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Analysis of antibiotic resistance of *KPC-2*-positive *Klebsiella pneumoniae* strains isolated from blood cultures in Van, Turkey

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Abstract. – OBJECTIVE: Recently, *Klebsiella pneumoniae* strains causing bacteremia and showing significant antibiotic resistance have raised serious health concerns. Especially carbapenem-resistant *K. pneumoniae* has spread worldwide and caused an increase in mortality rates. In this study, we aimed to present information about *KPC-2* carriage and molecular characteristics of *K. pneumoniae* strains showing multiple antibiotic resistance among patients in our hospital.

PATIENTS AND METHODS: Blood samples were collected from patients hospitalized in the intensive care units (ICU) of Van Regional Training and Research Hospital between 2020-2021. Culture, biochemical tests, antibiotic susceptibility tests, and molecular tests were performed to identify *K. pneumoniae* strains isolated from blood culture samples.

RESULTS: Two hundred and sixteen *K. pneumoniae* were isolated from patients with positive blood cultures. Twenty-seven of these isolates showed multidrug resistance. Carbapenem, β-lactam, and quinolone resistance were particularly high. On the contrary, almost all of these isolates were susceptible to Amikacin (AK), Gentamicin (CN), Colistin (CT) and Tigecycline (TGC). Molecular analysis revealed that all of these isolates were *KPC-2*-positive and ST11 variants.

CONCLUSIONS: It was observed that *KPC-2*-positive *K. pneumoniae* strains with multi-drug resistance may pose a serious risk in patients hospitalized in ICU in our hospital. It was concluded that surveillance and personnel training regarding the hospital and community-acquired infections due to these isolates that show pandemic spread would be important.

Key Words:
KPC-2, Blood, *Klebsiella*, Phylogenetic analysis.

Introduction

Over the last two decades, the occurrence and transmission of carbapenem-resistant Enterobacteriaceae (CRE) has attracted attention worldwide as it has become clear that the majority of currently used broad-spectrum antibiotics may no longer be a therapeutic option for some patients[1]. CRE has spread rapidly worldwide, resulting in high morbidity and mortality rates[2]. Various healthcare organizations have implemented strict infectious control programs along with the identification of patients with CRE to fight this problem[3,4]. At the same time, many hospitals cannot provide individual patient rooms and specialized nurses for CRE-positive patients[5], as intensive infection control programs may require significant resources and staffing capabilities, especially in developing countries due to the lack of adequate healthcare facilities[3,4].

Klebsiella pneumoniae is a common pathogen that causes invasive infections such as sepsis, liver abscess, pneumonia and urinary tract infections. *K. pneumonia* carbapenems (KPC)-producing bacteria, in which carbapenemases are produced, often cause mortality rates as high as 50% to 66%[6,7]. The presence of high rates of carbapenem and colistin resistance and virulence factors make the infection difficult to eradicate. When carbapenem resistance in *K. pneumoniae* is examined, it consists of carbapenemase enzymes such as New Delhi metallo-β-lactamase (*NDM*), *KPC*, *OXA-48* and similar carbapenemases and Verona integron-encoded metallo-β-lactamase (*VIM*). The KPC enzyme is the most common cause of carbapenem resistance in the USA, China, South America, and Europe but has rarely been documented in India, where *NDM* and *OXA48*-like carbapenemases are endemic[8,9]. VIM has been rarely reported[10,11] among *K. pneumoniae* isolates from different specimens in India. Globally, 24 KPC variants have been

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identified to date (www.lahey.org/Studies/other.asp). For example, the *KPC-2* gene, identified among 24 *KPC* genes, has been reported to be carried on various plasmid types (such as IncX3, IncFIIK and IncFIA) and to have a different genetic background[12]. *KPC* gene has been shown[13,14] to associate with genetic constructs, including transposon Tn4401 and its eight genetic variations; other non-Tn4401 element constructs have also been reported[15]. Tn4401 is known to possess the *ISKpn6* and *ISKpn7* structures that surround *blaKPC*. *blaKPC*-carrying ST101 is an international epidemic clone among *K. pneumoniae* isolated from various regions of the world[16,17].

