

# KPC-Like Carbapenemase-Producing *Enterobacteriaceae* Colonizing Patients in Europe and Israel

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**In a 2008–2011 survey, 17,945 patients in 18 hospital units in Europe and Israel were screened for carriage of *Klebsiella pneumoniae* carbapenemase (KPC)-producing *Enterobacteriaceae*, resulting in identification of 124 positive patients. The isolates were dominated by *Klebsiella pneumoniae* sequence type 258 (ST258) KPC-2 and ST512 KPC-3, mainly from Greece and Italy, respectively, whereas Israeli isolates were of diverse species, clones, and KPC variants. Various *bla*<sub>KPC</sub> platforms were observed, among which IncFII<sub>K</sub>-FIB<sub>K</sub> plasmids with *bla*<sub>KPC-2/3</sub> genes in the Tn4401a transposon prevailed.**

Carbapenemase-producing *Enterobacteriaceae* (CPE) constitute an urgent epidemiological issue (1). One of their major, globally spread mechanisms is *Klebsiella pneumoniae* carbapenemases (KPCs), which hydrolyze most  $\beta$ -lactams (1, 2). KPC-2 and -3 are the most prevalent variants, while *K. pneumoniae* is their predominant host species (3, 4). KPCs have occurred in many *K. pneumoniae* clones (sequence types [STs]) (5–8), but ST258 and its close relative ST512 are key players in the pandemic spread (2–4, 6, 9–11). *bla*<sub>KPC</sub> genes are located in Tn4401 transposon variants (12–15) and inserted into plasmids of various replicon types and transmission potentials (5, 7, 16–20). One type of these, pKpQIL, found first in KPC-3-producing *K. pneumoniae* ST258 in Israel, has two specific replicons, FII<sub>K</sub> and FIB<sub>K</sub>, and low conjugation efficiency (21–23). Later, KPC-2- or -3-encoding pKpQIL-like molecules were observed in other countries, usually in *K. pneumoniae* ST258 (2, 3, 10, 24, 25).

During the European Union project MOSAR (Mastering hOSPital Antimicrobial Resistance in Europe), patients in intensive care units (ICUs) and rehabilitation units (RUs) in Europe and Israel were screened for *Enterobacteriaceae* resistant to expanded-spectrum cephalosporins (ESCs) (26). Since KPCs and metallo- $\beta$ -lactamases (MBLs) confer resistance to ESCs (1), the project allowed performance of a large-scale comparative study of the KPC and MBL CPE carriage. A previous report concerned MBL CPE (27), while here we present the KPC data.

Between mid-2008 and mid-2011, all patients in 13 ICUs and five RUs in nine countries ( $n = 17,945$ ) were screened for ESC-resistant (ESC-R) *Enterobacteriaceae* (Table 1). Rectal swabbing was performed regularly from admission until discharge. Swabs were plated onto Brilliance ESB agar (Oxoid, Basingstoke, United Kingdom); enterobacterial colonies were stored for definite analysis. Species were identified with Vitek 2 (bioMérieux, Marcy l'Etoile, France). All isolates were tested for extended-spectrum  $\beta$ -lactamases (ESBLs) and AmpC-type cephalosporinases by the ESB double-disk synergy test (DDST) without and with 250  $\mu$ g/ml cloxacillin (28) and for susceptibility to ertapenem, imipenem, and meropenem. Carbapenemase screening breakpoints were from EUCAST (<http://euca.org>). All suspected CPE isolates were subjected to KPC, MBL, and OXA-48 phenotypic detection, using the combined disk test with phenylboronic acid (PBA CDT) (29), the DDST with EDTA (30), and the temocillin

disk (31), respectively. All nonduplicate PBA CDT-positive organisms were tested by PCR for *bla*<sub>KPC</sub> genes (32), and this test was performed also for putative MBL producers (27).

