Novel Carbapenem-Resistant *Klebsiella pneumoniae* ST147 Coharboring *bla*<sub>NDM-1</sub>, *bla*<sub>OXA-48</sub> and Extended-Spectrum β-Lactamases from Pakistan

Aamir Jamal Gondal, Sidrah Saleem, Shah Jahan, Nakhshab Choudhry, Nighat Yasmin

**Purpose:** The emergence of multidrug-resistant *Klebsiella pneumoniae* (*K. pneumoniae*) is associated with the acquisition of multiple carbapenemases. Their clonal spread is a worldwide concern due to their critical role in nosocomial infections. Therefore, the identification of high-risk clones with antibiotic resistance genes is very crucial for controlling its global spread.

**Materials and Methods:** A total of 227 *K. pneumoniae* strains collected during April 2018 to November 2019 were confirmed by PCR. Carbapenemases and extended-spectrum β-lactamases (ESBL) were detected phenotypically. Confirmation of carbapenemases was carried out by PCR and Sanger sequencing. The clonal lineages were assigned to selected isolates by multilocus sequence typing (MLST), and the plasmid analysis was done by PCR-based detection of the plasmid replicon typing.

**Results:** Of the total *K. pneumoniae*, 117 (51.5%) were carbapenem resistant (CRKP) and 140 (61.7%) were identified as ESBL producers. Intermediate to high resistance was detected in the tested β-lactam drugs while polymyxin-B and tigecycline were found to be susceptible. Among CRKP, 91 (77.8%) isolates were detected as carbapenemase producing, while 55 (47%) were positive for *bla*<sub>NDM-1</sub>, 23.9% (n=28), *bla*<sub>OXA-48</sub> 22.2% (n=26) and *bla*<sub>VIM</sub> 0.85% (n=1) while 12.7% (n=7) carried both *bla*<sub>NDM-1</sub> and *bla*<sub>OXA-48</sub> genes. The CRKP coharboring *bla*<sub>NDM-1</sub> and *bla*<sub>OXA-48</sub> genes (n=7) were positive for *bla*<sub>CTX-M</sub>, *bla*<sub>SHV</sub> (n=3), *bla*<sub>SHV</sub> (n=1) and *bla*<sub>CTX-M</sub> (n=3). The novel CRKP with the coexistence of *bla*<sub>NDM-1</sub>, *bla*<sub>OXA-48</sub>, *bla*<sub>CTX-M</sub> and *bla*<sub>SHV</sub> genes were associated with the high-risk clone ST147 (n=5) and ST11 (n=2). The assigned replicon types were IncI/M, IncFII, IncA/C and IncH1.

**Conclusion:** This is the first report of the coexistence of *bla*<sub>NDM-1</sub>, *bla*<sub>OXA-48</sub>, *bla*<sub>CTX-M</sub> and *bla*<sub>SHV</sub> genes on a high-risk lineage ST147 from Pakistan. This study highlights the successful dissemination of carbapenemase resistance genes in the high-risk clones that emphasizes the importance of monitoring and controlling the spread of these diverse clones globally.

**Keywords:** high-risk clone, New Delhi metallo-β-lactamase, MLST, *K. pneumoniae*, carbapenem resistance

**Introduction**

Accelerated emergence and effective propagation of carbapenem-resistant *Klebsiella pneumoniae* (CRKP) across the world have become a prominent public health challenge due to high mortality rate in healthcare-associated nosocomial
infections. The CRKP has a unique ability to acquire multiple resistance encoding genes through horizontal gene transfer interceded by broad-host-range plasmids, transposons and insertion sequences thereby turning out as one of the most successful nosocomial pathogen. Lack of stewardship and irrational use of carbapenems for the infections of ESBL producing K. pneumoniae has led to the evolution of transmissible plasmid-encoding resistance genes that supported the selection of high-risk clones of CRKP involving diverse geographic regions and populations. During 2014, the World Health Organization declared CRKP as the third most critical nosocomial pathogen for future concern. As carbapenemases and ESBL/AmpC β-lactamases are critical in the acquisition of multidrug resistance, the identification of such broad-spectrum resistance genes is required for the development of new intervention strategies.

Clinically important carbapenemase genes encompass blaKPC-2, blaVIM, blaIMP, blaNDM-1 and blaOXA-48. Global dissemination of such plasmid-encoded carbapenemases has increased alarmingly yet their geographic prevalence varies significantly. Clinical literature remains expressive about the linkage of NDM-1, most common MBL-type carbapenemase and its transmission to other parts of the world from the endemic areas of Indian subcontinent since the first isolation of blaNDM-1 producing K. pneumoniae ST14 and Escherichia coli (E. coli) in a patient treated in India and later shifted to Sweden in 2001. Frequent reports of NDM-1, KPC-2 and OXA-48 type carbapenemase are available from Pakistan during the past decade. Similarly, the OXA-48 is endemic in several countries since its first identification from Turkey in 2001. CRKP co-harboring at least two carbapenemases were reported globally such as KPC-3 and VIM-2 in Italy, NDM-1 and KPC-2 from Brazil and Pakistan, NDM-1 and OXA-48 in Morocco, Switzerland, China and Sultanate of Oman. However, the understanding of molecular and genetic context of the carbapenemases is scarce especially in the developing countries.

