Letters to the Editor

Detection of a VIM-27-Producing *Klebsiella pneumoniae* Isolate in a Patient following Surgical Tourism in Greece[▽]

Very recently, Papagiannitsis et al. described VIM-27, a new metallo- β -lactamase (MBL) single-point variant of VIM-1, identified in three *Klebsiella pneumoniae* isolates of sequence type 147 (ST147) recovered at three different Greek hospitals (6). We report here that VIM-27-producing *K. pneumoniae* already spread outside Greece following “surgical tourism.”

In 2010, a 25-year-old patient living in Luxembourg traveled to Greece to undergo plastic surgery. She stayed for 15 days in a general hospital in Athens. Eventually, she was repatriated and admitted to a hospital in Luxembourg for postoperative wound infection, and she was immediately nursed in a single-occupancy room with isolation precaution barriers.

Microbiological analysis of a surgical wound swab revealed the concomitant presence of carbapenem-resistant *Acinetobacter baumannii*, *Pseudomonas aeruginosa*, and *Klebsiella pneumoniae* isolates, each of these producing a different type of carbapenemase. An OXA-58-producing *A. baumannii* isolate and a VIM-2-producing *P. aeruginosa* isolate were rapidly identified (Table 1), but more attention was focused on a multidrug-resistant *K. pneumoniae* isolate (Kp10445) for which a synergy was evidenced by double-disk test between imipenem and EDTA, suggesting the presence of an MBL.

MIC determination by Etest or microdilution interpreted according to updated 2011 CLSI breakpoints (3) confirmed that Kp10445 was highly resistant to multiple classes of antimicrobials (Table 1), including carbapenems and colistin, remaining susceptible to aztreonam, tigecycline (EUCAST and FDA breakpoints), and gentamicin only. Analysis of β -lactamase genes (5) detected the presence of *bla*_{VIM} in addition to the chromosomal non-ESBL (extended-spectrum β -lactamase) *bla*_{SHV-11}. PCR sequencing of the integron (In10445, accession number JF803952) revealed the presence of *bla*_{VIM-27} located upstream to *aacA7*, *dhfrI*, and an incomplete *aadA1* gene. In10445 matches perfectly with the VIM-1-harboring integron described by Samuelsen et al. (7) in *K. pneumoniae* isolated in Scandinavia except for the single G-to-T transversion within *bla*_{VIM-1}, resulting in the Ala57-to-Ser mutation specific to VIM-27. Interestingly, the sequence of this integron differed from the In541-like integron reported for VIM-27 by Papagiannitsis et al. by the fact that *aadA1* was truncated in In10445 but not in the In541-like integron (6). Plasmid extracts revealed the presence of a 50.5-kb *bla*_{VIM}-harboring nontypeable plasmid (2) which could be transferred by mating-out experiments with *Escherichia coli* J53 according to a protocol previously described (1). The VIM-27-expressing transconjugant displayed lower MIC values than the clinical isolate, especially against carbapenems (Table 1).

Multilocus sequence typing (MLST) performed according to <http://www.pasteur.fr/recherche/genopole/PF8/mlst/Kpneumoniae.html> showed that Kp10445 belonged to ST147, an ST that was reported for the three VIM-27-producing *K. pneumoniae* isolates recovered in Greece as well as for other carbapenemase-producing *K. pneumoniae* isolates reported in this country and in Scandinavia (4, 7).

Subsequently the patient underwent surgical debridement of the wound and had a favorable clinical outcome following a

14-day course of therapy with meropenem, colistin, and amikacin.

The simultaneous detection of these three resistant Gram-negative isolates in the same patient underscores the potential public health threat that is associated with surgical tourism in foreign countries where multidrug-resistant organisms are highly endemic.

Systematic screening upon admission along with mandatory declaration of the occurrence of such resistance by the hospitals could help to slow down the spread of such worrisome organisms.

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We report no conflicts of interest.

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TABLE 1. Clinical and plasmid data and MICs as evaluated by Etest or microdilution (Sensititre; Trek Diagnostic Systems) for Kp10445, its transconjugant, and Pa10446 and Ab10447 clinical isolates^a

Reference isolate	Organism	Origin (transferred from)	Specimen	Resistance mechanism	MLST	Plasmid size (kb)	Inc group	MIC by Etest (µg/ml)														Colistin MIC by microdilution (µg/ml)		
								Ticarcillin	Ticarcillin-clavulanate	Temocillin	Piperacillin	Piperacillin-tazobactam	Ceftazidime	Cefepime	Aztreonam	Imipenem	Meropenem	Ertapenem	Doripenem	Amikacin	Gentamicin		Ciprofloxacin	Tigecycline
Kp10445	<i>K. pneumoniae</i>	Luxembourg (Greece)	Wound swab	VIM-27	ST147	201.5/115/50.5	Not typeable	>256	>256	256	>256	>256	>256	>256	8	0.125	32	>32	>32	32	4	>4	0.75	>4
Conj10445	<i>E. coli</i> J53	Transconjugant of Kp10445		VIM-27		50.5	Not typeable	>256	>256	128	96	64	192	8	0.047	3	0.38	0.5	0.5	16	2	<0.25	0.5	0.5
<i>E. coli</i> J53	<i>E. coli</i> J53	Acceptor strain						2	1.5	8	1	1.5	0.5	0.064	0.19	0.19	0.032	0.032	0.016	<4	<1	<0.25	0.38	0.25
Pa10446	<i>P. aeruginosa</i>	Luxembourg (Greece)	Wound swab	VIM-2	NA	NA	NA	>256	>256	NT	128	64	>256	64	8	>32	>32	NT	>32	>32	32	>32	NT	1
Ab10447	<i>A. baumannii</i>	Luxembourg (Greece)	Wound swab	OXA-58	NA	NA	NA	>256	>256	NT	>256	>256	>256	16	>32	16	8	NT	8	128	<2	32	NT	0.5

^a NT, not tested; NA, not applicable.**O. Denis**

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