A total of 124 patients carrying 127 unique KPC CPE organisms were identified in 6 of 18 clinical sites, located in Greece (centers AT,  $n = 44$ , and LA,  $n = 35$ ), France (center RP,  $n = 1$ ), Israel (center LH,  $n = 6$ , and TA,  $n = 16$ ), and Italy (center FS,  $n = 22$ ) (Table 1). They were 59.0% of all patients with CPE. Four Greek patients had *K. pneumoniae* strains coproducing KPC and MBL (VIM-1) and were reported previously too (27). The results for individual countries concurred with those of other reports. Since 2008, after the nationwide outbreak in 2006 and 2007, KPCs in Israel have been endemic at a lower level (2, 33, 34). Consistently, the KPC cases in the Israeli RUs were scattered during the study, being  $\sim 1\%$  of all patients screened and  $\sim 2\%$  of those with ESC-R organisms (Table 1). The KPC spread in Greece commenced in 2007 and was much advanced by mid-2008 (2, 34–36). Both Greek ICUs recorded KPC cases from the survey start, and their contribution to all patients screened and to ESC-R *Enterobacteriaceae* carriers was  $\sim 6\%$  and  $\sim 35\%$ , respectively. Italy reported the first KPC case in 2008, followed by an outbreak progressing rapidly from 2010 (2, 34, 37). The RU FS, screening patients from February 2009 to February 2011, had its first 2 cases late in 2009 and then 12 in 2010 and 8 in the first 2 months of 2011, being  $\sim 3\%$  of all patients and  $\sim 6\%$  of those with ESC-R organisms.

The *bla*<sub>KPC</sub> amplicons were digested by RsaI (Fermentas, Vilnius, Lithuania), which distinguishes *bla*<sub>KPC-2</sub> and *bla*<sub>KPC-3</sub> (38),

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TABLE 1 Occurrence of patients colonized by KPC CPE in study centers

Country	Center	Unit type	No. of patients enrolled in the study <sup>a</sup>	No. (%) of patients colonized by <i>Enterobacteriaceae</i> producing acquired ESC-hydrolyzing $\beta$ -lactamases <sup>b,c,d</sup>	No. (%) of patients colonized by CPE <sup>b,d,e</sup>	No. (%) of patients colonized by KPC CPE <sup>d</sup>
France	HM	ICU	2,373	256 (10.8)	1 (0.04) <sup>e</sup>	
France	RP	ICU	1,328	85 (6.4)	1 (0.08) <sup>f</sup>	1 (0.08)
France	SJ	ICU	1,049	51 (4.9)	4 (0.4)	
Greece	AT	ICU	796	117 (14.7)	53 (6.7) <sup>g</sup>	44 (5.5)
Greece	LA	ICU	558	99 (17.7)	83 (14.9) <sup>h</sup>	35 (6.3)
Italy	CA	ICU	788	49 (6.2)	2 (0.3)	
Latvia	RI	ICU	1,464	526 (35.9)	10 (0.7)	
Luxemburg	LU	ICU	1,823	54 (3.0)		
Portugal	PO	ICU	910	18 (2.0)		
Portugal	VR	ICU	628	24 (3.8)	1 (0.2)	
Slovenia	GO	ICU	919	32 (3.5)		
Slovenia	LJ	ICU	685	115 (16.8)		
Spain	BA	ICU	1,069	41 (3.8)		
France	BM	RU	410	76 (18.5)		
Israel	LH	RU	564	177 (31.4)	6 (1.1) <sup>i</sup>	6 (1.1)
Israel	TA	RU	1,650	870 (52.7)	16 (1.0) <sup>j</sup>	16 (1.0)
Italy	FS	RU	704	340 (48.3)	28 (4.0)	22 (2.8)
Spain	GI	RU	227	104 (45.8)	5 (2.2)	
Total			17,945	3,034 (16.9)	210 (1.2)	124 (0.7)

<sup>a</sup> All patients that were swabbed at least once at a clinical center, regardless of the length of hospitalization.

<sup>b</sup> These numbers were shown also in the report on colonization by MBL CPE in MOSAR centers (27).

<sup>c</sup> Acquired ESC-hydrolyzing  $\beta$ -lactamases include ESBLs, AmpC-type cephalosporinases, MBLs, and KPCs.

<sup>d</sup> Patients in this column include both those who were colonized at admission and those who were colonized due to in-hospital transmission.

<sup>e</sup> Carbapenemases include KPCs and MBLs except in one patient in the French ICU HM who was colonized with *E. coli* coproducing OXA-48 carbapenemase and ESBL.

