

## Letter to the Editor

**First clonal spread of KPC-producing *Pseudomonas aeruginosa* in Buenos Aires, Argentina**

Sir:

*Pseudomonas aeruginosa* is one of the leading gram negative bacteria associated with hospital acquired infections, causing life threatening processes particularly in compromised patients at intensive care units ([www.aam.org.ar](http://www.aam.org.ar)). It may express a wide repertoire of resistance mechanisms and is able to acquire additional resistance genes (Bebrone, 2007; Juan Nicolau and Oliver, 2008). The increasing detection of carbapenemases, which exhaust therapeutic options avoiding carbapenem activity, is of great concern although the loss of the outer membrane protein OprD, overexpression of efflux pumps and hyperproduction of chromosomal class C β-lactamase may also contribute to develop full resistance to carbapenems (Quale et al., 2006; Santella et al., 2010a,b).

KPC enzymes hydrolyze at significant levels penicillins, cephalosporins, monobactams and carbapenems, and are weakly inhibited by clavulanic acid and tazobactam (Sacha et al., 2009; Walsh, 2010). Since the first detection of KPC-1/2 in *Klebsiella pneumoniae* in 2001 in USA, they have been encountered in many other *Enterobacteriaceae* from the Americas, Europe, Asia and Middle East (Yigit et al., 2001; Nordmann et al., 2009). Their wide propagation across multiple continents has been related to a mobile genetic element, Tn4401 (Naas et al., 2008) and to the successful dissemination of a single *K. pneumoniae* sequence type (ST) 258 clone (Kitchel et al., 2009; Cejas et al., 2012).

In 2007, KPC-2 emerged in a clinical *P. aeruginosa* isolate recovered in Colombia (Villegas et al., 2007), soon after, this enzyme was reported from *P. aeruginosa* from Trinidad y Tobago (Alpaka et al., 2009), USA (Poirel et al., 2010) and China (Ge et al., 2011). KPC-5 was described in *P. aeruginosa* isolated at Puerto Rico (Wolter et al., 2009).

Although KPC-2 producing *K. pneumoniae* are wide distributed in Buenos Aires hospitals and other regions of Argentina (Pasterán et al., 2008; Cejas et al., 2012), the presence of this enzyme has been only once reported from *P. aeruginosa* isolated in Bariloche placed 1700 km from Buenos Aires (Pasterán et al., 2011).

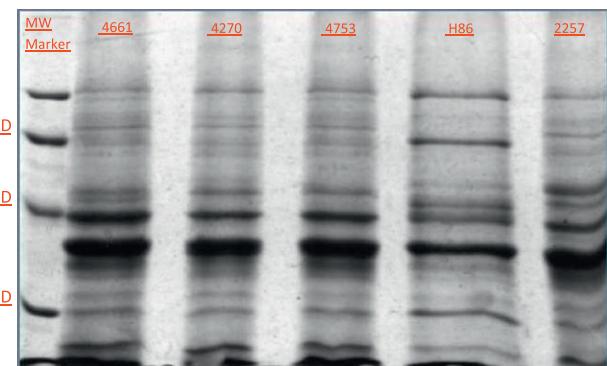
We report the first outbreak of clonally related KPC-producing *P. aeruginosa* in Buenos Aires, Argentina, which belong to the same sequence type of those isolates recovered previously in our country.

There were included three carbapenem resistant *P. aeruginosa* isolates from patients at the Intensive Care Unit (ICU) of a single hospital at Buenos Aires, Argentina, from July to September 2010. Susceptibilities to piperacillin, piperacillin-tazobactam, ceftazidime, cefepime, aztreonam, imipenem, meropenem, ciprofloxacin, levofloxacin, colistin, gentamicin and amikacin were determined by the disk diffusion test according to the CLSI recommendations (Clinical and Laboratory Standards Institute, 2010). Screening for metallo-β-lactamases (MBL) and KPC β-lactamases were per-

formed by a double disk diffusion method using 1 μmol EDTA (Santella et al., 2010a,b) and 300 μg phenyl boronic acid containing disks, respectively. PCR amplification of MBL coding genes and *kpc* were carried out as previously described (Bradford et al., 2004; Ellington et al., 2007). Amplified fragments were sequenced in both strands using an ABI Prism DNA 3700 sequencer and compared with databases using the NCBI Basic Local Alignment Search Tool (Blast). Pulsed-field gel electrophoresis (PFGE) of *Xba*I-digested genomic DNA of *P. aeruginosa* isolates was carried out with a CHEF-DRIII system (Bio-Rad, Hemel Hempstead, UK), as described previously (Tsakris et al., 2000). Multi-Locus Sequence-Typing (MLST) with seven housekeeping genes (*acs*, *aro*, *gua*, *mut*, *nuo*, *pps*, *trp*) was performed according to published protocols (Curran et al., 2004). Sequence type (ST) numbers were assigned using the pubMLST database (<http://pubmlst.org/paeruginosa>).

Epidemiological data and antimicrobial susceptibility patterns of the isolates are shown in Table 1. The three isolates were susceptible to gentamicin, amikacin and colistin, intermediate to ceftazidime and resistant to piperacillin, piperacillin/tazobactam, cefepime, aztreonam, carbapenemes and fluoroquinolones. Synergy tests with EDTA were negative in all cases, also the multiplex PCR performed did not detect any alleles encoding VIM, IMP, SIM, SPM or GIM families of acquired MBLs. Screening of KPC enzymes using phenyl boronic acid was not reproducible even when it was performed with the same strain; however, the presence of *kpc-2* was confirmed in all isolates.

