Detection of an IncA/C plasmid encoding VIM-4 and CMY-4 β-lactamases in Klebsiella oxytoca and Citrobacter koseri from an inpatient cardiac rehabilitation unit

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SUMMARY

A 62-year-old patient was transferred to the cardiac rehabilitation unit of the I.R.C.C.S. Fondazione S. Maugeri after undergoing a heart transplantation at the Acute Care Hospital I.R.C.C.S. S. Matteo of Pavia. On 1 August 2013 and during hospitalization in the rehabilitation unit, Klebsiella oxytoca and Citrobacter koseri clinical isolates were simultaneously recovered from the patient's preputial swab. Both the K. oxytoca and C. koseri strains were carbapenem-resistant by MicroScan System (Beckman Coulter). Carbapenem-resistant K. pneumoniae had previously been reported in the same rehabilitation facility.

The aim of the study was to identify the carbapenem resistance mechanisms among the enterobacterial species recovered. Phenotypic screening tests useful to detect the β-lactamases/carbapenemases were performed. Carbapenem MICs were obtained by Etest. AmpC and MBL encoding genes were identified by PCR and sequencing. Conjugation assays and plasmid characterization were performed.

Both of the K. oxytoca and C. koseri isolates were multi-drug resistant, showing resistance to amoxicillin-clavulanic acid, three generation cephalosporins, ertapenem (K. oxytoca MIC, >32 mg/L; C. koseri MIC, 4 mg/L), imipenem (K. oxytoca MIC, 4 mg/L; C. koseri MIC, 12 mg/L), thrimethoprim-sulphamethoxazole and gentamicin. Susceptibility was retained to fluoroquinolones, colistin and tigecycline. Molecular characterization confirmed the co-presence of blaCMY-4 and blaVIM-4 determinants in a 150 Kb transferable plasmid of IncA/C group.

This case is the first detection in Italy of the K. oxytoca and C. koseri clinical isolates co-producing the CMY-4 and VIM-4 enzymes.

KEY WORDS: Metallo-β-lactamases, Cephalosporinases, Multi-drug resistant Enterobacteriaceae, Rehabilitation unit.

INTRODUCTION

Klebsiella oxytoca and K. pneumoniae are opportunistic pathogens increasingly implicated in clusters of community and nosocomial outbreaks, particularly in specific medical units (Watson et al., 2005; Migliavacca et al., 2013).

The acquisition of an extended-spectrum β-lactamase (ESβL) is the most common mechanism of resistance to broad-spectrum cephalosporins in K. oxytoca (Romero et al., 2007; Sturm et al., 2010), while acquired AmpC cephalosporinases are less frequently detected in this species (Yamasaki et al., 2010). Since AmpC β-lactamase production is frequently accompanied by multi-drug resistance, therapeutic options became limited. In addition, failure to identify AmpC β-lactamase producers may lead to inappropriate antimicrobial treatment and may result in increased mortality (Tsakris et al., 2011). Citrobacter koseri, an environmental Gram-neg-
On 1 August 2013, Candida glabrata derwent a heart transplantation at the Acute Care Hospital I.R.C.C.S. S. Matteo of Pavia, were he unwell in February 2013. The man had been previously admitted to hospital in (Northern Italy) with a diagnosis of cardiac complications, septic shock, pneumonia and preputial edema.

On 18 July 2013, a 62-year-old male patient was admitted to the cardiac rehabilitation unit of the I.R.C.C.S. Fondazione S. Maugeri in Pavia (Northern Italy) with a diagnosis of cardiac complications, septic shock, pneumonia and preputial edema. The objective of this study was to evaluate the localization of \( \text{bla}_{\text{VIM}} \) and \( \text{bla}_{\text{CMY4}} \) resistance genes and to assess their spreading potential.

**MATERIALS AND METHODS**

On 18 July 2013, a 62-year-old male patient was admitted to the cardiac rehabilitation unit of the I.R.C.C.S. Fondazione S. Maugeri in Pavia (Northern Italy) with a diagnosis of cardiac complications, septic shock, pneumonia and preputial edema. The man had been previously admitted to hospital in February 2013, at the Acute Care Hospital I.R.C.C.S. S. Matteo of Pavia, were he underwent a heart transplantation.

On 1 August 2013 Candida glabrata, Pseudomonas aeruginosa, K. oxytoca and C. koseri were also isolated from both preputial swab and urine samples of the patient. The patient was then treated with colistin in monotherapy (EV 1.000.000 U 4/die). After the antibiotic therapy, both the samples resulted negative for the three bacterial species previously identified.

