

Cluster of *Escherichia coli* Isolates Producing a Plasmid-Mediated OXA-48 β-Lactamase in a Spanish Hospital in 2012

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Three unrelated sequence type 131 (ST131), ST58, and ST83 *Escherichia coli* isolates with low-level resistance to impenem and resistance to ertapenem were recovered in a Spanish hospital from July to October 2012. They were positive for *bla*_{OXA-48} carried by an IncL/M conjugative plasmid, which may have been acquired from *Klebsiella pneumoniae*.

esistance to carbapenem antibiotics in Gram-negative bacte-Rria has become an increasingly important problem worldwide over the last 2 decades (1). The most relevant mechanism for this resistance is the production of carbapenemases, with the responsible genes often carried by plasmids which contribute to their spread by horizontal gene transfer (2). OXA-48 is a class D β -lactamase which confers resistance to penicillins and weak, but nonetheless significant, resistance to carbapenems but not to extendedspectrum cephalosporins (3). This enzyme was first identified in 2004 in Turkey and since then has been reported in many other countries, mainly those of the Middle East, North Africa, and Europe, but also in the United States (4-6). OXA-48 is most often detected in Klebsiella pneumoniae, although other members of the Enterobacteriaceae family, including Escherichia coli, also produce it (3). In K. pneumoniae, the bla_{OXA-48} gene has been located in a conjugative plasmid of about 60 kb assigned to the IncL/M group (7). Here, we report the characterization of three E. coli OXA-48producing isolates, each obtained from a different patient at a Spanish hospital (Hospital Universitario Central de Asturias [HUCA]) over a 3-month period (Table 1). These are the first OXA-48-producing E. coli isolates detected in our region, and only one was previously reported in Spain (8). The three patients underwent surgery, were hospitalized for long periods, were coinfected with other bacteria, and received prolonged treatment with numerous antimicrobials.

The first *E. coli* isolate (*Ec*-HUCA 1) was recovered in July 2012 from a colostomy specimen from a 46-year-old female (patient 1) with postsurgical septic shock. The colostomy specimen was also positive for *K. pneumoniae* (isolate *Kp*-HUCA 4, which was addi-

tionally detected in blood cultures for the same patient and partially characterized in this study) and *Morganella morganii*. The second isolate (*Ec*-HUCA 2) was recovered in October 2012 from a surgical wound in a 57-year-old male (patient 2) with intestinal obstruction. After empirical treatment with meropenem, the isolate was detected in the wound drainage, as was *Enterococcus faecalis*. The third isolate (*Ec*-HUCA 3) was found in a urine sample from a 68-year-old male (patient 3) with several complications after septic shock caused by multidrug-resistant *Pseudomonas aeruginosa* secondary to a surgical wound infection (Table 1).

Antimicrobial susceptibility tests were performed by disk diffusion assays (Becton Dickinson, Sparks, MD, USA). The Microscan system (Neg Combo Panel Type 53; Siemens Healthcare Diagnostics, Deerfield, IL, USA) was applied for the identification of bacterial isolates and the determination of MICs. The Etest (bioMérieux, Marcy-l'Étoile, France) was used to determine the MIC for tigecycline and to confirm the MIC for ertapenem. The results of the disk diffusion assays (not shown) and the MICs (Table 2) were interpreted according to CLSI breakpoints that

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TABLE 1 Characteristics of patients and clinical samples positive for *E. coli* or for *E. coli* and *K. pneumoniae* isolates carrying the *bla*_{OXA-48} gene and recovered in a Spanish hospital

Patient no. (sex ^{<i>a</i>} /age [yr])	Hospital unit	Disease/outcome	Sample origin	Isolate(s) ^b	Date of isolation (day/mo/yr)	Final therapy
1 (F/46)	General surgery	Surgical wound infection/discharged	Colostomy	Ec-HUCA 1, Kp-HUCA 4 (Morganella morganii)	16/7/2012	Ciprofloxacin
2 (M/57)	ICU ^c	Surgical wound infection/discharged	Wound exudate	<i>Ec</i> -HUCA 2 (<i>Enterococcus faecalis</i>)	15/10/2012	Ciprofloxacin, cefoxitin, vancomycin
3 (M/68)	Reanimation	Septic shock ^d / discharged	Urine	Ec-HUCA 3	26/10/2012	Colistin, meropenem, amikacin

^{*a*} F, female; M, male.