The aim of this study was to analyze the antibiotic resistance characteristics of *K. pneumoniae* strains isolated from blood cultures of patients hospitalized in the intensive care unit of Van Training and Research Hospital in Van, Turkey. In addition, it aimed to reveal the *KPC-2* carriage of *K. pneumoniae* isolates and to investigate the sequence and multilocus sequence types (MLST).

Patients and Methods

Microbiological Analysis of K. Pneumoniae Strains (Isolation, Identification, and Analysis of Antibiotic Susceptibilities)

Carbapenem-resistant *K. pneumoniae* strains were isolated from patients with bacteremia at the ICU of Van Regional Training and Research Hospital between 2020-2021. Bactec/Alert 3D (Biomerieux, Cambridge, Boston, USA) system was used, and blood culture flasks were observed for five days. Five percent sheep blood agar (Acumedia, CA, USA), McConkey Agar (Oxoid, Hamshire, UK) and Eosin Methylene Blue (EMB, Oxoid, Hamshire, UK) agar were used for inoculations from blood culture flasks. Petri plates were incubated at 37°C for 48-72 hours. The colony morphology of the cultures was assessed appropriately and carefully. Important biochemical analyses such as catalase, oxidase, indole, hydrogen sulfide (H_2S) and gram staining were performed immediately afterward. Vitek 2 Compact (Biomerieux, Cambridge, Boston, USA) was used for the two important steps of antibiogram testing and bacterial identification[18]. Ampicillin (AM), Amoxicillin/Clavulanic Acid (AMC), Amikacin (AK), Piperacillin (PRL), Piperacillin/Tazobactam (TPZ), Cefepime (FEP), Cefazolin (CZ), Cefoxitin (FOX), Cefuroxime (CXM), Ciprofloxacin (SPX), Cefuroxime Axetil (CXA), Colistin (CT), Ceftazidime (CAZ), Ceftriaxone (CRO), Ertapenem (ETP), Imipenem (IPM), Gentamicin (CN), Levofloxacin (LEV), Meropenem (MEM), Nitrofurantoin (F), Netilmicin (NET), Aztreonam (ATM), Tobramycin (TOB), Tigecycline (TGC) and Trimethoprim/Sulfamethoxazole (SXT) were used. Tests were performed using the minimum inhibitory concentration (MIC, mg/L) threshold table of the European Committee for Microbiological Resistance[19]. The modified Hodge test (MHT) was chosen to determine the presence of carbapenemases, and CLSI 2012 guidelines were applied[20,21].

Analysis of the Molecular Properties of the KPC-2 Gene

DNA extraction was performed at Van Yüzüncü Yıl University Pharmaceutical Microbiology Laboratory. Bacteria were grown on Tryptone Soy Agar (Acumedia, California, USA) and then incubated at 37°C for 24-48 hours. Then, EcoSpin Bacterial Genomic DNA kit (Echotech Biotechnology, Erzurum, Turkey) methodology was used to extract DNA from multidrug-resistant carbapenem-resistant *K. pneumoniae* strains. Bacterial DNA samples were stored at -20°C.

May Taq™ DNA Polymerase (Bioline, Bio-21105, Tenessee, USA) kit protocol was applied for DNA amplification of bacteria. For Polymerase Chain Reaction (mPCR), a set of chemical solutions and substances were used, respectively, 10 µL 5x MyTaq reaction buffer [5 mM deoxyribonucleoside-triphosphates (dNTPs), 15 mM MgCl2], 5 µL template DNA, 1 µL of each primer (20 µM), 1 µL MyTaq DNA polymerase and 8 µL nuclease-free water, calculated as 25µl of the final solution. PCR conditions for *KPC-2* were 94°C for 10 minutes, 94°C for 30 seconds, 52°C for 40 seconds, 72°C for 50 seconds and 72°C for 5 minutes for 40 cycles. The HyperLadderTM marker (50 Base Pair, Bioline, USA) was used to analyze the size of the amplicon accurately. For accurate visualization of bacterial amplicon products, a Thermo EC300XL2 electrophoresis device was operated at 100 Volts on a 1.5% agarose gel for 1 hour. Amplicons were visualized using Bio-Print-ST4 (Vilber Lourmant, France). *KPC-2* gene amplification of *K. pneumoniae* strains was performed using the F: 5'- CGTCTAGTTCTGCTGTCTTG-3'; R: 5'- CTTGTCATCCTTGTTAGGCG -3' primer.