Species identification and susceptibility testing were carried out using the MicroScan AutoSCAN4 automated-system (Beckman Coulter). Ertapenem (ETP), meropenem (MER) and imipenem (IPM) MICs were determined by Etest (bioMérieux); the results were interpreted according to EUCAST 2014 criteria (The European Committee on Antimicrobial Susceptibility Testing, Version 3.1, 2014). Escherichia coli ATCC 25922 and P. aeruginosa ATCC 27853 were routinely included during testing for quality assurance.

The K. oxytoca and C. koseri strains were screened and than phenotypically confirmed for carbapenemase production by the Modified Hodge test (MHT) - using both ETP and IPM - and the KPC/MBL Confirm kit (Rosco Diagnostic).

Phenotypic ESBL and AmpC detection were performed with both the double disk synergy test (DD) (Jarlier, 1988), using piperacillin-tazobactam (TZP), cefotaxime (CTX), ceftazidime (CAZ) and aztreonam (ATM), and with the ESBL + AmpC Screen kit (Rosco Diagnostic). The β-lactamase preliminary identification was performed by Isoelectric focusing (IEF), as described elsewhere (Pagani et al., 2002).

Crude sonic extracts from E. coli harbouring TEM-1 (pI, 5.4), SHV-2 (pI., 7.6) and SHV-12 (pI,8.2) were used as Isoelectric point (pI.) markers. Conjugal transfer of resistance determinants was performed in liquid medium using the E. coli K12 strain J62 (\( \text{pro}, \text{his}, \text{trp}, \text{lac}, \text{Sm}^r \)) and J53 (\( \text{met}, \text{pro}, \text{Rif}^r \)) as recipients. The initial donor/recipient ratio was 0.01.

The transconjugants were selected on MacConkey agar containing CTX (8 mg/L) plus streptomycin (1000 mg/L) or rifampin (100 mg/L). Species identification and susceptibility testing of the obtained E. coli transconjugants were carried out by MicroScan AutoSCAN4 automated-system.

Transconjugants MICs against MER, ETP and IPM were determined by Etest (bioMérieux). The presence of \( \text{bla}_{\text{VIM}}, \text{bla}_{\text{TIM}} \) and \( \text{bla}_{\text{AMPc}} \) genes was assessed by multiplex PCR analysis using the primers and the conditions described elsewhere (Rossolini et al., 2008; Pérez-Pérez et al., 2002; Hujer et al., 2006; Koeleman et al., 2001).

PCR products were purified using the kit Quantum Prep PCR Kleen Spin Columns (BioRad) and subjected to double-strand sequencing (Macrogen Inc., Seoul, South Korea). The nucleotide sequences were analyzed according to...
the BLAST program (http://www.ncbi.nlm.nih.gov/blast/).
Plasmid DNA was extracted and purified by PureLink™ HiPure Plasmid Filter Purification Kits (Life technologies™).
Plasmids were subsequently typed according to their incompatibility group using the PBRT kit-PCR based replicon typing scheme, as described previously (Carattoli et al., 2006). The sizes of the plasmids were estimated using the S1 nuclease PFGE method (Barton et al., 1995).

RESULTS
The antimicrobial susceptibility results by MicroScan System showed that both of K. oxytoca and C. koseri isolates were characterized by multi-drug resistance, retaining susceptibility only to fluoroquinolones, colistin and tigecycline, and showing resistance to amoxicillin-clavulanic acid (AMC), third generation cephalosporins (3GC), cefoxitin, trimethoprim-sulfamethoxazole and gentamicin (according to the 2014 EUCAST breakpoints). The C. koseri isolate resulted resistant to ETP (MIC, >1 mg/L), IPM (MIC, >8 mg/L) and MER (MIC, >8 mg/L) by MicroScan System, while K. oxytoca was only ETP (MIC, >1 mg/L) and MER (MIC, >8 mg/L) resistant, showing a IPM MIC, 8 mg/L, using the same tool. These values were not always coherent with those of the Etest for K. oxytoca, ETP MIC being >32 mg/L; IPM MIC, 6 mg/L but MER MIC, 0.75 mg/L, lower than expected. The values for C. koseri were consistent only in the case of the ETP MIC >32 mg/L; with IPM MIC, 1 mg/L,

TABLE 1 - In vitro activity of selected antimicrobial agents tested against Citrobacter koseri, Klebsiella oxytoca and their transconjugants.

<table>
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<td>≤2/38</td>
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MIC: Minimum Inhibitory Concentration; According to European Committee on Antimicrobial Susceptibility Testing (EUCAST 2014) criteria: MIC values were determined using NBC46 card, AutoScan4 System (Beckman Coulter).
and a MER MIC lower than the expected, being equal to 0.5 mg/L.
MHT carbapenemase screening test showed positive results for both the isolates studied.
KPC/MBL Confirm kit and ESBL + AmpC Screen kit tests showed synergistic effect with both dipicolinic and boronic acid; this is typical of MBL and AmpC producers respectively.