Carbapenemases have spread worldwide through evolution of high-risk clones by acquiring, retaining and efficiently transmitting resistance genes. Such globally identified high-risk K. pneumoniae clones for the dissemination of carbapenemases include ST258, ST11 and ST147 co-harboring broad range of plasmids. Several STs were found to be associated with blaNDM-1 producing K. pneumoniae such as ST258, ST340, ST512 and ST147 along with different plasmids IncF, IncAC and IncL/M. Therefore, careful detection and treatment strategies are required especially in developing countries where carbapenemase-producing strains have diverse opportunities.

However, insufficient data are available from Pakistan that describes molecular versatility of resistance genes in relation to genetic analysis and prevalence of high-risk clones. Hence, it is imperative to promptly detect and examine these successful clones to get insights into the global spread of antimicrobial drug resistance. Therefore, the current study aimed to ascertain the prevalence of carbapenemases and to analyze their clonal relatedness.

**Materials and Methods**

**Bacterial Collection and Identification**

Clinical strains were collected during the course of routine diagnostic bacterial cultures from tertiary care hospitals of Lahore, Pakistan. A total of 227 clinical strains of K. pneumoniae were included from different sample types from April 2018 to November 2019. The isolates were characterized phenotypically by colony morphology, Gram’s staining and biochemical characteristics by using API-20E according to the manufacturer’s instructions (BioMerieux, France). The study was sanctioned by institutional review board of the University of Health Sciences, Lahore, Pakistan.

**Antimicrobial Susceptibility Testing (AST)**

AST was carried out by standard disc diffusion method according to the CLSI guidelines using the following antibiotic discs: imipenem (IPM), meropenem (MEM), ertapenem (ETP), ceftazidime (CAZ), ampicillin (AMP), amoxicillin-clavulanic acid (AMC), cefepime (FEP), cefotaroline (CTP), aztreonam (ATM), gentamicin (CN), amikacin (AK), ciprofloxacin (CIP), doxycycline (DO), polymyxin-B (PB), tigecycline (TGC), cefotaxime (CTX), trimethoprim-sulfamethoxazole (SXT) and piperacillin-tazobactam (TZP) (Oxoid, UK). E. coli ATCC 25922 and Pseudomonas aeruginosa ATCC 27853 were used as quality control strains.

**Minimal Inhibitory Concentrations (MICs)**

MIC of antibiotics was determined by standard broth microdilution method using cation-adjusted Mueller-Hinton broth in accordance with CLSI guidelines with antibiotic concentrations ranging from 0.5 to 1024 μg/mL.
Phenotypic Characterization
Carbapenemases were identified phenotypically by carbapenem inactivation method (CIM) while the detection of ESBLs was carried out by double-disc synergy test (DDST) using amoxicillin-clavulanic acid alone and in combination with cefazidime as per the guidelines of CLSI.\textsuperscript{18}

DNA Isolation from Bacterial Strains
Genomic DNA was prepared from pure bacterial culture plates by heat lysis method as reported previously and stored at \textasciitilde20°C for onward processing.\textsuperscript{19}

Molecular Profile Analysis by Polymerase Chain Reaction (PCR)
Klebsiella species, carbapenemase resistance genes (\textit{blaNDM-1}, \textit{blaVIM}, \textit{blaTEM} and \textit{blaOXA-48}) and ESBL encoding genes (\textit{blaTEM}, \textit{blaCTX-M} and \textit{blaSHV}) were detected through PCR using specific primers as given in Table 1. PCR reaction mixture of 50 μL consisting of 25 μL of 2x PCR Master Mix, 1 μL of each primer, 2 μL of DNA and dH\textsubscript{2}O upto 50 μL. Amplification was carried out in thermal cycler (Proflex, ABI) with different annealing temperatures given in Table 1. Agarose gel (1–1.5%) was used to resolve and analyze the PCR products. \textit{blaNDM-1} genes were further analyzed for allelic discrimination by Sanger’s sequencing method. \textit{K. pneumoniae} ATCC BAA-2146 was used as NDM positive control.

Multilocus Sequence Typing (MLST) of Klebsiella Species
MLST of CRKP strains coharboring \textit{blaNDM-1} and \textit{blaOXA-48} was performed using seven housekeeping genes (\textit{gapA}, \textit{infB}, \textit{mdh}, \textit{pgi}, \textit{phoE}, \textit{rpoB} and \textit{tonB}) as described by \textit{K. pneumoniae} MLST website.\textsuperscript{20} The mutation analysis of NDM-1 was carried out by cycle sequencing using specific primers given in Table 1. The cycle sequencing was performed by BigDye terminator v3.1 kit on Proplex thermal cycler while the sequencing products were analyzed through capillary electrophoresis on Genetic Analyzer AB-3500 (Life Technologies by Thermo Fisher, USA) as per the kit instructions. Data were analyzed by using the sequencing analysis software v6.1 and checked on basic local alignment (BLAST) at NCBI for allele identification. CRKP STs were assigned using the MLST database (http://bigsdb.pasteur.fr/klebsiella/klebsiella. html).