<sup>f</sup> This patient was colonized by KPC-producing *K. pneumoniae* and MBL-producing *E. coli*.

<sup>g</sup> One patient was colonized by KPC-producing *E. coli* and MBL-producing *K. pneumoniae*.

<sup>h</sup> Four patients were colonized by *K. pneumoniae* coproducing KPC and MBL.

<sup>i</sup> One patient was colonized by KPC-producing *E. coli* and *K. pneumoniae*.

<sup>j</sup> Two patients were colonized by two different KPC producers: either *C. freundii* and *E. coli* or *E. coli* and *K. pneumoniae*.

followed by sequencing for representative isolates. KPC-producing isolates were typed by pulsed-field gel electrophoresis (PFGE) as described previously (39). PFGE types and subtypes were distinguished visually according to the method of Tenover et al. (40). Selected isolates were analyzed also by multilocus sequence typing (MLST) (41–44); databases available at <http://pubmlst.org/cfreundii/> (*Citrobacter freundii*), <http://pubmlst.org/e cloacae> (*Enterobacter cloacae*), <http://mlst.warwick.ac.uk/mlst/dbs/Ecoli> (*Escherichia coli*), and <http://bigsdw.web.pasteur.fr/klebsiella/klebsiella.html> (*K. pneumoniae*) were used for assigning STs. *E. cloacae* STs and  $\beta$ -lactamases were shown previously (45).

*K. pneumoniae* isolates, being the predominant species ( $n = 110$ ; 86.6%), were classified into 10 STs (Table 2). ST258 prevailed ( $n = 76$ ; 69.1%) and was observed in all but one of the sites (FS, Italy), dominating in Greece with  $bla_{KPC-2}$  ( $n = 73$ ; 93.6%). The next-most-prevalent clone, ST512 ( $n = 21$ ; 19.1%), was originally identified in this study in an Israeli isolate from 2008 (<http://bigsdw.web.pasteur.fr/klebsiella/klebsiella.html>). This single-locus variant (SLV) of ST258 carried  $bla_{KPC-3}$  and dominated in the Italian RU FS ( $n = 19$ ; 86.4%) but was sporadic in Israel. Four KPC-2- and VIM-1-positive Greek isolates belonged to ST147, the major VIM producer in Greece (27), while the remaining STs represented single isolates with KPC-2 or -3 in individual sites. *C. freundii*, *E. cloacae*, and *E. coli*, usually producing KPC-2s, were identified vastly in Israel and were clonally diverse, except for *E.*

*coli* ST131, of which there were three KPC-2 or -3 isolates. Most of the *E. cloacae*, *E. coli*, and *K. pneumoniae* isolates represented international clones (45, 46). For *C. freundii*, the clonality data are scarce (27, 41, 47), but KPC-producing *C. freundii* ST14, originally identified in this study, was found in 2015 in Malaysia [<http://pubmlst.org/cfreundii/>]. In general, the clonality plus KPC type data were congruent with data in national reports. The high KPC CPE diversity in the Israeli centers corresponds to the endemicity situation following the polyclonal outbreak of KPC-2 and the clonal spread of *K. pneumoniae* ST258 KPC-3 (7, 19, 22, 48, 49), even if other studies still indicate the importance of *K. pneumoniae* ST258/ST512 (50). In contrast, the high prevalence of ST258 KPC-2 in Greece and ST512 KPC-3 in Italy reflected their clonal dissemination in real time (35–37). This study is also yet another report on KPC-producing *E. coli* ST131, which has been repeatedly identified in Israel (4, 49, 51, 52).

