolated bacteria, with *qnrS1* being the most common (n=50). Genes related to sulfonamide resistance, *sul1* and *sul2*, were detected in 67.5% (52/77) and 63.6% (49/77) of the isolated bacteria, respectively. In addition, resistance genes related to other antimicrobial agents were detected in this study, such as *tet(A)* encoding tetracycline resistance. The gene *tet(X)* related to tigecycline resistance was not detected in any of the isolated strains (Figure 3).

Virulence Genes

CRKP strains carried a rich variety of virulence genes (more than 60 types) and showed a high degree of similarity in our study. For instance, they all carry aerobactin gene (*iutA*), salmochelin genes (*iroEN*), type I fimbriae genes (*fimABCDEFGHIK*), type III fimbriae genes (*mrkCDFIJ*), Yersiniabactin genes (*fyuA-irp1-irp2-ybtAEPQSTUX*), siderophore gene (*entABCEFS-fepABCDG-fes*), efflux pump genes (*AcrAB*), and secretion system-related gene (*clpV/tssH*). None of the strains carried the salmochelin genes (*iroBCD*), Allantoin utilization genes (*allABCDRS*), or Colibactin genes (*clbABCDEFGHIJKLMNOPS*). The *rmpA*, *rmpA2* and *iucABCD* genes were found in 1.3%, 72.7% and 76.6% of the strains, respectively. Notably, we identified 72.7% (n=56) Hv-CRKP, which were defined as carrying both *iucA* and *rmpA/ rmpA2* (Figure 3).

Plasmid Replicons

In this study, 16 different plasmid replicons were identified in CRKP isolates. Each CRKP isolate contained 2 to 8 different plasmid replicons. The most common plasmid replicons were IncFII (pHN7A8) (97.4%, n = 75), followed by IncR (96.1%, n=74). All isolates carrying carbapenemase genes contained IncFII (pHN7A8). Two isolates without any carbapenemase resistance genes only contained IncFIB(K) and IncFII(K). IncFIB (pB171) was only found in 3 isolates carrying *bla*_{NDM}. All isolates carrying the *rmpA2* virulence gene contained IncFII (pHN7A8) and IncR. Notably, all isolates carrying both carbapenemase resistance genes and the virulence gene *rmpA2* contained IncFII (pHN7A8) (Figure 3).

MLST and Capsular Serotype

In this study, whole genome sequencing data were used for MLST and capsular serotype. Among the 77 CRKP isolates, only three different ST types were identified. The predominant type was ST11 (96.1%, 74/77), followed by ST39 (2.6%, 2/77). None of the ST39 CRKP isolates carried any carbapenemase genes. Notably, we detected a rare ST genotype, ST3336 (1.3%), in 1 CRKP isolate. The KPC-2-ST11 type CRKP strain accounted for as high as 93.5% (n=72). Five different capsular serotypes were detected in the CRKP, among which KL64 (81.8%, 63/77) was the most common capsular serotype, followed by KL47 (11.7%, 9/77), KL25 (2.6%, 2/77), KL23 (2.6%, 2/77) and KL155 (1.3%, 1/77). The ST11-KL64 (81.8%, 63/77) and ST11-KL47 (11.7%, n=9) clones are the most common isolates of CRKP in bloodstream infections among older adults (Figure 4).