Before the analysis of the results, the *KPC-2*-positive samples were separated using a purification

kit (High Pure PCR Cleanup Micro Kit, Roche, Germany). Primers and PCR samples of the *KPC-2* gene region were carefully coated and sent to Sentebiolab in Ankara city for DNA sequencing. Although it is a reference laboratory where genetic studies are carried out, the Sanger sequencing method and ABI Prism 3130 (Thermo Fisher Scientific, Norristown, USA) genetic device were used in this study. Bioedit Software (https://bioedit.software.informer.com) was used to adjust the samples before analysis of nucleotide sequences[22]. "BLAST analysis" (http://www.ncbi.nlmn.nih.gov/BLAST) was performed on the final structural sequences of a total of four isolates [Surgery (MW766897); Internal Medicine (MW766898); Reanimation (MW766899) and Neonatal (MW766900)] selected from each of the ICU. During the MEGA 7.0 (http://www.megasoftware.net) application, the Clustal W model parameter was selected to reveal genetic distances. The nucleotide sequences of a total of 30 isolates were used to generate the *KPC-2* phylogenetic analysis dataset. The 30 isolates we used in the phylogenetic analysis were selected based on the country, where they were isolated from and their *KPC* feature. "Outgroups" of some bacterial sequences were used to construct the phylogenetic tree. With 1000 bootstrap replicates, phylogenetic analyses and tree construction were performed in MEGA 7.0 using the Maximum Likelihood Technique[23]. The phylogenetic tree consists of sequences of strains from Turkey and several other countries (such as Brazil, Argentina, South Korea, America, Japan, Austria, China, England, and Cambodia). At the same time, the FASTAs of our *KPC-2*-positive *K. pneumonia* isolates with reference numbers MW766897, MW766898, MW766899 and MW766900 from the World Gene Bank were used for the phylogenetic analysis.

Sequence types (STs) were allocated using the Institut Pasteur (Paris, France) database (//bigsdb.pasteur.fr/klebsiella/klebsiella.html) in line with the approach of Diancourt et al[24]. DIVEIN was used to analyze the differences between individual locus sequences and concatenated sequences of the seven MLST loci of each isolate[24]. eBURST (http://ebrust.mlst.net) was applied to generate clonal clusters that meet STs sharing six loci (single locus variations)[25]. The first step of the eBURST algorithm is to divide STs into groups. Each ST within an eBURST group has a user-defined minimum number of identical alleles in common with at least one other ST in the group. The eBURST groups are, therefore, mutually exclusive; no ST can belong to more than one group. The default setting in eBURST is the most specific group definition, where STs are included in the same group only if they share the same alleles at six or seven of the seven MLST loci with at least one other ST in the group. Defined this way, each group equals a single clonal complex. eBURST was utilized to produce an overview of a population regarding the clonal connections between these Sequence Types (STs) and those present in the Institut Pasteur database[26].

Ethics Committee Approval

The research Ethics Committee of Van Training and Research Hospital authorized our study (decision dated 25/01/2018 and numbered 2018/02) by evaluating the accuracy of our research.

Results

As a result of the analysis of blood cultures (total sample=2,638), 216 (8.2%) isolates that were considered to be *KPC*-positive *K. pneumoniae* were identified. Subsequently, 27 of these isolates (1.02%) were identified as multidrug-resistant *K. pneumoniae* strains. Furthermore, these strains were found to be carriers of the *KPC-2* gene and were included in the study (Figure 1). These isolates were analyzed for antibiotic susceptibility.

