Molecular Epidemiology of NDM-1-Producing Enterobacteriaceae and Acinetobacter baumannii Isolates from Pakistan

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The molecular epidemiology of 66 NDM-producing isolates from 2 Pakistani hospitals was investigated, with their genetic relatedness determined using repetitive sequence-based PCR (Rep-PCR). PCR-based replicon typing and screening for antibiotic resistance genes encoding carbapenemases, other β-lactamases, and 16S methylases were also performed. Rep-PCR suggested a clonal spread of Enterobacter cloacae and Escherichia coli. A number of plasmid replicon types were identified, with the incompatibility A/C group (IncA/C) being the most common (78%). 16S methylase-encoding genes were carborked in 81% of NDM-producing Enterobacteriaceae.

With the worldwide spread of the NDM-1 gene and its variants (NDM-2 to NDM-8) (1, 2), molecular epidemiological studies of global isolates using various genotyping techniques are essential for gaining a better understanding of how this spread is occurring. India, Pakistan, and Bangladesh are clearly major reservoir countries for blaNDM, with numerous factors, such as antibiotic selection pressure, contributing to this current situation (3, 4). This study examines a group of 66 NDM-1-producing isolates from Pakistan for their genetic relatedness, phylotype, plasmid replicon type, and plasmid transferability.

All isolates were acquired from stool samples from 37 distinct patients at two military hospitals in Rawalpindi, Pakistan (5). The samples were collected from inpatients (35%) and outpatients (65%). The isolates were tested for susceptibility to 17 antimicrobials using the Vitek 2 system. The MICs for meropenem, doripenem, fosfomycin, and amdinocillin were determined using a standard agar dilution methodology (5).

The isolates were reconfirmed for the presence of the carbapenem resistance gene blaNDM-1 by PCR, as previously described (6). PCR was also performed to detect blaCTX-M-15, blaVIM, blaIMP, blablaKPC, blaOXA-1, blablaSHV, blablaTEM, blablaCTX-M-15 group, AmpC β-lactamases, blablaCMY-2, and the 16S rRNA methylase genes armA, rmtB, rmtC, and rmtF (6–9). The phylogenetic groups of Escherichia coli were determined using a multiplex (PCR)-based method (10).

Replicative sequenced-based PCR (Rep-PCR)-based typing by the DiversiLab system (bioMérieux, Oakleigh, Australia) was used for assessing clonal relatedness. A cluster of closely related isolates was defined as isolates sharing >95% similarity and indistinguishable isolates of >97% (11, 12). PCR-based replicon typing analysis (PBRT) was performed to determine the plasmid incompatibility (Inc) groups for all Enterobacteriaceae isolates (13).

Ten genetically diverse E. coli isolates, based on different Rep-PCR profiles and phylgroups, were selected for transformation studies and typing by multilocus sequence typing (MLST). MLST

<table>
<thead>
<tr>
<th>Resistance genes and plasmid replicon types of NDM-1-producing isolates</th>
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<tr>
<td><strong>NDM-producing isolates (no.)</strong></td>
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<tr>
<td>-----------------------------------------------</td>
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<tr>
<td>Escherichia coli (30)</td>
</tr>
<tr>
<td>Enterobacter cloaceae (21)</td>
</tr>
<tr>
<td>Citrobacter freundii (4)</td>
</tr>
<tr>
<td>Acinetobacter baumannii (3)</td>
</tr>
<tr>
<td>Klebsiella pneumoniae (3)</td>
</tr>
<tr>
<td>Pseudomonas aeruginosa (2)</td>
</tr>
<tr>
<td>Providencia rettgeri (2)</td>
</tr>
<tr>
<td>Citrobacter braakii (1)</td>
</tr>
<tr>
<td>Total no. of isolates</td>
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All isolates were negative for blablaCTX-M-15, blablaIMP, blablaSHV, and blablaKPC.

ND, not determined.

A. baumannii excluded from this total.
included seven conserved housekeeping genes and was performed according to the *E. coli* MLST Database (see http://mlst.warwick.ac.uk/mlst/dbs/Ecoli).

The transferability of *bla* \textsubscript{NDM-1}-carrying plasmids was investigated by electroporation. Plasmid DNA was prepared and electroporated into the recipient TOP10 *E. coli* (Invitrogen, Melbourne, Victoria, Australia), as previously described (6). Successful electrotransformants carrying *bla* \textsubscript{NDM-1} were confirmed by PCR. The plasmid replicon type of the transformants acquiring *bla* \textsubscript{NDM-1} carrying plasmids was confirmed by PBRT. Plasmid size was determined by performing S1 endonuclease (Promega; Madison, WI, USA) restriction digestion using pulsed-field gel electrophoresis (PFGE) (14). PCR-amplified DNA probes of *bla* \textsubscript{NDM-1} were labeled with digoxigenin nucleic acid (Roche, Mannheim, Germany).