^b Ec, Escherichia coli; Kp, Klebsiella pneumoniae; HUCA, Hospital Universitario Central de Asturias.

^c ICU, intensive care unit.

^d Septic shock was caused by *Pseudomonas aeruginosa*, which was not recovered from urine.

TABLE 2 MICs for bla _{OX}	A-48-positive is	solates and th	eir transconj	ugants ^a								
	MIC (µg/ml)	for:										
	Ec-HUCA 1			Ec-HUCA 2			Ec-HUCA 3					
Antimicrobial agent	(ST131)	Tc-1/1	Tc-1/2	(ST58)	Tc-2/1	Tc-2/2	(ST83)	Tc-3/1	Tc-3/2	<i>Kp</i> -HUCA 4	Tc-4/1	Tc-4/2
Amoxicillin	>16	>16	>16	>16	>16	>16	>16	>16	>16	>16	>16	>16
Amoxicillin-clavulanic	>16/8	>16/8	>16/8	>16/8	>16/8	>16/8	>16/8	>16/8	>16/8	>16/8	>16/8	>16/8
acid												
Piperacillin-tazobactam	> 64	64	64	> 64	> 64	> 64	> 64	64	> 64	> 64	16	32
Cefazolin	> 16	8	8	>16	>16	8	>16	8	>16	>16	8	8
Cefuroxime	> 16	8	8	>16	>16	8	8	8	8	>16	8	8
Cefoxitin	8	8	8	8	8	8	8	8	8	8 = 8	8	8
Cefotaxime	∐ I	<u>IV</u>	IV IV	>32	>32	IV	IV IV	IV IV	<u>IV</u>	>32	<u>IV</u>	ΙΛ
Ceftazidime	<u>I</u>	IV IV	IV IV	>16	>16	IV IV	IV IV	<u> </u> \	IV IV	>16	IV IV	ΙΛ
Cefepime	ΙΛ	IV IV	$\stackrel{[\Lambda]}{=}$	>16	>16	IV IV	∐ I	IV I	<u>I</u>	>16	IV IV	١٨ ١
Aztreonam	<u>IV</u>	<u>I</u> V	IV I	>16	>16	ΙΛ	<u>IV</u>	IV I	<u>IV</u>	>16	IV I	ΙΛ
Imipenem	2	[]	\mathbb{N}	2	2	2	2	[]	2	∐ I	\mathbb{N}	1
Ertapenem	2	2	2	2	2	4	2	2	2	2	1	1
Gentamicin	≤ 2	≦2	≤ 2	8	≤ 2	≤ 2	≤2	≦2	≦2	≤ 2	≦2	≤ 2
Tobramycin	≤ 2	≦2	≤ 2	8	8	≤2	≤2	≦2	≦2	8	≦2	≤ 2
Amikacin	8	8	8	32	8∐	8≥	8	8	8	8≥	8	8
Acid nalidixic	> 16	≤ 16	≤ 16	≤ 16	≤ 16	≤ 16	≤ 16	≤ 16	≤ 16	>16	≤ 16	≤ 16
Ciprofloxacin	1	≤ 0.5	≤ 0.5	≤ 0.5	≤ 0.5	≤ 0.5	≤ 0.5	≤ 0.5	≤ 0.5	>2	≤ 0.5	≤ 0.5
Trimethoprim-	$\leq 2/38$	$\leq 2/38$	$\leq 2/38$	>2/38	>2/38	$\leq 2/38$	$\leq 2/38$	$\leq 2/38$	$\leq 2/38$	>2/38	$\leq 2/38$	$\leq 2/38$
sulfamethoxazole												
Tigecycline	<u>I</u>	IV IV	IV IV	ĬV	ĬV	<u>IV</u>	Ш	IV IV	IV IV	ĬV	١ <u>٨</u>	IV IV
β-Lactamase gene(s)	bla _{OXA-48} , bla _{TEM-1}	bla _{OXA-48}	bla _{OXA-48}	bla _{OXA-48} , bla _{TEM-1} ,	bla _{OXA-48} , bla _{CTX-M-15}	bla _{OXA-48} , bla _{CTX-M-15}	bla _{OXA-48}	bla _{OXA-48}				
Relevant plasmid(s) (kb)	ca. 60	ca. 60	ca. 60	ca. $60, <150$	ca. 60, <150	ca. 60	ca. 60	ca. 60	ca. 60	ca. 60, >150	ca. 60	ca. 60
" Four and 20 transconjugants ((Tc) were analyze	ed in matings us	ing as donors cl	inical isolates of Esci	herichia coli (Ec) and	Klebsiella pneur	noniae (Kp) recove	ered in the Hosp	ital Universitari	io Central de Asturia chown (see the text f	s (HUCA). A ri for details)	fampin-