Plasmid Analysis
CRKP coharboring \textit{blaNDM-1} and \textit{blaOXA-48} were further analyzed for the presence of plasmids. Plasmid DNA was extracted from single colony of CRKP by using the plasmid isolation kit (Thermo Fisher Scientific) and DNA was stored at \textasciitilde20°C. The samples were run on 0.8% agarose gel for the detection of plasmids. Plasmids were classified according to their incompatibility groups by using the PCR-based replicon typing method as described before.\textsuperscript{21}

Results
During the 19-month study period, 227 clinical strains of Klebsiella were identified by phenotypic and genotypic methods. Of the total, 129 (56.8%) were isolated from males while remaining 98 (43.2%) were from females. These isolates were collected from wound 29.5% (\textit{n}=67), pus 17.6% (\textit{n}=40), blood 15.5% (\textit{n}=35), tracheal secretion 13.2% (\textit{n}=30), sputum 11% (\textit{n}=25), urine 7.04% (\textit{n}=16) and tissue 6.16% (\textit{n}=14). Isolates originated from different sections of the hospital such as general surgery 26.4% (\textit{n}=60), SICU 18.5% (\textit{n}=42), general medicine 15.8% (\textit{n}=36), dermatology 5.72% (\textit{n}=13), nephrology 4.40% (\textit{n}=10), chest medicine 8.37% (\textit{n}=19), cardiology 3.96% (\textit{n}=9), pediatric medicine 7.04% (\textit{n}=16), oncology 5.28% (\textit{n}=12) and orthopedic surgery 4.40% (\textit{n}=10).

Antimicrobial Susceptibility Testing and Phenotypic Confirmatory Tests
As high as 51.5% (\textit{n}=117) clinical strains of \textit{K. pneumoniae} were carbapenem resistant (CRKP) while remaining 48.5% (\textit{n}=110) were susceptible (CS). Out of 117 CRKP, 77.7% (\textit{n}=91) were detected as carbapenemase-producing strains (CPKP). Most of the CRKP exhibited resistant to intermediate resistant profile for the β-lactam combination agents, carbapenems, fluoroquinolones, aminoglycosides and trimethoprim/sulfamethoxazole. Antimicrobial resistance pattern of CRKP strains was as follows: meropenem (96.9%), imipenem (98%), ertapenem (90%), amoxicillin/clavulanic acid (93.5%), ceftazidime (91.2%), ceftriaxone (96%), cefotaxime (95%), aztreonam (90.3%), ciprofloxacin (87%), amikacin (37.1%), tigecycline (21.1%) and polymyxin-B (13.7%). The MIC values of the tested β-lactam antibiotics were as follows: 4 to >1024 mg/L for ertapenem, 8 to >1024 mg/L for meropenem, 8 to >1024 mg/L for imipenem in all tested strains. All of the isolates were recognized as MDR (72%) or XDR (28%). The MIC results of the selected strains are given in Table 2.
## Table 1 Primer Sequences Used for PCR