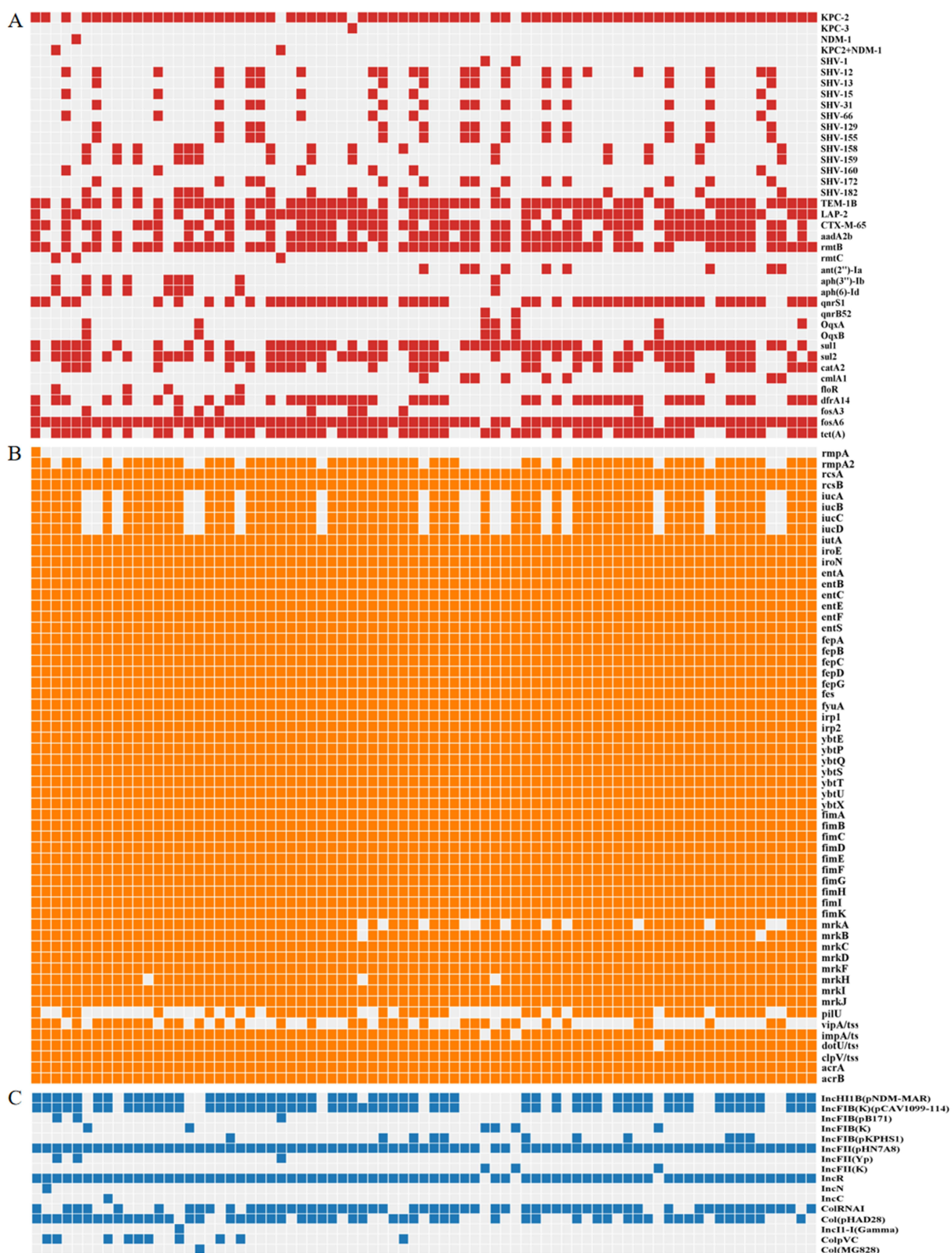


Figure 3 The distribution of antimicrobial resistance genes, virulence genes and plasmid replicons in CRKP strains. Each column represents a CRKP isolate. **(A)** Antimicrobial resistance genes. **(B)** Virulence genes. **(C)** Plasmid replicons.