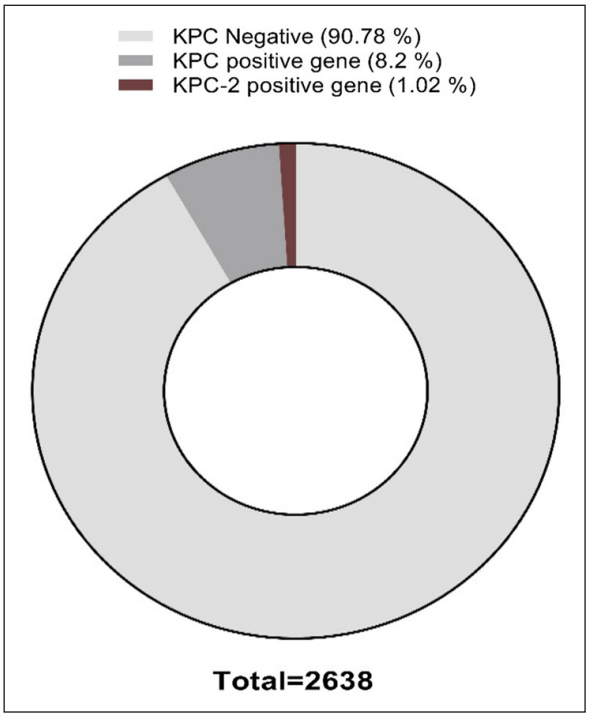

Figure 1. *KPC* gene distribution in analyzed samples.

It was found that almost all of these isolates were susceptible to AK, CN, CT and TGC, while they were completely resistant to all other antibiotics. All of these isolates were found to have extended resistance against all β-lactam antibiotics, including CAZ and CRO. In addition, the distribution rates of ETP, IPM and MEM resistance in *KPC-2*-positive *K. pneumoniae* isolates were high and similar. In addition, it was revealed that all of these isolates showed a high level of quinolone resistance (Table I).

The images of *KPC-2* gene amplicons (761 bp) of *K. pneumoniae* isolates are given in Figure 2. The phylogenetic tree results of *KPC-2*-positive *K. pneumoniae* strains isolated from different ICUs [Surgery (MW766897); Internal Medicine (MW766898); Reanimation (MW766899) and Neonatal (MW766900)] are shown in Figure 3. It was determined that our four *KPC-2*-positive strains isolated from blood were highly genetically similar and were in the same clade as *KPC-2*-positive strains isolated from the blood of patients coming to the hospital in Edirne City, Turkey. At the same time, our *KPC-2*-positive strains were genetically similar to *KPC-2*-positive *K. pneumoniae* strains from other parts of the world (such as Brazil, Argentina, South Korea, America, Japan, Austria, China, England, and Cambodia). As a result of this analysis, it was determined that *KPC-2*-positive *K. pneumoniae* isolates were in the same clade as *KPC-2*-carrying *Pseudomonas*, *Citrobacter*, and *Stenotrophomonas* species. *KPC-2*-positive *K. pneumoniae* isolates were found to be in different clades, with *KPC-2* carrying *Serratia marcescens* and *K. pneumoniae*. Finally, the *KPC-2* gene carried by our *K. pneumoniae* strains was similar to *KPC-3* and *KPC-4* genes, but different from *KPC-5* (Figure 3). As a result of the analysis by MLST, it was determined that all 27 *KPC-2*-positive *K. pneumoniae* isolates were ST11 variants. ST11-positive *K. pneumoniae* is one of the most common isolates causing hospital-acquired infections in different parts of the world[27].