<table>
<thead>
<tr>
<th>Gene</th>
<th>Primer Sequence (5′–3′)</th>
<th>Annealing (°C)</th>
<th>Amplicon Size (bp)</th>
<th>Reference</th>
</tr>
</thead>
</table>
| `rpoB` (K. pneumoniae) | F: CAA CGG TGT GGT TAC TGA CG  
R: TCT ACG AAG TGG CCG TTT TC                                                                 | 55              | 108                | 53        |
| `pehX` (K. oxytoca) | F: GAT ACG GAG TAT GCC TTT ACG GTG  
R: TAG CCT TTA TCA AGC GGA TAC TGG                                                                 | 55              | 343                | 53        |
| `gyrA` (Klebsiella genus) | F: CGC GTA CTA TAC GCC ATG AAC GTA  
R: ACC GTT GAT CAC TTC GGT CAG G                                                                 | 55              | 441                | 53        |
| `blaSHV` | F: CTT TAT CGG CCC TCA CTC AA  
R: AGG TGC TCA TCA TGG GAA AG                                                                 | 55              | 237                | 54        |
| `blaTEM` | F: CGC CGA ATA CAC TAT TCT CAG AAT GA  
R: ACG CTC ACC GGC TCC AGA TTT AT                                                                 | 55              | 445                | 54        |
| `blaCTX-M` | F: ATG TGC AGY ACC AGT AAR GTK ATG GC  
R: TGG GTR AAR TAR GTS ACC AGA AYC AGC GG                                                                 | 55              | 593                | 54        |
| `blaNDM-1` | F: ATG GAA TTG CCC AAT ATT ATG CAC  
R: TCA GGC CAG CTT GTC GGC                                                                 | 52              | 813                | 55        |
| `blaVIM` | F: GAT GGT TGT TGG TCG CAT A  
R: CTA ATG CGC AGC ACC AG                                                                 | 52              | 390                | 56        |
| `blaOXA-48` | F: GGC TGG TTA AGG ATG AAC AC  
R: CAT CAA GTT CAA CCC AAC CG                                                                 | 52              | 438                | 56        |
| `blaIMP` | F: GGA ATG GAG TGG CCT AAY TCT C  
R: GGT TTA AYA AAA CAA CCA CC                                                                 | 52              | 232                | 56        |
| `blaNDM-1` | F: TGGGTTTTGAAACTGCTGCACC  
R: CTTGACACTCGAAATGCAGCCA                                                                 | 60              | 1000               | 57        |
| `gapA` | F: TGA AGT ATG ACT CCA CTC ACG G  
R: AAC GCC TTT CAT TGC GCC TTC GGA A                                                                 | 60              | 662                | 20        |
| `infB` | F: CTC TCT GCT GGA CTA CAT TCG  
R: CGC TTT CAG CTC CAG AAC TTC                                                                 | 52              | 462                | 20        |
| `mdh` | F: CCC AAC TGC CTT CAG GTT CAG  
R: CCT TCC ACG TAG GGC CAT TCC                                                                 | 52              | 756                | 20        |
| `pgi` | F: GAG AAA AAC CTG CCG GTG CTG CTG  
R: CAG TTA ATC AGG CCG TTA GTG GAG C                                                                 | 52              | 566                | 20        |
| `phoE` | F: ACC TGG CGC AAC ACC GAT TCC TTC  
R: TTC AGC TGG TTG ATT TTG TAA TCC AC                                                                 | 52              | 602                | 20        |
| `rpoB` | F: GCC GAA ATG GCC GAA AAC CA  
R: GAG TCT TCG AAG TTG TAA CC                                                                 | 52              | 1075               | 20        |
| `tonB` | F: CTC TAT ACT TCG GTA CAT CAG GTT  
R: CCT GTT TGG CCG CCA GCA CTT GGT                                                                 | 48              | 539                | 20        |

Significantly higher frequency of CPKP was observed in wound samples 49.4% (n=45; p=0.002), pus samples 27.4% (n=25; p=0.026) and tracheal secretion samples 23.2% (n=21; p=0.029). Clinical strains of CRKP from wound and pus samples were significantly associated with the general surgery (p<0.001) while those from tracheal secretion samples were significantly associated with the SICU (p=0.008) as compared to the other samples obtained from the general surgery and SICU.

Out of 227 K. pneumoniae strains, 61.6% (n=140) were ESBL producers and 38.3% (n=87) were non-ESBL producers. Among the 140 strains of ESBL producing K. pneumoniae, 9.28% (n=13) isolates were resistant to one of the third-generation cephalosporins (3GCs), 28.5% (n=40) were resistant against 2 of the 3GCs and 62.1% (n=87) were resistant to all the 3GCs. Association analysis demonstrated that 80% (n=112) ESBL producers were collected from the samples of wound, pus and tracheal secretions (p=0.003).

**Antibiotic Resistance Genes**

Out of 117 CRKP, 47% (n=55) were positive for the carbapenemase resistance genes by PCR including bla<sub>NDM-1</sub> 23.9% (n=28), bla<sub>OXA-48</sub> 22.2% (n=26) and bla<sub>VIM</sub> 0.85% (n=1); bla<sub>IMP</sub> was not detected. However, 12.7% (n=7) of CPKP coharbored bla<sub>NDM-1</sub> and bla<sub>OXA-48</sub> genes. bla<sub>NDM-1</sub> positive strains were further confirmed by DNA sequencing. The presence of the β-lactamase-encoding genes bla<sub>CTX-M</sub>, bla<sub>TEM</sub> and bla<sub>SHV</sub> was detected in the ESBL-producing K. pneumoniae strains (n=140). Single ESBL gene was detected in 38.5% (n=54): bla<sub>CTX-M</sub> 10.7% (n=15), bla<sub>SHV</sub> 22.8% (n=32), bla<sub>TEM</sub> 5% (n=7) and double ESBL genes were detected in 61.4% (n=86): bla<sub>CTX-M</sub>, bla<sub>SHV</sub> 32.1% (n=45), bla<sub>TEM</sub>, bla<sub>SHV</sub> 12.1% (n=17), bla<sub>TEM</sub>, bla<sub>CTX-M</sub>...
Table 3 Resistance Profile of Carbapenem-Resistant K. pneumoniae