Outer membrane proteins were extracted and resolved in 12% SDS-PAGE (Lambert, 1988). Previously characterized, *P. aeruginosa* H86 that produced OprD and *P. aeruginosa* 2257 that lack this protein were included as controls (Santella et al., 2010a,b). KPC producing isolates included in this study displayed an altered outer membrane protein profiles, lacking OprD.



Outer membrane protein profiles: 2257: *P. aeruginosa* that lack OprD; H86: *P. aeruginosa* that produce OprD; 4661, 4270 and 4753: this study.

**Table 1**  
Epidemiological data and antimicrobial susceptibility profile of KPC-2 producing *P. aeruginosa*.

Isolate number	Culture source	Date of isolation	Antimicrobial susceptibility (inhibition zone; mm)									Therapeutic treatment	Outcome			
			PIP	PTZ	CAZ	FEP	AZT	IMI	MER	COL	AKN	GEN	CIP	LEV		
4661	Respiratory secretions /Blood	22/07/10	13	13	15	6	6	6	6	15	23	19	6	6	COL	Favorable
4270	Respiratory secretions	30/08/10	13	13	15	6	6	6	6	15	23	19	6	6	COL	Favorable
4753	Respiratory secretions	05/09/10	13	13	14	6	6	6	6	15	24	19	6	6	COL	Favorable

PIP: piperacillin, PTZ: piperacillin-tazobactam, CAZ: ceftazidime, FEP: cefepime, AZT: aztreonam, IMI: imipenem, MER: meropenem, CIP: ciprofloxacin, LEV: levofloxacin, COL: colistin, GEN: gentamicin, AKN: amikacin.

PFGE profiles were identical, revealing clonal relatedness. Allele sequences and STs were verified at <http://pubmlst.org/paeruginosa> and corresponded to sequence type ST 654 (allelic profile: *acs*:17, *aro*: 5, *gua*: 26, *mut*: 3, *nuo*: 4, *pps*: 4, *trp*:26).

We report the first outbreak of clonally related KPC-producing *P. aeruginosa* in Buenos Aires, Argentina. Since phenotypic detection of this resistance marker is still difficult and has not been yet standardized (Cuzon et al., 2011; Pasterán et al., 2011), it remains uncertain to what extent KPC-producing *P. aeruginosa* have spread in our country. Some epidemiological studies performed in carbapenemase producing *P. aeruginosa* indicate that some sequence types (ST) like ST654, ST175, ST235, ST621, among others, have been associated to the presence of MBL (Koh et al., 2010; Samuels et al., 2010; Santella et al., 2010a,b). To our knowledge, little is known about the clonal relationship and genetic background of KPC-producing *P. aeruginosa* isolates. ST654 (clonal complex CC244) correspond to an internationally disseminated clone previously associated to both IMP and VIM enzymes (Samuels et al., 2010), however *P. aeruginosa* ST654 has been also reported as a KPC producer in those isolates recovered in 2008 in Bariloche, Argentina.

Recent studies have provided evidence that KPC producing *P. aeruginosa* have a non-clonal population structure interspersed by geographically distributed clones (Cuzon et al., 2011). The dissemination of *kpc* into genetically unrelated *P. aeruginosa* isolates has already been described in Puerto Rico and Colombia (Wolter et al., 2009; Cuzon et al., 2011). However our findings indicate the presence of a successful *P. aeruginosa* ST 654 clone disseminated in our country.

## Acknowledgements

This work was partially supported by grants from UBACyT and ANPCyT to G. Gutkind. G. Gutkind and M. Radice are members of Carrera del Investigador Científico (CONICET). M. Papalia is recipient of a doctoral fellowship from UBA.

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- Gisela Santella  
Facultad de Farmacia y Bioquímica, Universidad de Buenos Aires,  
Junín 956, Ciudad Autónoma de Buenos Aires, CP 1113, Argentina
- Roxana Cittadini  
Sanatorio Mater Dei, San Martín de Tours 2952,  
Ciudad Autónoma de Buenos Aires, CP 1425, Argentina
- Mariana Papalia  
Facultad de Farmacia y Bioquímica, Universidad de Buenos Aires,  
Junín 956, Ciudad Autónoma de Buenos Aires, CP 1113, Argentina
- Cecilia Vera Ocampo  
Sanatorio Mater Dei, San Martín de Tours 2952,  
Ciudad Autónoma de Buenos Aires, CP 1425, Argentina
- Marcelo Del Castillo  
Sanatorio Mater Dei, San Martín de Tours 2952,  
Ciudad Autónoma de Buenos Aires, CP 1425, Argentina
- Carlos Vay  
Facultad de Farmacia y Bioquímica, Universidad de Buenos Aires,  
Junín 956, Ciudad Autónoma de Buenos Aires, CP 1113, Argentina
- Sanatorio Mater Dei, San Martín de Tours 2952,  
Ciudad Autónoma de Buenos Aires, CP 1425, Argentina
- Gabriel Gutkind  
Facultad de Farmacia y Bioquímica, Universidad de Buenos Aires,  
Junín 956, Ciudad Autónoma de Buenos Aires, CP 1113, Argentina  
Tel.: +5411 49648285; fax: +5411 45083645.  
E-mail address: ggukind@ffyb.uba.ar
- Marcela Radice  
Facultad de Farmacia y Bioquímica, Universidad de Buenos Aires,  
Junín 956, Ciudad Autónoma de Buenos Aires, CP 1113, Argentina

Available online 5 April 2012