The location of  $bla_{KPC}$  genes within Tn4401-like transposons and polymorphism of these was analyzed by PCR mapping (12). For the Tn4401g variant (15), an additional primer was designed (5'-GTTCCACTGAGCGTCAGAC-3') for use with primer 3781L (12) (expected product size, 370 bp). All  $bla_{KPC}$  genes were located in Tn4401 variants (12). The main type was Tn4401a (12), observed in all isolates from Greece, Italy, and France and in 9/22 Israeli isolates, including most *K. pneumoniae* isolates with  $bla_{KPC-2}$  or  $bla_{KPC-3}$  (Table 2). Tn4401c (14) and Tn4401g (15)

**TABLE 2** Geographic distribution, species, clones, pulsotypes, S1 plasmid profiles, plasmids and Tn4401 transposons with *bla*<sub>KPC</sub> genes, and other acquired β-lactamases of KPC CPE isolates<sup>a</sup>

Center	Species	ST (CC or CG) <sup>b</sup>	No. of isolates	No. of pulsotypes (no. of subtypes)	S1 profile <sup>c</sup>	Size of plasmid (kb); replicon(s) of plasmid with <i>bla</i> <sub>KPC</sub> gene(s) <sup>d</sup>	<i>bla</i> <sub>KPC</sub> <sup>e</sup>	Tn4401 variant <sup>f</sup>	MBL, ESBL, and/or AmpC (no. of isolates) <sup>g</sup>
AT (Greece)	<i>E. coli</i>	ST10 (CC10)	1	1	Eco1	~130; <b>FII<sub>K</sub> + FIB<sub>K</sub></b>	<i>bla</i> <sub>KPC-2</sub>	Tn4401a	TEM-1
	<i>K. pneumoniae</i>	ST258 (CG258)	43	2 (18)	Kpn1 Kpn2	~120; <b>FII<sub>K</sub> + FIB<sub>K</sub></b> ~115; <b>FII<sub>K</sub> + FIB<sub>K</sub></b>	<i>bla</i> <sub>KPC-2</sub> <i>bla</i> <sub>KPC-2</sub>	Tn4401a Tn4401a	SHV-12 + TEM-1 SHV-12 + TEM-1
LA (Greece)	<i>K. pneumoniae</i>	ST17 (CG17)	1	1	Kpn4	~115; <b>FII<sub>K</sub> + FIB<sub>K</sub></b>	<i>bla</i> <sub>KPC-2</sub>	Tn4401a	SHV-5 + TEM-1
	<i>K. pneumoniae</i>	ST147 (CC147) <sup>h</sup>	4	1 (2)	Kpn6	~115; <i>FII<sub>K</sub> + FIB<sub>K</sub></i>	<i>bla</i> <sub>KPC-2</sub>	Tn4401a	VIM-1 + TEM-1
	<i>K. pneumoniae</i>	ST258 (CG258)	30	1 (12)	Kpn9 Kpn2 Kpn10	~100; <i>FII<sub>K</sub> + FIB<sub>K</sub></i> ~115; <i>FII<sub>K</sub> + FIB<sub>K</sub></i> ~70; NT	<i>bla</i> <sub>KPC-2</sub> <i>bla</i> <sub>KPC-2</sub> <i>bla</i> <sub>KPC-2</sub>	Tn4401a Tn4401a Tn4401a	SHV-12 + TEM-1 SHV-12
FS (Italy)	<i>K. pneumoniae</i>	ST16 (CG17)	1	1	Kpn7	~90; NT	<i>bla</i> <sub>KPC-3</sub>	Tn4401a	CTX-M-15
	<i>K. pneumoniae</i>	ST45 (CG485)	1	1	Kpn3	~115; <i>FII<sub>K</sub> + FIB<sub>K</sub></i>	<i>bla</i> <sub>KPC-3</sub>	Tn4401a	TEM-1
	<i>K. pneumoniae</i>	ST383 (CC42)	1	1	Kpn8	~100; <b>FII<sub>K</sub></b>	<i>bla</i> <sub>KPC-2</sub>	Tn4401a	CMY-4 + TEM-1
	<i>K. pneumoniae</i>	ST512 (CG258)	19	1 (9)	Kpn2/6	~115; <b>FII<sub>K</sub> + FIB<sub>K</sub></b>	<i>bla</i> <sub>KPC-3</sub>	Tn4401a	TEM-1 (19); SHV-12 + CMY-2 (1); OXA-1 (1) <sup>i</sup>
RP (France)	<i>K. pneumoniae</i>	ST258 (CG258)	1	1	ND	ND	<i>bla</i> <sub>KPC-2</sub>	Tn4401a	CTX-M-15 + SHV + TEM-1