<table>
<thead>
<tr>
<th>Strain ID</th>
<th>Ward</th>
<th>Sample Type</th>
<th>MIC (μg/mL)</th>
<th>Resistance Profile</th>
<th>Profile of Resistance Genes</th>
<th>Replicon and Sequence Type</th>
</tr>
</thead>
<tbody>
<tr>
<td>KP-17</td>
<td>SICU</td>
<td>Wound</td>
<td>256</td>
<td>MDR</td>
<td>blaNDM-1 (MT312213)*, blaOXA-48, blaCTX-M, blaSHV</td>
<td>ST147, IncL/M, IncF11, IncA/C, IncF1H</td>
</tr>
<tr>
<td>KP-97</td>
<td>SICU</td>
<td>Pus</td>
<td>64</td>
<td>XDR</td>
<td>blaNDM-1 (MT320894)*, blaCTX-M, blaSHV</td>
<td>-</td>
</tr>
<tr>
<td>KP-104</td>
<td>OPD</td>
<td>Wound</td>
<td>32</td>
<td>MDR</td>
<td>blaNDM-1 (MT320895)*, blaCTX-M, blaSHV</td>
<td>-</td>
</tr>
<tr>
<td>KP-188</td>
<td>SICU</td>
<td>Tracheal secretion</td>
<td>64</td>
<td>MDR</td>
<td>blaNDM-1 (MT320896)*, blaSHV</td>
<td>-</td>
</tr>
<tr>
<td>KP-191</td>
<td>GS</td>
<td>Wound</td>
<td>16</td>
<td>MDR</td>
<td>blaNDM-1 (MT320897)*, blaCTX-M</td>
<td>-</td>
</tr>
<tr>
<td>KP-194</td>
<td>GS</td>
<td>Wound</td>
<td></td>
<td>MDR</td>
<td>blaNDM-1 (MT320898)*, blaSHV</td>
<td>-</td>
</tr>
<tr>
<td>KP-199</td>
<td>OPD</td>
<td>Pus</td>
<td>&gt;1024</td>
<td>XDR</td>
<td>blaNDM-1 (MT320899)*, blaOXA-48, blaCTX-M, blaSHV</td>
<td>ST147, IncL/M, IncF11, IncA/C, IncF1H</td>
</tr>
<tr>
<td>KP-222</td>
<td>GS</td>
<td>Sputum</td>
<td>128</td>
<td>MDR</td>
<td>blaNDM-1 (MT320900)*, blaOXA-48, blaCTX-M, blaSHV</td>
<td>ST147, IncL/M, IncF11, IncA/C, IncF1H</td>
</tr>
<tr>
<td>KP-246</td>
<td>GS</td>
<td>Wound</td>
<td>32</td>
<td>XDR</td>
<td>blaNDM-1 (MT320901)*, blaCTX-M</td>
<td>-</td>
</tr>
<tr>
<td>KP-268</td>
<td>SICU</td>
<td>Tip cells</td>
<td>64</td>
<td>XDR</td>
<td>blaNDM-1 (MT320902)*, blaTEM, blaCTX-M, blaSHV</td>
<td>-</td>
</tr>
<tr>
<td>KP-272</td>
<td>GS</td>
<td>Wound</td>
<td>32</td>
<td>MDR</td>
<td>blaNDM-1 (MT320903)*, blaCTX-M, blaSHV</td>
<td>-</td>
</tr>
<tr>
<td>KP-284</td>
<td>GS</td>
<td>Wound</td>
<td>8</td>
<td>MDR</td>
<td>blaNDM-1 (MT320904)*, blaCTX-M, blaSHV</td>
<td>-</td>
</tr>
<tr>
<td>KP-289</td>
<td>GS</td>
<td>Wound</td>
<td>16</td>
<td>XDR</td>
<td>blaNDM-1 (MT320905)*, blaTEM</td>
<td>-</td>
</tr>
<tr>
<td>KP-315</td>
<td>SICU</td>
<td>Tracheal secretion</td>
<td>32</td>
<td>XDR</td>
<td>blaNDM-1 (MT320906)*, blaSHV</td>
<td>-</td>
</tr>
<tr>
<td>KP-333</td>
<td>GS</td>
<td>Pus</td>
<td>32</td>
<td>MDR</td>
<td>blaNDM-1 (MT320908)*, blaSHV</td>
<td>-</td>
</tr>
<tr>
<td>KP-426</td>
<td>BURN</td>
<td>Tracheal secretion</td>
<td>64</td>
<td>MDR</td>
<td>blaNDM-1 (MT320909)*, blaCTX-M</td>
<td>-</td>
</tr>
<tr>
<td>KP-443</td>
<td>GS</td>
<td>Wound</td>
<td>64</td>
<td>MDR</td>
<td>blaNDM-1 (MT320910)*</td>
<td>-</td>
</tr>
<tr>
<td>KP-494</td>
<td>SICU</td>
<td>Tracheal secretion</td>
<td>64</td>
<td>MDR</td>
<td>blaNDM-1 (MT320912)*, blaOXA-48, blaCTX-M, blaSHV</td>
<td>ST147, IncL/M, IncF11, IncA/C</td>
</tr>
<tr>
<td>KP-544</td>
<td>GS</td>
<td>Blood</td>
<td>32</td>
<td>XDR</td>
<td>blaNDM-1 (MT320913)*</td>
<td>-</td>
</tr>
<tr>
<td>KP-562</td>
<td>SICU</td>
<td>Tracheal secretion</td>
<td>64</td>
<td>MDR</td>
<td>blaNDM-1 (MT320914)*, blaCTX-M</td>
<td>-</td>
</tr>
<tr>
<td>KP-611</td>
<td>PS</td>
<td>Pus</td>
<td>128</td>
<td>XDR</td>
<td>blaNDM-1 (MT320915)*, blaCTX-M</td>
<td>-</td>
</tr>
<tr>
<td>KP-663</td>
<td>GS</td>
<td>Wound</td>
<td>64</td>
<td>MDR</td>
<td>blaNDM-1 (MT320916)*, blaSHV</td>
<td>-</td>
</tr>
<tr>
<td>KP-675</td>
<td>SICU</td>
<td>Tracheal secretion</td>
<td>128</td>
<td>MDR</td>
<td>blaNDM-1 (MT320917)*, blaOXA-48, blaCTX-M</td>
<td>ST11, IncL/M, IncF11, IncA/C</td>
</tr>
</tbody>
</table>