Discussion

The use of carbapenems has become widespread globally due to their safety and effectiveness in the treatment of multidrug-resistant bacterial infections, which can be life-threatening. It is now leading to the development of carbapenem resistance among numerous Gram-negative bacterial pathogens such as *Enterobacteriaceae*, *Pseudomonas aeruginosa* and *Acinetobacter baumannii*[28]. The rising incidence and prevalence of carbapenem-resistant *Enterobacteriaceae* (CRE), *P. aeruginosa,* and *A. baumannii* worldwide, with notable mortality rates ranging from 6.6% to 20%, is considered a global threat affecting human and animal health[29,30]. All of these bacteria were subsequently reported by the World Health Organization as priority critical pathogens[31]. The importance of carbapenems in the treatment of MDR infections is well known, but the emergence and rapid spread of CREs resistant to fluoroquinolones, aminoglycosides and colistin significantly reduces the treatment options[32,33]. In fact, although CREs are usually detected in healthcare-acquired (hospital) infections, *Enterobacteriaceae* also cause community-acquired infections, which is an important indicator to explain the spread of CREs in the community[34]. *K. pneumoniae*, which causes community-acquired and hospital-acquired infections, was found to be common among patients in our hospital. Twenty-seven of these isolates showed high rates of antibiotic resistance. It was predicted that strains of K. pneumoniae, which are resistant to multiple antibiotics, could cause serious problems in the spread of antibiotic resistance and the maintenance of healthcare services. It is crucial to handle surveillance information about nosocomial infections in wards and ICUs with utmost diligence.

Carbapenem resistance is mainly controlled by carbapenem enzymes located in mobile genetic elements (MGE). MGEs include integrons, insertion sequences, transposons and mobile plasmids that can transfer carbapenemase expression genes within and between cellular structures of bacteria of the same or different species[35,36]. The capacity and ability of plasmids to carry multiple antibiotic resistance genes (ARGs) and mobility between the same and different species through conjugation makes them highly important and unique in the molecular epidemiology of CREs[36,37]. This can be further complicated by the fact that multiple plasmids can reside in a single CRE cell, depending on their incompatibility (Inc). Plasmids use their extrachromosomal and self-replicative properties for bacterial adaptation and survival in adverse conditions[37,38]. *KPCs*, along with carbapenems, show broad-spectrum activity against many β-lactams, but mostly occur in clinical isolates of *K. pneumoniae*[39,40]. In addition, *KPC* has recently been detected[40,41] in Gram-negative bacteria such as *Escherichia coli*, *Enterobacter* spp., *Klebsiella oxytoca*, *Proteus mirabilis*, *Serratia marcescens*, *Morganella morganii* and *Cit-*

Table I. Antibiotic resistance characteristics of *KPC-2* positive *K. pneumoniae* isolates.

No.	AM	AMC	PRL	TPZ	CZ	CXM	CXA	FOX	CAZ	CRO	FEP	ETP	IPM	MEM	TOB	AK	NET	CN	ATM	SPX	LEV	TGC	CT	F	SXT
1	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	S	R	S	R	R	R	S	S	R	R
2	R	R	R	I	R	R	R	I	R	R	R	R	R	R	R	S	R	S	R	R	R	S	S	S	R
3	R	R	R	I	R	R	R	R	R	R	R	R	R	R	R	S	S	S	R	R	R	S	S	S	R
4	R	R	R	I	R	R	R	R	R	R	R	S	R	R	R	S	R	S	R	R	R	S	S	S	R
5	R	I	R	R	R	R	R	R	R	R	R	R	S	R	R	S	R	S	R	S	R	S	S	R	R
6	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	S	S	S	R	S	R	S	S	R	R
7	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	S	S	S	R	S	R	S	S	R	S
8	R	R	R	R	R	R	R	R	R	R	R	S	R	R	R	S	S	S	R	S	R	S	S	R	S
9	R	R	R	R	R	I	R	R	R	R	R	S	R	R	R	S	R	S	R	R	I	S	S	R	R
10	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	S	R	S	S	R	I	S	S	R	R
11	R	R	R	R	R	R	R	I	R	R	R	R	R	R	R	S	R	S	S	R	I	S	S	R	R
12	I	I	R	R	R	R	R	I	R	R	R	R	R	R	R	S	R	S	S	R	I	S	S	R	R
13	R	R	R	R	R	R	R	I	R	R	R	R	R	R	S	S	R	S	S	R	R	S	S	R	R
14	R	R	R	R	R	I	R	I	R	R	R	R	R	S	R	S	R	S	S	R	R	S	S	R	I
15	I	R	R	R	R	R	R	R	R	R	R	R	R	S	S	S	R	S	R	R	R	S	S	R	I
16	R	R	R	R	R	R	R	R	R	R	R	R	S	S	R	S	R	S	R	R	R	S	S	R	S
17	R	R	R	R	R	R	R	R	R	R	R	R	S	R	R	S	R	S	R	R	S	S	S	S	S
18	R	R	R	R	R	R	R	R	R	R	I	R	S	R	R	S	R	S	R	S	S	S	S	S	R
19	R	I	R	I	R	R	R	R	R	R	I	R	R	R	R	S	R	S	S	R	S	S	S	S	R
20	R	R	R	R	R	R	R	R	R	R	I	R	R	S	R	S	R	S	S	R	R	S	S	S	R
21	R	R	R	R	R	R	R	R	R	R	I	R	R	S	R	S	S	S	S	S	R	S	S	R	R
22	R	R	R	R	R	R	R	R	R	R	R	R	R	R	S	S	S	S	R	R	R	S	S	R	R
23	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	S	R	S	R	R	R	S	S	R	R
24	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	S	R	S	S	R	R	S	S	R	R
25	R	R	R	R	R	R	R	R	R	R	R	R	R	R	S	S	R	S	R	R	R	S	S	R	R
26	R	R	R	R	R	R	R	R	R	R	R	R	R	R	S	S	R	S	R	R	R	S	S	R	R
27	R	R	R	R	R	R	R	R	R	R	R	R	R	R	S	S	R	S	R	R	R	S	S	R	R