FIG 1 Plasmid profiles of *Klebsiella pneumoniae* (*Kp*) and *Escherichia coli* (*Ec*) isolates producing OXA-48 carbapenemase (a) and hybridization with bla_{OXA-48} (b) and $bla_{CTX-M-15}$ (c) probes. Lanes λ , phage λ DNA digested with PstI, used as reference for the hybridization experiments (the sizes of some of the linear fragments are shown in parentheses); lanes i and ii, plasmids obtained from *E. coli* V517 (NCTC 50192) and plasmid RP4 used as molecular size standards for undigested DNA; lanes 1, *Kp*-HUCA 4; lanes 2, *Ec*-HUCA 1; lanes 3, *Ec*-HUCA 2; lanes 4, *Ec*-HUCA 3.

were updated in January 2013 (9). As shown in Table 2, the resistance pattern was different for each of the three *E. coli* isolates. Note that each isolate showed intermediate susceptibility to imipenem (MICs of 2 mg/liter) and resistance to ertapenem (MICs of 2 mg/liter), and they were positive for the modified Hodge test recommended for the detection of carbapenemases (9). *Ec*-HUCA 2 was also resistant to third-generation cephalosporins. The *K. pneumoniae* isolate recovered from patient 1 was resistant to third-generation cephalosporins and ertapenem but susceptible to imipenem. Apart from resistance to β -lactam antibiotics, resistance to nalidixic acid, ciprofloxacin, tobramycin, and/or trimethoprim-sulfamethoxazole was detected in some of the isolates (Table 2).

The genes responsible for resistance to carbapenems and extended-spectrum cephalosporins were identified by PCR amplification (10, 11) followed by sequencing. The presence of bla_{OXA-48} was demonstrated in the three E. coli isolates and Kp-HUCA 4, and bla_{CTX-M-15} was detected in Ec-HUCA 2 and Kp-HUCA 4. To establish the location of these genes, plasmid DNA extracted from each isolate (12) was hybridized with probes specific for the two genes amplified from Kp-HUCA 4 and labeled as previously reported (13). The same gel was also hybridized with phage λ DNA (Fermentas GmbH, Madrid, Spain), included as a control. The λ probe was generated by random-primed DNA labeling with digoxigenin-dUTP using the DIG DNA labeling kit (Roche Applied Sciences). As shown in Fig. 1a, each isolate displayed a distinct profile, including a common plasmid of ca. 60 kb accompanied by one or more plasmids of various sizes. The ca. 60-kb plasmid hybridized with the bla_{OXA-48} probe in the four isolates (Fig. 1b), while the *bla*_{CTX-M-15} mapped on plasmids slightly larger or slightly smaller than 150 kb in Kp-HUCA 4 and Ec-HUCA 2, respectively (Fig. 1c).