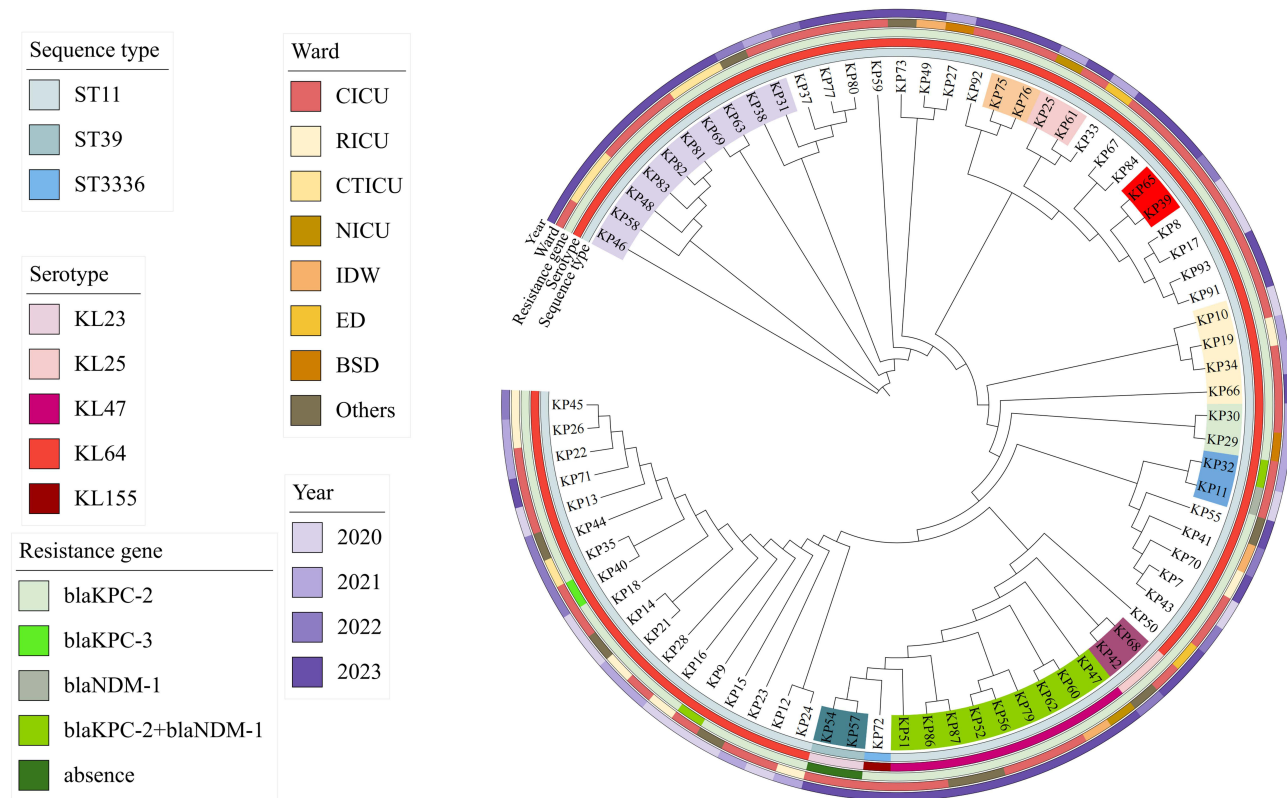


Figure 4 The phylogenetic tree was constructed based on the SNPs of the core genes of 77 CRKP strains. The five different colors in the phylogenetic tree denote five separate clusters. CRKP strains with the same color background belong to the same clonal transmission event.

Abbreviations: CICU, Central ICU; RICU, Respiratory ICU; CTICU, Cardiothoracic Surgery ICU; IDW, Infectious Diseases Department; BSD, Burn Surgery Department; ED, Epilepsy Department.

Phylogenetic Tree and Clone Strain Analysis

Based on phylogenetic tree analysis and paired SNP distances (SNPs = 21 as the threshold), we inferred that there were likely 10 clonal transmission events of CRKP within the hospital (Figure 4). Among the 37 strains involved in clonal transmission, 67.6% (25/37) were isolated in 2023, and 83.8% (31/37) were isolated from ICU, including CICU (n=24), CTICU (n=4), NICU (n=2), RICU (n=1). Additionally, among the strains involved in clonal transmission, 94.6% (35/37) were of ST11 type, and 5.4% (2/37) were of ST39 type.

Discussion

In recent years, CRKP-BSIs have seriously threatened global public health. However, few studies have focused on older adults with CRKP-BSIs, which have a worse prognosis. In this study, we collected the clinical data and CRKP isolates of 77 older adults with CRKP-BSIs hospitalized in a large tertiary hospital in China, analyzed the clinical characteristics of the patients, and utilized whole-genome sequencing data to analyze the genomic characteristics of CRKP.

The all-cause mortality rate of 77 older adults with CRKP BSIs was 64.9%, which was higher than that of the cohort without age screening in previous studies.^{9–12} Therefore, we should pay more attention to older adults population with CRKP-BSIs. Our research confirmed that mechanical ventilation is an independent risk factor for patient mortality, which is consistent with previous studies in the general population.^{10,21} Patients on mechanical ventilation tend to have more severe conditions and greater exposure to antibiotics, which may be the reasons for their poor treatment outcomes and adverse consequences.

Genomic analysis was conducted using the whole-genome sequencing data of 77 CRKP strains isolated from BSIs in older adults. Our study confirmed that the production of carbapenemases is the main cause of carbapenem resistance in *K. pneumoniae*, with KPC-2 being the most common, which is similar to most studies in China.^{22–25} These CRKP strains

carry over 60 kinds of resistance genes, which is consistent with their high proportion (94.8%, 73/77) of XDR phenotype. However, certain bacterial strains lacking extended-spectrum β -lactamases still exhibit resistance to aztreonam, which may be attributed to alternative resistance mechanisms, including the production of AmpC-type β -lactamases, loss of porin, and overexpression of efflux pumps. Furthermore, these CRKP strains simultaneously contain abundant virulence genes, among which the proportion of Hv-CRKP strains was as high as 72.7% (56/77), and all Hv-CRKP were ST11. During the evolution of ST11 CRKP, it often carries more virulence genes, which is consistent with previous studies.^{26,27} We speculate that the higher proportion of Hv-CRKP in older adults might be an important reason for its higher mortality rate than the general population.

A study on CRKP-BSIs in an unselected Chinese population identified seven different ST types among 61 isolates, with the predominant strain being ST11 (60.7%), followed by ST15 (27.9%).²⁸ Another similar study from China found that among 85 CRKP strains isolated from ICU wards, 12 different ST types were identified, with ST11 being the predominant type (61.18%), followed by ST15 (25.88%).²⁹ Obviously different from the above studies, in a cohort study from the United States, 74 ST types were detected in 94 strains of *K. pneumoniae* causing bloodstream infections, and no obvious dominant ST type was found. This indicates that *K. pneumoniae* causing BSIs originates from a genetically heterogeneous bacterial population.³⁰ In this study, only three different ST types were found, with ST11 being the predominant type, accounting for as high as 96.1%, significantly higher than the proportion of ST11 in the general population (61%). The CRKP-BSIs in older adults are mainly driven by the ST11 lineage, which may be related to the fact that the convergence of drug resistance can lead to the expansion of specific lineage bacteria.