(Continued)
15% (n=21) and bla\textsubscript{TEM}, bla\textsubscript{SHV}, bla\textsubscript{CTX-M} 2.14% (n=3). The CRKP strains coharboring bla\textsubscript{NDM-1} and bla\textsubscript{OXA-48} genes (n=7) were positive for bla\textsubscript{CTX-M}, bla\textsubscript{SHV} (n=3), bla\textsubscript{SHV} (n=1) and bla\textsubscript{CTX-M} (n=3). The results are shown in Table 3.

### Sequence Type Analysis and Plasmid Detection of NDM-1 Producing Isolates

CRKP coharboring bla\textsubscript{NDM-1} and bla\textsubscript{OXA-48} (n=7) were further analyzed for sequence typing. High-risk \textit{K. pneumoniae} clones ST147 coharbored bla\textsubscript{NDM-1}, bla\textsubscript{OXA-48}, bla\textsubscript{CTX-M}, bla\textsubscript{SHV} (n=3), bla\textsubscript{NDM-1}, bla\textsubscript{OXA-48} bla\textsubscript{CTX-M} (n=2), while ST11 coharbored bla\textsubscript{NDM-1}, bla\textsubscript{OXA-48}, bla\textsubscript{SHV} (n=1) and bla\textsubscript{NDM-1}, bla\textsubscript{OXA-48}, bla\textsubscript{CTX-M} (n=1). Plasmid analysis of CRKP coharboring bla\textsubscript{NDM-1} and bla\textsubscript{OXA-48} identified the following replicon types: IncL/M, IncFII, IncA/C and IncH1.

### Discussion

The emergence of CRKP has resulted in limited effective treatment strategies thus posing a major healthcare threat worldwide.\textsuperscript{1} Global dissemination of transmissible carbapenemases by virtue of horizontal gene transfer involving certain high-risk clones\textsuperscript{9} has become alarming especially in developing countries in the backdrop of inconsistent antibiotic policies. \textit{K. pneumoniae} is among one of the most commonly detected multidrug-resistant member of the Enterobacteriaceae family.\textsuperscript{22}

In the present study, we identified 51.1% CRKP strains that consisted of 77.7% carbapenemase producers. A large-scale study conducted in Turkey has detected only 3.1% (n=45/1452) CRKP isolates,\textsuperscript{2} while from the European cohort study, 55% (n=944/1717) isolates were carbapenem resistant and 39.84% (n=684/1717) were carbapenemase producers.\textsuperscript{23} Similarly, 10.69% (n=247/2310) CRKP strains were reported previously.\textsuperscript{24} However, the highest percentages of carbapenem resistant and carbapenemase producers are reported from Pakistan such as another study identified 88% carbapenemase producers.\textsuperscript{25} Due to the presence of high carbapenem resistance among \textit{K. pneumoniae} in Pakistan, it is tempting to speculate that \textit{K. pneumoniae} strains have the ability to retain diverse resistance determinants especially in a situation of uncontrolled use of high amounts of antibiotics. Wound samples (49.4%) were the major source of the CRKP infection that were significantly associated with the general surgery ward. In line with our study, 40% of wound samples with carbapenemase production were reported recently in association with the emergency department.\textsuperscript{26} However, blood, urine, sputum, tracheal secretion and pus were the major source of CRKP in other studies.\textsuperscript{11,24,25,27-29} The identification of CRKP strains from different anatomical sites highlights the importance of diverse set of sampling sites for the surveillance studies.

In consistent with the previous studies,\textsuperscript{2,11,30-32} the most effective antibiotics against the isolates were polymyxin-B (13.7%) and tigecycline (21.1%). However, intermediate to high resistance levels were observed against carbapenemases (meropenem, imipenem and ertapenem) 90% to 98%, cephalosporins 86% to 92%, aztreonam 90.3%, ciprofloxacin 87% and amikacin 37.1% that counts for 72% MDR and 28% XDR isolates. Sattar et al\textsuperscript{12} have reported 45% MDR \textit{K. pneumoniae} strains with 85% to 90% resistance to cephalosporins and 30% resistance to imipenem. Another study from Pakistan reported 22.5% MDR \textit{K. pneumoniae} strains among the study population in 2013.\textsuperscript{13} The detailed analysis of antibiotic resistance among the \textit{K. pneumoniae} from Pakistan suggested that the resistance has been increasing.