Widespread dissemination of NDM-1 in Pakistan was first described in 2010 (15). In this study, we investigated the molecular epidemiology of a group of NDM-1-producing isolates from Pakistan, and we report here on the clonal relatedness of these isolates, providing an insight into the molecular characterization of *bla* \textsubscript{NDM-1}-carrying plasmids.

The majority of the NDM-1-producing *Enterobacteriaceae* isolates cohabored an extended-spectrum \( \beta \)-lactamase (ESBL) gene,
β-lactamase.

16S rRNA methylase gene

Phytype, MLST type Replicon Inc type

blaCTX-M-15 (70%), blaCMY-2 and the cooccurrence of 16S rRNA methylase genes encoding broad-spectrum aminoglycoside resistance, rmtB, rmtC, or armA, was detected in 47 (75%) isolates (Table 1). AmpC β-lactamase production coexisting with an ESBL was also high (n = 36 [73%]). The novel 16S rRNA methylase rmtF (16) was not detected; however, rmtB was found in 8 E. coli strains. A strong association between NDM-producing isolates harboring a 16S rRNA methylase-encoding gene has been well documented, particularly with rmtC. More recent studies in India, the United Kingdom, South Africa, and Nepal have reported the carriage of rmtF among NDM-harboring isolates (9, 17–19).

Of the 10 E. coli isolates subjected to electroporation, the blaNDM-1 plasmids in 4 isolates were successfully electroporated. Plasmid replicon typing of these transformants confirmed that blaNDM-1 resides on IncA/C-, IncN-, IncFIB-, and IncFII-type plasmids. These replicon types have been reported in Enterobacteriaceae in many regions of the world (4).

Southern hybridization (Fig. 1) of the E. coli donors and their transformants revealed blaNDM-1 plasmid sizes ranging from ~50 kb to ~350 kb. The majority of the blaNDM-1 plasmids were ~140 kb in size. Among the 30 E. coli isolates, there was a predominance of the phylogenetic group B1 (57%), followed by phylotypes A (40%) and D (3%). It has been suggested that the distribution of E. coli phylotypes may be geographically dependent (22). Mushtaq et al. (23) found a prevalence of phytype B1 among NDM isolates in Pakistan and no phytype B2. Our study shows similar results.

Rep-PCR revealed two dominant clones among Enterobacter cloacae, one large cluster (n = 17), designated ECLI, and one small cluster of three isolates (ECLII) (see Fig. 2). Three clonal types were observed among 17 E. coli isolates, and the remaining E. coli
isolates were diverse (Fig. 3). The three Klebsiella pneumoniae isolates were genetically diverse, while the three Acinetobacter baumannii isolates were considered identical (>99% similarity) (data not shown). Figure 4 shows the dendrogram for Citrobacter spp. and Pseudocitrobacter faecalis isolates (>99% similarity).

MLST differentiated the 10 representative E. coli strains into seven sequence types and one unknown sequence type (ST) (un-typeable). The sequence types included ST10 (n = 2), ST101 (n = 2), and single isolates representing STs 211, 226, 1431, 2598, and 3032. MLST studies on NDM-1-producing E. coli in the literature provide an incomplete and heterogeneous global distribution, suggesting a nonclonal pattern of spread for blaNDM-1 (24). In this study, the clinical isolates of E. coli representing STs 211, 226, 1431, 2598, and 3032 to our knowledge have not been reported in NDM-1-producing E. coli.

There were a number of limitations in our study, including the lack of clinical patient data and using fecal samples from 2 hospitals at a single point in time. It is difficult in this respect to obtain a clear epidemiological picture of NDM-producing isolates more widely in Pakistan.

The spread of blaNDM-1 is frequently associated with common and highly promiscuous plasmids resulting in a diverse range of species and clones harboring blaNDM-1. However, the molecular epidemiology of our study may indicate that blaNDM-1 additionally disseminates via dominant clones. The potential role of such dominant clones as a factor of blaNDM-1 spread may be underrepresented due to the lack of large-scale surveillance and molecular epidemiological studies monitoring blaNDM-1 dissemination. In this scenario, we can see a situation in which a single clone of NDM-1 may become epidemic or pandemic.

REFERENCES