R: Resistant, I: Intermediate, S: Susceptible, Ampicillin (AM), Amoxicillin/Clavulanic Acid (AMC), Amikacin (AK), Piperacillin (PRL), Piperacillin/Tazobactam (TPZ), Cefepime (FEP), Cefazolin (CZ), Cefoxitin (FOX), Cefuroxime (CXM), Ciprofloxacin (SPX), Cefuroxime Axetil (CXA), Colistin (CT), Ceftazidime (CAZ), Ceftriaxone (CRO), Ertapenem (ETP), Imipenem (IPM), Gentamicin (CN), Levofloxacin (LEV), Meropenem (MEM), Nitrofurantoin (F), Netilmicin (NET), Aztreonam (ATM), Tobramycin (TOB), Tigecycline (TGC), Trimethoprim/Sulfamethoxazole (SXT).

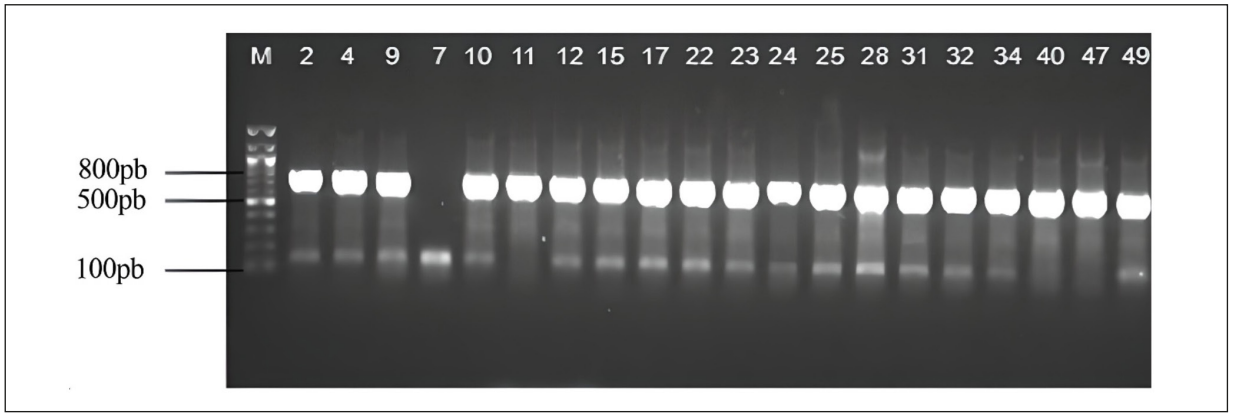

Figure 2. PCR image of *KPC-2* gene positive (761 bp) *K. pneumoniae* isolates. M: Marker; 7: KPC-2 negative sample.