The most frequently detected carbapenemases among \textit{K. pneumoniae} are bla\textsubscript{KPC} enzymes followed by bla\textsubscript{NDM-1}, bla\textsubscript{OXA-48-like} and bla\textsubscript{VIM} in \textit{K. pneumoniae}.\textsuperscript{22} In our study, the detailed resistome analysis revealed the presence of carbapenemase resistance genes in 55 out of 117 CRKP strains. The most commonly detected carbapenemase

---

**Table 3 (Continued).**

<table>
<thead>
<tr>
<th>Strain ID</th>
<th>Ward</th>
<th>Sample Type</th>
<th>MIC (g/mL)</th>
<th>Resistance Profile</th>
<th>Profile of Resistance Genes</th>
<th>Replicon and Sequence Type</th>
</tr>
</thead>
<tbody>
<tr>
<td>KP-668</td>
<td>GS</td>
<td>Pus</td>
<td>64</td>
<td>MDR</td>
<td>bla\textsubscript{NDM-1} (MT320918)*, bla\textsubscript{TEM}, bla\textsubscript{SHV}</td>
<td>-</td>
</tr>
<tr>
<td>KP-687</td>
<td>SICU</td>
<td>Tracheal secretion</td>
<td>32</td>
<td>MDR</td>
<td>bla\textsubscript{NDM-1} (MT320919)*, bla\textsubscript{SHV}</td>
<td>-</td>
</tr>
<tr>
<td>KP-704</td>
<td>CM</td>
<td>Sputum</td>
<td>32</td>
<td>XDR</td>
<td>bla\textsubscript{NDM-1} (MT320920)*, bla\textsubscript{CTX-M}</td>
<td>-</td>
</tr>
</tbody>
</table>

*Note:* *GenBank Accession Number.

**Abbreviations:** GS, general surgery; PS, plastic surgery; SICU, surgical ICU; CM, chest medicine.
genes were \textit{bla}_{NDM-1} (23.9%; n=28/55) and \textit{bla}_{OXA-48} (22.2%; n=26/55) while \textit{bla}_{IMP} was identified in only 1 isolate and \textit{bla}_{IMP} was not detected. In consistent with our results, several studies from Pakistan reported that the most prevalent carbapenemase genes in Enterobacteriaceae/\textit{K. pneumoniae} are \textit{bla}_{NDM-1} 83.3% (n=30/37),\textsuperscript{25} 70% (n=10),\textsuperscript{28} 14.6% (n=13/82)\textsuperscript{34} followed by \textit{bla}_{OXA-48} 86% (n=49/57),\textsuperscript{35} 50% (n=5/10)\textsuperscript{28} and \textit{bla}_{VIM} 13.4% (n=11/82),\textsuperscript{34} 3.5% (n=2/57).\textsuperscript{35} The results of our study are also in line with the observations that India, Bangladesh and Pakistan are the major reservoir countries for the widespread dissemination of carbapenemase genes such as \textit{bla}_{NDM-1} and \textit{bla}_{OXA-48}.\textsuperscript{36} Since the first report of \textit{bla}_{NDM-1} detection in Pakistan in 2010,\textsuperscript{37} carbapenemase genes have spread significantly. Moreover, in the present study, the \textit{bla}_{NDM-1} and \textit{bla}_{OXA-48} coproduction was detected in 7 out of 55 CRKP. The co-occurrence of \textit{bla}_{NDM-1} and \textit{bla}_{OXA-48} has been reported previously in Asian and European countries.\textsuperscript{16,24,38-40} However, in Pakistan the coexistence of carbapenem-resistant genes is not commonly detected in \textit{K. pneumoniae}. In clinical isolates of \textit{K. pneumoniae}, \textit{bla}_{KPC-2}, \textit{bla}_{NDM-1} (n=2/20),\textsuperscript{12} \textit{bla}_{NDM-1}, \textit{bla}_{OXA-48} (n=2/10)\textsuperscript{28} and \textit{bla}_{VIM}, \textit{bla}_{NDM-1} (n=4/28) encoding genes in community-based E. coli isolates\textsuperscript{41} have been identified.

The CRKP strains cohaboring \textit{bla}_{NDM-1} and \textit{bla}_{OXA-48} examined in our study belonged to either ST11; single locus variant of ST258\textsuperscript{42} or emerging ST147 high-risk CRKP clone with resistance genes located on different plasmids.\textsuperscript{9} NDM-type carbapenemases have been described associated with ST11, ST14, ST147, ST340, ST149 and ST231.\textsuperscript{2} The ST11 is typically associated with the acquisition of multidrug resistance due to its ability to capture multiple plasmids\textsuperscript{42} and \textit{K. pneumoniae} strains with multiple resistance genes have been reported previously.\textsuperscript{43} In concurrence with this study, our data also revealed that different antimicrobial resistance and replicon type exist within the identified ST11 isolates. One of the ST11 isolate was polymyxin-B resistant while other was susceptible. Our results are in line with the previously reported study from Pakistan where out of 3 ST11 strains, 2 strains were colistin resistant and 1 strain was colistin susceptible.\textsuperscript{28} The ST11 isolates identified in our study cohabored \textit{bla}_{NDM-1} and \textit{bla}_{OXA-48} genes, whereas ST11 isolates positive for \textit{bla}_{NDM-1} (n=7), \textit{bla}_{NDM-7} (n=2) and \textit{bla}_{NDM-5} (n=1) were recently reported from Pakistan.\textsuperscript{25}