LH (Israel)	<i>E. cloacae</i>	ST78 (CC74) <sup>j</sup>	1	1	Ecl1	ND	<i>bla</i> <sub>KPC-2</sub>	Tn4401c	SHV-12 + TEM-1 <sup>k</sup>
	<i>E. coli</i>	ST131 (CC131)	2	1 (2)	Eco2	~75; N	<i>bla</i> <sub>KPC-2</sub>	Tn4401g	TEM-1
	<i>E. coli</i>	ST167 (CC10)	1	1	Eco4	~90; <b>FII<sub>K</sub> + FIB<sub>K</sub></b>	<i>bla</i> <sub>KPC-3</sub>	Tn4401a	SHV-12 + TEM-1
	<i>E. coli</i>	ST1571	1	1	Eco3	ND	<i>bla</i> <sub>KPC-2</sub>	Tn4401c	SHV-12 + TEM-1
	<i>K. pneumoniae</i>	ST258 (CG258)	1	1	Kpn5	~115; <i>FII<sub>K</sub> + FIB<sub>K</sub></i>	<i>bla</i> <sub>KPC-3</sub>	Tn4401a	TEM-1
	<i>K. pneumoniae</i>	ST512 (CG258)	1	1	Kpn11	~150; N	<i>bla</i> <sub>KPC-3</sub>	Tn4401a	-
TA (Israel)	<i>C. freundii</i>	<b>ST14</b>	1	1	Cfr1	~80; N	<i>bla</i> <sub>KPC-2</sub>	Tn4401g	TEM-1 + OXA-1
	<i>C. freundii</i>	<b>ST12</b>	1	1	Cfr2	~80; N	<i>bla</i> <sub>KPC-2</sub>	Tn4401g	CTX-M-15 + TEM-1
	<i>C. freundii</i>	ND	1	1	Cfr3	~80; N	<i>bla</i> <sub>KPC-2</sub>	Tn4401g	SHV-12 + TEM-1 + OXA-1
	<i>C. freundii</i>	<b>ST10</b>	1	1	Cfr4	~300; ND	<i>bla</i> <sub>KPC-2</sub>	Tn4401c	TEM-1 + OXA-1
	<i>C. freundii</i>	<b>ST15</b>	1	1	Cfr4	~300; ND	<i>bla</i> <sub>KPC-2</sub>	Tn4401c	TEM-1 + OXA-1
	<i>E. cloacae</i>	<b>ST118</b> <sup>l</sup>	1	1	Ecl3	~320; ND	<i>bla</i> <sub>KPC-2</sub>	Tn4401c	CTX-M-27 + SHV-12 + TEM-1 <sup>k</sup>
	<i>E. cloacae</i>	<b>ST146</b> <sup>l</sup>	1	1	Ecl2	~300; ND	<i>bla</i> <sub>KPC-2</sub>	Tn4401c	TEM-1 <sup>k</sup>
	<i>E. coli</i>	ST69 (CC69)	1	1	Eco8	~70; N	<i>bla</i> <sub>KPC-2</sub>	NT	TEM-1
	<i>E. coli</i>	ST131 (CC131)	1	1	Eco5	~115; <b>FII<sub>K</sub> + FIB<sub>K</sub></b>	<i>bla</i> <sub>KPC-3</sub>	Tn4401a	TEM-1
	<i>E. coli</i>	ST216	1	1	Eco6	~60; N	<i>bla</i> <sub>KPC-2</sub>	Tn4401g	TEM-1 + OXA-1
	<i>E. coli</i>	<b>ST3541</b>	1	1	Eco7	ND	<i>bla</i> <sub>KPC-2</sub>	Tn4401c	CTX-M-15 + SHV-12 + CMY-2 + TEM-1 + OXA-1
	<i>K. pneumoniae</i>	ST17 (CG17)	1	1	Kpn12	~140; N	<i>bla</i> <sub>KPC-2</sub>	Tn4401g	TEM-1 + OXA-1
	<i>K. pneumoniae</i>	ST34 (CC34)	1	1	Kpn13	ND	<i>bla</i> <sub>KPC-2</sub>	Tn4401c	CTX-M-15 + SHV-12 + TEM-1 + OXA-1
	<i>K. pneumoniae</i>	ST36 (CG485)	1	1	Kpn14	~115; <b>FII<sub>K</sub> + FIB<sub>K</sub></b>	<i>bla</i> <sub>KPC-3</sub>	Tn4401a	TEM-1
	<i>K. pneumoniae</i>	ST258 (CG258)	1	1	Kpn2	~115; <i>FII<sub>K</sub> + FIB<sub>K</sub></i>	<i>bla</i> <sub>KPC-3</sub>	Tn4401a	TEM-1
	<i>K. pneumoniae</i>	ST383 (CC42)	1	1	Kpn15	~115; <b>FIB<sub>K</sub></b>	<i>bla</i> <sub>KPC-2</sub>	Tn4401a	CTX-M-15 + CMY-4 + TEM-1
<i>K. pneumoniae</i>	<b>ST512</b> (CG258)	1	1	Kpn16	~140; <b>FII<sub>K</sub> + FIB<sub>K</sub></b>	<i>bla</i> <sub>KPC-3</sub>	Tn4401a	TEM-1 + OXA-1	
<i>K. pneumoniae</i>	ST833 (CG258)	1	1	Kpn17	~100; <b>FII<sub>K</sub> + FIB<sub>K</sub></b>	<i>bla</i> <sub>KPC-2</sub>	Tn4401a	SHV-12	