In our study, five different capsular serotypes were detected, with KL64 (81.8%) being the most common, followed by KL47 (11.7%), which is consistent with the results of most CRKP molecular epidemiological studies in China.^{17,24} In contrast to our research findings, another study from China on CRKP-BSIs without age restrictions showed that KL47 (55.5%) was the most dominant serotype, followed by KL64 (29.5%).³¹ This indicates that there are differences in the capsular serotypes of CRKP-BSIs among different populations, with KL64 being the dominant serotype in older adults. Investigating the serotypes of CRKP in bloodstream infections among older adults can provide a theoretical basis for vaccine research.

Phylogenetic analysis suggests that there were likely 10 clonal transmission events of these CRKP strains within the hospital. 94.6% (35/37) of the clonal transmission strains were of ST11 type, and 70.3% (26/37) were isolated in 2023. The most frequent occurrence was in the ICU, accounting for 83.8% (31/37). Therefore, we speculate that the clonal spread of ST11 CRKP is an important cause of the spread of CRKP, which is similar to a large-scale study in Europe in 2019.¹⁸ A study in China also confirmed that ST11 *K. pneumoniae* isolates are associated with hospital outbreaks and transmission.³² The ICU is a high-risk area for the clonal spread of CRKP within hospitals, which is similar to the findings of Chen et al.² ICU patients are more prone to colonization and infection with CRKP.^{28,33} ICU patients often require invasive procedures such as mechanical ventilation, central venous catheterization, and bronchoscopy, which provide conditions for the colonization and spread of CRKP. The ICU environment serves as a reservoir, and the contact between patients and medical staff can easily lead to cross-infection, which may be an important source of clonal spread of CRKP. Therefore, for the high-risk clonal type ST11, clinical monitoring and prevention and control should be strengthened, especially in the ICU. For example, regular sampling and testing should be conducted in the hospital environment, and active screening of patients should be carried out to reduce the risk of clonal spread.

Our research systematically revealed the genomic characteristics of CRKP-BSIs among older adults using whole-genome sequencing. However, there are certain limitations. Firstly, this study was a single-center study that only included older adults, which might lead to certain biases in the results. Secondly, there may be some undetected resistance genes or mechanisms in this study, and the sensitivity of CRKP to new antibacterial drugs such as ceftazidime and averbactam was not evaluated. This provides limited suggestions for treatment strategies. Additionally, our research was retrospective and could not promptly trace and control the clonal spread of CRKP.

Conclusions

A single-center study from Changsha, China, showed that the all-cause mortality rate of CRKP bloodstream infection in older adults was as high as 64.9% (50/77), and the risk factor for 30-day mortality was mechanical ventilation. CRKP-BSIs in older adults are driven by a limited genetic lineage, ST11, which is prone to clonal spread through hospital pathways, thereby triggering the prevalence of CRKP. Furthermore, ST11 CRKP shows a convergence phenomenon of XDR phenotype and high virulence. Among all the strains, the proportion of Hv-CRKP was as high as 72.7% (56/77). The treatment options for Hv-CRKP are extremely limited, which may be an important reason for the high mortality rate in older adults with CRKP-BSIs. Therefore, in Changsha, China, there is an urgent need to enhance active screening and continuous monitoring of high-risk clone ST11 CRKP, especially for older adults and the ICU environment, in order to curb the further spread of CRKP in the future.

Data Sharing Statement

The sequencing data supporting this study have been deposited in the NCBI GenBank under BioProject ID PRJNA1277461, and can be accessed via the website <http://www.ncbi.nlm.nih.gov/bioproject/1277461>.

Ethics Approval and Consent to Participate

This study was retrospective. Patient identifiers were not used to ensure the privacy or rights of participants. Therefore, written informed consent from individuals was not required, and it was approved by the Ethics Committee of Xiangya Hospital, Central South University (Ethics no. 2025061050). This research design was carried out in accordance with the provisions of the Declaration of Helsinki.

Author Contributions

All authors made a significant contribution to the work reported, whether that is in the conception, study design, execution, acquisition of data, analysis and interpretation, or in all these areas; took part in drafting, revising or critically reviewing the article; gave final approval of the version to be published; have agreed on the journal to which the article has been submitted; and agree to be accountable for all aspects of the work.

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Disclosure

The authors declare no competing interests in this work.

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