robacter freundii, and other *Enterobacteriaceae* species. *KPC* carbapenemases show a wide distribution worldwide, but more commonly, the majority of cases have been reported in the United States[42,43]. In the United States, *KPC* production has been associated with hospital outbreaks that have caused patient-to-patient transmission of resistant bacteria that are often clonally similar and related to each other in the biological system[44]. There are more than 20 *KPC* variants worldwide, but *KPC-2* and *KPC-3* are the most commonly reported and widespread variants[40,45]. Different KPCs have been reported in several *K. pneumoniae* sequence types (ST), although the major clones associated with pandemic spread are ST258, ST11, and, more recently, ST101[36,44,46,47]. It was observed that the *KPC-2* gene identified in our *K. pneumoniae* strains isolated from our

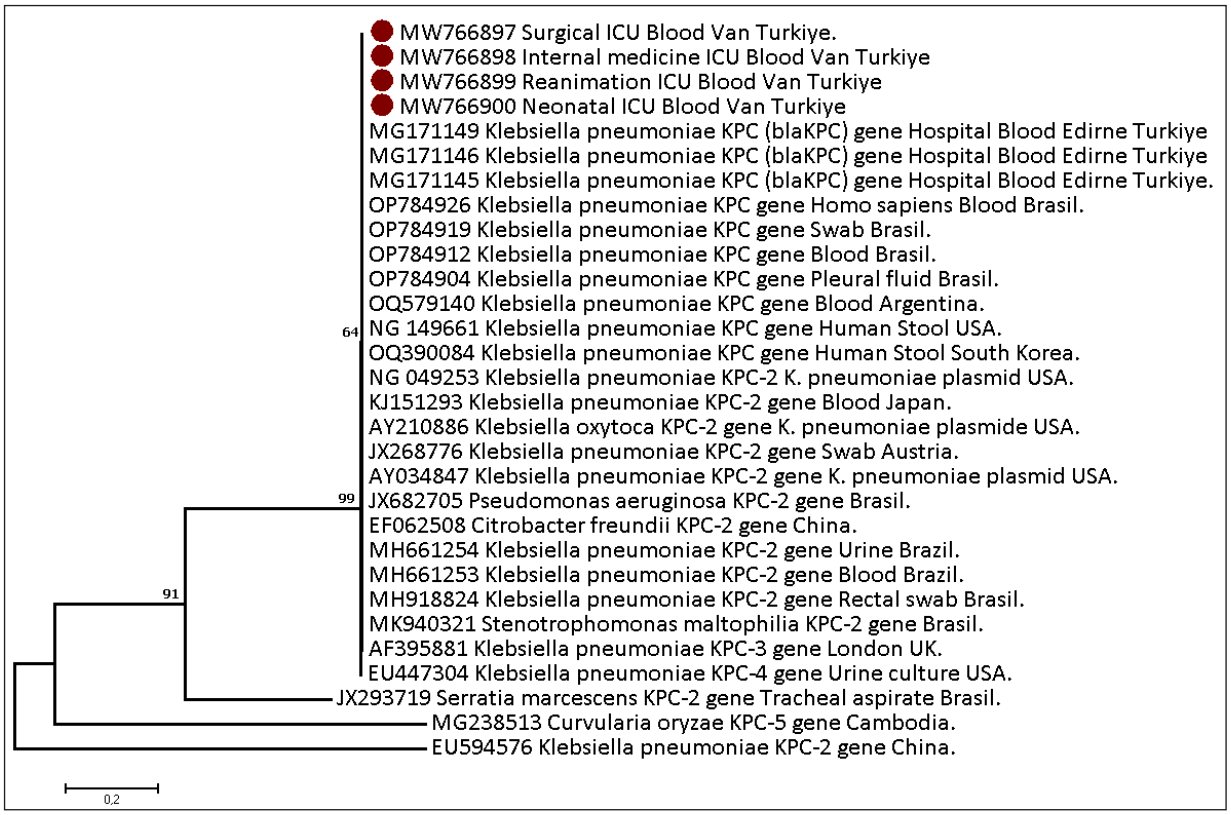

Figure 3. Phylogenetic analysis of *KPC-2* positive *K. pneumoniae* isolates.

hospital was similar to the variants obtained from different regions of the world. However, it was revealed that the isolated *KPC-2* genes may be different from other *KPC-2* variants. It was also discovered that *KPC-2*-positive *K. pneumoniae* isolates are ST11 clones and may cause pandemic spread. In addition to the health services provided, it was seen that it is very important to inform hospital personnel about this issue.