The isolates were then further studied for β-lactamase production by biochemical and molecular assays.
Analytical IEF performed using crude enzymatic extracts from the clinical isolates and nitrocefin as chromogenic substrate, showed the presence of a unique β-lactamase band with pI 9.2. Both of the K. oxytoca and C. koseri donor strains were able to transfer the resistance plasmid to E. coli K12 strain J62 (pro, his, trp, lac, Smr) and J53 (met, pro-, Rifr) as recipients. Transfer of CTX resistance was observed at a frequency of approximately 10^3 transconjugants per recipient from both K. oxytoca and C. koseri.

Compared to the recipient E. coli J53 and J62 strains, the transconjugants exhibited a decreased susceptibility to several β-lactams (including carbapenems), trimethoprim-sulphamethoxazole and aminoglycosides. The resistance phenotypes of transconjugants were similar to those of the donors K. oxytoca and C. koseri for the other antimicrobial agents tested (Table 1).

PCR analysis performed on both donors and transconjugant strains yielded positive results for the co-presence of the \( bla_{VIM} \) and \( bla_{CMY} \) determinants in all the isolates. Amplicons sequencing revealed that K. oxytoca, C. koseri and E. coli transconjugants carried both \( bla_{VIM} \) and \( bla_{CMY} \) genes.

Plasmid analysis showed that the above resistance determinants were located in a 150 kb conjugative plasmid belonging to the IncA/C incompatibility group. The IncP and IncN incompatibility groups were also observed in K. oxytoca.

The IncA/C multi-resistance plasmid, from the E. coli transconjugant, was characterized. PCR results showed that the plasmid contained two distinct resistant loci carrying the VIM-4 and CMY-4 β-lactamase genes, with \( bla_{VIM} \) found as the first gene cassette of a class 1 integron.

**DISCUSSION**

Although VIM-type carbapenemases have already been described as widely spread in K. pneumoniae in Italian rehabilitation hospitals (Nucleo et al., 2013), to our knowledge this is the first report on the detection of MDR K. oxytoca and C. koseri clinical isolates co-producing VIM-4 and CMY-4 enzymes in Italy. The above clinical strains were both recovered from the preputial sample of a patient admitted to the cardiac rehabilitation unit of I.R.C.C.S. Fondazione S. Maugeri of Pavia.

The susceptibility profiles of the studied strains were coherent with carbapenemase production (MER MIC ≥0.5 mg/L), and phenotypic tests used for screening/confirmation of carbapenemase production yielded positive results. The co-presence of a CMY-type enzyme was suggested by IEF results (pI 9.2) and confirmed by PCR and sequencing.

CMY-4 enzyme differs from CMY-2 by one substitution (Arg for Trp at position 221) and from CMY-3 by two substitutions (Glu for Gly at position 42 and Ser for Asn at position 363). The deduced amino acid sequence is 98-99% identical to CMY-3 and to those of the plasmid-mediated AmpC-type β-lactamases originated from C. freundii.

The K. oxytoca and C. koseri MDR strains retained complete susceptibility to colistin. The administration of colistin monotherapy led to a positive outcome, with a complete resolution of the infection.

The \( bla_{VIM} \) and \( bla_{CMY} \) resistance genes were co-transferred to E. coli during conjugation. The high transfer frequency highlights the plasmid potential of diffusion and dissemination among susceptible isolates, also of different species.

The variability of plasmids mediating antimicrobial resistance in Enterobacteriaceae is high. There are plasmid families that are largely prevalent and also plasmids prevalently associated with specific resistance genes. The IncFII, IncA/C, IncL/M and IncI1 plasmids showed the highest occurrence among typed resistance plasmids. These plasmids can be considered “epidemic”, being detected in different countries, and in bacteria of different origins and sources. The occurrence of these plasmid types
seems closely linked to the selective pressure exerted by antimicrobial use, incrementing their prevalence compared to that observed in bacterial populations that are not preselected for antimicrobial resistance. Incompatibility group IncA/C plasmids are large, low copy, plasmids that have been described in the literature for over 40 years. However, they have only recently been intensively studied at the genomic level because of their association with the emergence of multi-drug resistance in enteric pathogens of humans and animals. These plasmids are unique among other enterobacterial plasmids in many aspects, including their modular structure and gene content.

Circulation of IncA/C plasmids in Gram-negative pathogens is now common, and these plasmids bring with them the ability to encode resistance to broad arrays of antimicrobial agents. Incompatibility group IncA/C plasmids are large, low copy, plasmids that have been described in the literature for over 40 years. However, they have only recently been intensively studied at the genomic level because of their association with the emergence of multi-drug resistance in enteric pathogens of humans and animals. These plasmids are unique among other enterobacterial plasmids in many aspects, including their modular structure and gene content.

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