Previously, the pandemic lineage ST147 in \textit{K. pneumoniae} has been correlated with the spread of carbapenemase resistant genes such as \textit{bla}_{CTX-M}, \textit{bla}_{VIM}, \textit{bla}_{OXA-48}, \textit{bla}_{KPC} and \textit{bla}_{NDM-1}.\textsuperscript{44,45} ST147 has also been associated with \textit{bla}_{NDM-1}, \textit{bla}_{CTX-M}, \textit{bla}_{SHV},\textsuperscript{30} \textit{bla}_{CMY-4}, \textit{bla}_{OXA-48},\textsuperscript{46} \textit{bla}_{NDM-1}, \textit{bla}_{OXA-48},\textsuperscript{38} \textit{bla}_{NDM-1} and \textit{bla}_{OXA-48}.\textsuperscript{47} Antecedently, two studies are available from Pakistan that reported the existence of ST147 \textit{K. pneumoniae} with \textit{bla}_{OXA-181} resistant gene\textsuperscript{10} and ST147 \textit{K. pneumoniae} isolate with \textit{bla}_{NDM-1}, \textit{bla}_{NDM-5}.\textsuperscript{25} The coexistence of \textit{bla}_{NDM-1}, \textit{bla}_{OXA-48} has also been detected in ST307 from China\textsuperscript{16} and \textit{bla}_{NDM-1}, \textit{bla}_{OXA-232} in ST231 from Pakistan.\textsuperscript{27} However, in our study we have identified the co-emergence of \textit{bla}_{NDM-1}, \textit{bla}_{OXA-48}, \textit{bla}_{CTX-M}, \textit{bla}_{SHV} among ST147 (n=5), a globally spread high-risk clone. The identification of ST147 with \textit{bla}_{NDM-1}, \textit{bla}_{OXA-48}, \textit{bla}_{CTX-M}, \textit{bla}_{SHV} is alarming as it indicates that strong selection has occurred towards the resistance in these clinical isolates from Pakistan.

Subsequently, four replicon types IncL/M, IncFII, IncA/C and IncH1 were detected in the present study. Previous studies have shown that IncL/M-type plasmid was related to the OXA-48-type carbapenemases and responsible for the \textit{bla}_{OXA-48} gene dissemination.\textsuperscript{48} The molecular studies have reported that the most frequent replicon type identified in \textit{K. pneumoniae} species is IncFII replicon\textsuperscript{9} while IncA/C type replicons are responsible for the horizontal spread of NDM-type carbapenemase along with IncFIIK, IncL/M and IncH1.\textsuperscript{49} Moreover, among the typed resistant plasmids, IncL/M and IncFII plasmids may be regarded as epidemic as they have been detected in different countries with different origins and sources.\textsuperscript{50} On the other hand, IncR, IncFIIK-type and IncA/C type replicons have been identified in OXA-48-type carbapenemases and IncR type replicons in NDM-type carbapenemases.\textsuperscript{51} Previously reported replicon types among the NDM-producing \textit{K. pneumoniae} from Pakistan include IncN, IncA/C\textsuperscript{52} and IncFII, IncR.\textsuperscript{11} In our study, the identified replicon types (IncL/M, IncFII, IncA/C and IncH1) are reported to be responsible for OXA-48-type and NDM-type carbapenemases dissemination.

**Conclusion**

We reported the first identification of high-risk CRKP clone ST147 cohaboring several carbapenem resistance genes \textit{bla}_{NDM-1}, \textit{bla}_{OXA-48}, \textit{bla}_{CTX-M}, \textit{bla}_{SHV} from Pakistan. Taken into account the presence of highest genetic diversity among \textit{K. pneumoniae} worldwide, the identification of high-risk clone with multidrug resistance and coexistence of different classes of β-lactamases in the same strain highlight the severity of health challenges
posed by *K. pneumoniae* worldwide. Our findings suggested that the high antimicrobial resistance existed among study isolates that can also be associated with the presence of several β-lactams genes in a high-risk clone. Therefore, the continuous monitoring of carbapenemases is necessary to prevent the national and transnational spread of these powerful isolates especially in case when the healthcare facilities are inadequate.

**Acknowledgments**

We are thankful to the University of Health Sciences, Lahore, and King Edward Medical University, Lahore for the provision of samples and research facilities.

**Author Contributions**

All authors made substantial contributions to conception and design, acquisition of data, or analysis and interpretation of data; took part in drafting the article or revising it critically for important intellectual content; gave final approval of the version to be published and agreed to be accountable for all aspects of the work.

**Disclosure**

The authors report no conflicts of interest in this work.

**References**