Klebsiella pneumoniae is becoming rapidly identified, often because it has shown resistance to many of the new antibiotics in clinical use. They are particularly problematic in hospitals where they cause acute infections in a number of patients. Rising trends in the number of isolations of *K. pneumoniae* are of concern. In economically developed countries (e.g., China, USA), the possibility of bacterial resistance may increase in a medical system where the latest antibiotics are used and the chances of exposure are increased. Although imipenem and meropenem show favorable activity against *Enterobacteriaceae*[48], the public health implications of *K. pneumoniae* seem to be reiterated for the observed situation. The worldwide presence and spread of antimicrobial resistance genes, such as extended-spectrum beta-lactamase (ESBL) and carbapenemase genes in *K. pneumoniae* isolates, pose a serious threat to public health. This is because infections caused by multidrug-resistant gram-negative bacteria have long been treated with carbapenems. The rapid global occurrence of *K. pneumoniae* strains resistant to almost all β-lactams, including carbapenems, demonstrates the organism's ability to rapidly respond to pressure differences in selective environmental conditions. Overuse and misapplication of carbapenems is one of the reasons for the development of plasmid-mediated carbapenemases, enzymes that hydrolyze all β-lactams, including carbapenems[49]. *BlaKPC* genes, which confer increased resistance to almost all β-lactam antibiotics in *K. pneumoniae*, are mostly carried by plasmids. The detection of carbapenemases is important from an epidemiological point of view as they are plasmid-mediated and can be horizontally transferred between different bacterial species[50]. Furthermore, the resistance of *K. pneumoniae* to a cephalosporin (e.g., ceftazidime, cefepime, and cefotaxime) may also be partly associated with the *KPC* gene since the KPC enzyme has the ability to hydrolyze broad-spectrum cephalosporins. Therefore, it may be an indicator to identify *KPC*-mediated genes resistant to these cephalosporins (e.g., ceftazidime, ceftriaxone, and cefotaxime). In our study, 27 *KPC-2*-positive *K. pneumoniae* isolates were resistant to most of the tested antibiotics. However, it is noteworthy that these isolates were susceptible to antibiotics such as AK, CN, CT and TGC. In particular, the lack of resistance to CT, which has been used extensively in recent years, is an important finding. On the contrary, it was observed that there was a high rate of β-lactam resistance in all of the *KPC-2*-positive strains obtained worldwide. It was also observed that quinolone resistance was common in all strains. It is inevitable that these high rates of resistance will cause serious problems in the treatment of patients.

Conclusions

In conclusion, it was observed that a significant proportion of *K. pneumoniae* strains were isolated from blood cultures of patients admitted to our hospital (especially intensive care unit patients). A significant proportion of these isolates were found to be resistant to different antibiotics at the same time. Especially cabapenem and extended-spectrum β-lactam resistance were determined as serious threats to the health of patients. The presence of *KPC-2* and ST11 variant features in *K. pneumoniae* strains showing multidrug resistance was found to be dangerous in terms of the potential for pandemic spread. These data were shared in our hospital in terms of surveillance and training of healthcare professionals.

Conflict of Interest

The authors declare that they have no conflict of interest.

Data Availability

All data generated or analyzed during this study are included in this published article; the datasets are available from the corresponding author upon reasonable request.

Ethics Approval

The research Ethics Committee of Van Training and Research Hospital authorized our study (decision dated 25/01/2018 and numbered 2018/02) by evaluating the accuracy of our research.

Informed Consent
Written informed consent was obtained from all participants prior to their inclusion in the study.

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Authors' Contribution
All authors equally contribute to the present manuscript preparation.

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