To investigate the self-transfer ability of the bla_{OXA-48} plasmids, conjugation experiments were performed using each of the four



FIG 2 XbaI pulsed-field electrophoresis profiles of *Klebsiella pneumoniae* (*Kp*) and *Escherichia coli* (*Ec*) isolates producing OXA-48 carbapenemase. Lane C, XbaI-digested DNA of *Salmonella enterica* serovar Braenderup H9812 used as size standard; lane 1, *Kp*-HUCA 4; lane 2, *Ec*-HUCA 1; lane 3, *Ec*-HUCA 2; lane 4, *Ec*-HUCA 3.

isolates as donors and a rifampin-resistant derivative of E. coli J53 as the recipient. Transconjugants were selected on eosin methylene blue (EMB) agar (Oxoid, Madrid, Spain) containing rifampin (100 mg/liter) plus ertapenem (0.5 mg/liter). At least four independent transconjugants were tested per conjugation with regard to plasmid content and antimicrobial susceptibility (see Table 2 for representative examples). As expected, each transconjugant carried the ca. 60-kb plasmid, either alone or together with other plasmid(s), and each was PCR positive for the *bla*_{OXA-48} gene. These self-transferable bla_{OXA-48} plasmids were assigned to incompatibility group IncL/M by PCR amplification using transconjugants carrying only this plasmid as the source of the template DNA and primers targeting the repA, traU, and parA genes specific for this group (7). Three out of four transconjugants tested from crosses involving Ec-HUCA 2 harbored the bla_{OXA-48} plasmid together with the larger *bla*_{CTX-M-15} plasmid, and they were resistant to cefotaxime and other extended-spectrum cephalosporins (Table 2). In contrast, all transconjugants analyzed from matings involving Kp-HUCA 4 (up to 20) were positive for the bla_{OXA-48} gene and plasmid only and showed a resistance pattern consistent with this (Table 2).

Multilocus sequence typing (MLST) (see mlst.warwick.ac.uk/ mlst/dbs/Ecoli/) assigned *Ec*-HUCA 1, *Ec*-HUCA 2, and *Ec*-HUCA 3 to ST131, ST58, and ST83, respectively (Table 2). Pulsedfield gel electrophoresis (PFGE) performed with XbaI (14) revealed a different profile for each of the three *E. coli* isolates, and the XbaI profile of *Kp*-HUCA 4 was also different (Fig. 2). Note that the cluster of *E. coli* isolates carrying the *bla*_{OXA-48} gene was detected in our hospital during the national outbreak of *K. pneumoniae* producing the OXA-48 carbapenemase (4, 8). As the responsible gene appeared to be carried by the same conjugative IncL/M plasmid in the two species, it may have been transferred from K. pneumoniae into E. coli isolates which had been circulating at the time in the same hospital. Such a transfer may have independently occurred more than once, as the E. coli isolates were not clonally related according to their STs. The presence of bla_{OXA-48} in Ec-HUCA 1 (ST131) is particularly worrisome, considering the ability of the pandemic ST131 clone to acquire genes encoding extended-spectrum β -lactamases, especially bla_{CTX-M} (15). In Spain, the only reported OXA-48-producing E. coli isolate was also ST131 (8). Note that the detection of carbapenem resistance was difficult, because the three E. coli isolates showed intermediate resistance to imipenem, and that treatment of the patients was complicated by additional resistances accompanying OXA-48 production in two out of the three isolates and by coinfection of the patients with other bacteria. Altogether, these facts highlight the risk of high antimicrobial pressure, in conjunction with long-term hospitalization, for the emergence of new resistant bacteria. Nevertheless, after the therapy indicated in Table 1, further cultures tested negative for OXA-48-producing Enterobacteriaceae, and the three patients were eventually discharged from the hospital.

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REFERENCES

- Patel G, Bonomo RA. 2013. "Stormy waters ahead": global emergence of carbapenemases. Front. Microbiol. 4:48. http://dx.doi.org/10.3389/fmicb .2013.00048.
- Nordmann P, Dortet L, Poirel L. 2012. Carbapenem resistance in *Entero-bacteriaceae*: here is the storm! Trends Mol. Med. 18:263–272. http://dx.doi.org/10.1016/j.molmed.2012.03.003.
- Poirel L, Potron A, Nordmann P. 2012. OXA-48-like carbapenemases: the phantom menace. J. Antimicrob. Chemother. 67:1597–1606. http://dx .doi.org/10.1093/jac/dks121.