<sup>a</sup> Other acquired β-lactamases include MBLs, ESBLs, AmpCs, and broad-spectrum β-lactamases. CC, clonal complex; CG, clonal group; ND, not determined; NT, nontypeable; FII<sub>K</sub>, FIB<sub>K</sub>, and N are plasmid replicon types.

<sup>b</sup> New STs are indicated in bold. Numerous reports on *K. pneumoniae* ST512 have been published since 2012 (2, 11, 34, 37); however, this ST was identified originally in this study (isolate identifier 578 in the *K. pneumoniae* MLST database [http://bigsdw.web.pasteur.fr]). In groups of four or more isolates, MLST was performed for representative isolates, based on the PFGE data.

<sup>c</sup> In large groups of isolates of the same ST/pulsotype (*K. pneumoniae* ST258 and ST512), the S1 analysis was performed for representative isolates. S1 plasmid profiles are numbered within species groups of isolates; profiles differed from each other by number and/or size of plasmids.

<sup>d</sup> Plasmids found in transformants are shown in bold. Replicons shown in italics represent the probable types of *bla*<sub>KPC</sub> plasmids (PBRT and pKpQIL PCR mapping was performed on DNA of clinical isolates).

<sup>e</sup> In groups of four or more isolates of the same ST/pulsotype, *bla*<sub>KPC</sub> sequencing was performed for representative isolates; for the remaining isolates, RsaI PCR-restriction fragment length polymorphism analysis distinguishing *bla*<sub>KPC-2</sub> and *bla*<sub>KPC-3</sub> sequences (38) was carried out.

<sup>f</sup> In groups of four or more isolates of the same ST/pulsotype, PCR mapping of Tn4401-like elements was performed for representative isolates.

<sup>g</sup> In groups of four or more isolates with the same ST/pulsotype and *bla* genes, PCR profile sequencing was performed for representative isolates.

<sup>h</sup> These isolates were also included in the study of MBL CPE isolates identified during the MOSAR project (27).

<sup>i</sup> All isolates of this group produced TEM-1; one isolate produced additionally SHV-12 and CMY-2, and another one produced OXA-1.

<sup>j</sup> STs and β-lactamases of the *E. cloacae* isolates from LH and TA were reported previously (45).

were found only in Israel in various species and clones, always containing *bla*<sub>KPC-2</sub>. Tn4401a has been the main type of Tn4401, strongly associated with *K. pneumoniae* ST258 worldwide (6, 10, 18, 21, 36), while Tn4401c has been observed in diverse KPC-2-producing organisms in Israel (15, 49). Interestingly, Tn4401c-derived Tn4401g was identified only recently in a single *K. pneumoniae* KPC-2 isolate recovered in Israel in 2008 (15), whereas in this study, it occurred frequently in *C. freundii*, *E. coli*, and *K. pneumoniae*.