- Canton R, Akova M, Carmeli Y, Giske CG, Glupczynski Y, Gniadkowski M, Livermore DM, Miriagou V, Naas T, Rossolini GM, Samuelsen O, Seifert H, Woodford N, Nordmann P, European Network on Carbapenemases. 2012. Rapid evolution and spread of carbapenemases among *Enterobacteriaceae* in Europe. Clin. Microbiol. Infect. 18:413–431. http://dx.doi.org/10.1111/j.1469-0691.2012.03821.x.
- Lascols C, Peirano G, Hackel M, Laupland KB, Pitout JD. 2013. Surveillance and molecular epidemiology of *Klebsiella pneumoniae* isolates that produce carbapenemases: first report of OXA-48-like enzymes in North America. Antimicrob. Agents Chemother. 57:130–136. http://dx.doi.org/10.1128/AAC.01686-12.
- Mathers AJ, Hazen KC, Carroll J, Yeh AJ, Cox HL, Bonomo RA, Sifri CD. 2013. First clinical cases of OXA-48-producing carbapenem-resistant *Klebsiella pneumoniae* in the United States: the "menace" arrives in the new world. J. Clin. Microbiol. 51:680–683. http://dx.doi.org/10.1128 /JCM.02580-12.
- Poirel L, Bonnin RA, Nordmann P. 2012. Genetic features of the widespread plasmid coding for the carbapenemase OXA-48. Antimicrob. Agents Chemother. 56:559–562. http://dx.doi.org/10.1128/AAC.05289 -11.
- Oteo J, Saez D, Bautista V, Fernandez-Romero S, Hernandez-Molina JM, Perez-Vazquez M, Aracil B, Campos J, Spanish Collaborating Group for the Antibiotic Resistance Surveillance P. 2013. Carbapenemase-producing *Enterobacteriaceae* in Spain in 2012. Antimicrob. Agents Chemother. 57:6344–6347. http://dx.doi.org/10.1128/AAC.01513-13.
- Clinical and Laboratory Standards Institute. 2013. Performance standards for antimicrobial susceptibility testing. NCCLS approved standard 23rd informational supplement, M100-S23. Clinical and Laboratory Standards Institute Wayne, PA.
- Batchelor M, Hopkins K, Threlfall EJ, Clifton-Hadley FA, Stallwood AD, Davies RH, Liebana E. 2005. *bla*_{CTX-M} genes in clinical *Salmonella* isolates recovered from humans in England and Wales from 1992 to 2003. Antimicrob. Agents Chemother. 49:1319–1322. http://dx.doi.org/10 .1128/AAC.49.4.1319-1322.2005.
- Dallenne C, Da Costa A, Decre D, Favier C, Arlet G. 2010. Development of a set of multiplex PCR assays for the detection of genes encoding important beta-lactamases in *Enterobacteriaceae*. J. Antimicrob. Chemother. 65:490–495. http://dx.doi.org/10.1093/jac/dkp498.
- Kado CI, Liu ST. 1981. Rapid procedure for detection and isolation of large and small plasmids. J. Bacteriol. 145:1365–1373.
- Herrero A, Rodicio MR, Echeita MA, Mendoza MC. 2008. Salmonella enterica serotype Typhimurium carrying hybrid virulence-resistance plasmids (pUO-StVR): a new multidrug-resistant group endemic in Spain. Int. J. Med. Microbiol. 298:253–261.
- 14. Ribot EM, Fair MA, Gautom R, Cameron DN, Hunter SB, Swaminathan B, Barrett TJ. 2006. Standardization of pulsed-field gel electrophoresis protocols for the subtyping of *Escherichia coli* O157:H7, *Salmonella*, and *Shigella* for PulseNet. Foodborne Pathog. Dis. 3:59–67. http://dx.doi .org/10.1089/fpd.2006.3.59.
- Qureshi ZA, Doi Y. 2014. Escherichia coli sequence type 131: epidemiology and challenges in treatment. Expert Rev. Anti Infect. Ther. 12:597-609. http://dx.doi.org/10.1586/14787210.2014.899901.