Plasmid profiling and identification of *bla*<sub>KPC</sub>-carrying plasmids was done with nuclease S1 (New England BioLabs, Beverly, MA) analysis (53) and hybridization with the *bla*<sub>KPC</sub> probe, using the enhanced-chemiluminescence (ECL) Random-Prime labeling and detection system (Amersham Pharmacia Biotech, Little Chalfont, United Kingdom). The analysis comprised 44 isolates of all species, STs, and pulsotypes (15 *K. pneumoniae* ST258/ST512 isolates), revealing highly varied plasmid profiles, with *bla*<sub>KPC</sub>-carrying plasmids ranging in size from ~60 to ~320 kb (Table 2). Plasmid DNA of 27 isolates of various species, STs, and S1 profiles was purified with the Qiagen plasmid midi kit (Qiagen, Hilden, Germany) and electroporated into *E. coli* DH5 $\alpha$ , with transformant selection with 0.5  $\mu$ g/ml imipenem or 1  $\mu$ g/ml cefotaxime. Subsequently, plasmids of the transformants were purified and subjected to PCR-based replicon typing (PBRT) (54–57). KPC-positive transformants were obtained for 22 isolates (Table 2). PBRT revealed that 12 of these had plasmids with FII<sub>K</sub> and FIB<sub>K</sub> replicons (alternating in two cases) of ~90 to ~140 kb. PCR mapping, performed as proposed by Baraniak et al. (10), showed that all these were of the pKpQIL type (21), and molecules positive in that assay were identified also in selected isolates for which no transformants were available (Table 2). The pKpQIL-like plasmids carried *bla*<sub>KPC-2</sub> or *bla*<sub>KPC-3</sub> (Tn4401a) and were hosted mainly in *K. pneumoniae* ST258 and ST512 isolates; however, these occurred also in other organisms (10, 22, 23). The other group was IncN plasmids of ~60 to ~150 kb, identified in various *C. freundii*, *E. coli*, and *K. pneumoniae* Israeli strains, usually carrying *bla*<sub>KPC-2</sub> (Tn4401g). These plasmids have been observed among diverse KPC-2-producing *E. coli* and non-CG258 *K. pneumoniae* isolates in Israel (15, 49). However, some of our isolates fell beyond this pattern, like *K. pneumoniae* ST833 (SLV of ST258), with *bla*<sub>KPC-2</sub> on a pKpQIL-like plasmid or *K. pneumoniae* ST512 with *bla*<sub>KPC-3</sub> on an IncN molecule. Finally, the *bla*<sub>KPC-2</sub> gene in the Tn4401c variant was observed in *C. freundii* and *E. cloacae* in large plasmids (~300 to ~320 kb) that could not be separated by transfer despite repeated attempts; their replicon types thus remained undetermined.

The KPC CPE isolates were analyzed for other acquired  $\beta$ -lactamase genes, namely, *bla*<sub>SHV-5/SHV-12</sub>, *bla*<sub>CTX-M</sub>, *bla*<sub>CMY-2</sub>, *bla*<sub>TEM</sub>, and *bla*<sub>OXA-1</sub> types, by PCR and sequencing (32, 58–60). The isolates had various  $\beta$ -lactamase combinations, including SHV- and CTX-M-like ESBLs, AmpCs of the CMY-2 type, and broad-spectrum TEM-1 and OXA-1 enzymes (Table 2).

We assessed the KPC CPE carriage among ICU and RU patients on a large international scale, using the same time frame and methodology. Not surprisingly, KPC producers were found mainly in the countries which reported their wide spread, i.e., Greece, Italy, and Israel (2, 33–37). Considering the study period, 2008 to 2011, the rhythm of occurrence of cases in individual centers and characteristics of the organisms reflected the situation in the countries, i.e., the onset and advanced stage of nationwide

outbreaks in Italy and Greece, respectively, and the postoutbreak endemicity in Israel (33, 35–37). The analysis provided a comparative snapshot of the geographic and quantitative distribution of species/clones, Tn4401 transposon variants, and *bla*<sub>KPC</sub>-carrying plasmids, often observed in national reports. Also, this has been one of the first studies of *C. freundii* and *E. cloacae* that included MLST data.

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