

Different phenotypic expression of KPC β -lactamase variants and challenges in their detection

Saoussen Oueslati, Linda Tlili, Cynthia Exilie, Sandrine Bernabeu, Bogdan

Iorga, Rémy Bonnin, Laurent Dortet, Thierry Naas

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2	Different phenotypic expressions of KPC eta -lactamases and
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5	Saoussen OUESLATI, ¹ Linda TLILI, ¹ Cynthia EXILIE, ¹ Sandrine BERNABEU, ^{1,2} Bogdan IORGA, ³
6	Rémy A. BONNIN, ^{1,4} Laurent DORTET ^{1,2,4} and Thierry NAAS ^{1,2,4*}
7	
8	1 EA7361 "Structure, dynamic, function and expression of broad spectrum β -lactamases", Faculty of Medicine
9	Université Paris-Sud, LabEx Lermit, Université Paris-Saclay, Le Kremlin-Bicêtre, France
10	² Bacteriology-Hygiene unit, Assistance Publique/Hôpitaux de Paris, Bicêtre Hospital, Le Kremlin-Bicêtre, France
11	³ Institut de Chimie des Substances Naturelles, CNRS UPR 2301, Université Paris-Saclay, Labex LERMIT, Gif-sur-
12	Yvette, France.
13	⁴ Associated French National Reference Center for Antibiotic Resistance: Carbapenemase-producing
14	Enterobacteriaceae, Le Kremlin-Bicêtre, France
15	
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19	*Corresponding author: Service de Bactériologie-Hygiène, Hôpital de Bicêtre 78 rue du Général Leclerc, 94275
20	Le Kremlin-Bicêtre, France.
21	Tel : +33 1 45 21 20 19 ;
22	Fax : +33 1 45 21 63 40,
23	thierry.naas@aphp.fr
24	

25 Sir,

26 Carbapenem-resistance among Enterobacteriaceae has become a major public health 27 issue owing to their rapid worldwide spread.¹ In Enterobacteriaceae this resistance is largely 28 due to the production of carbapenemases, the most prevalent throughout the world being 29 KPC-, VIM-, IMP-, NDM- and OXA-48 type variants. KPC-2, initially described in the USA in 30 2001,² went global in less than a decade likely as a result of being located on a transposon, 31 Tn4401 capable of high frequency transposition, itself inserted on self-conjugative plasmids, 32 and its frequent association with the highly successful K. pneumoniae clonal group 258.³ 33 Today, more than 44 natural KPC variants have been described, but only a few of them have 34 been characterized in terms of β-lactam hydrolytic properties.⁴ It is crucial to understand the 35 impact of single amino-acid changes on the hydrolytic profile of KPC-variants and the ability 36 of commercially-available diagnostic tests to efficiently detect them.

37 In this work, we have compared the phenotypic expressions of 14 KPC variants either 38 natural or generated by site-directed mutagenesis and evaluated the performance of several 39 diagnostic tests to detect them. Bla_{KPC-2} and bla_{KPC-3} alleles were cloned into pTOPO vector 40 along with its natural ribosomal binding site (RBS) upstream, and electroporated into 41 electrocompetent *E. coli* TOP10 as previously described.⁵ The resulting plasmids were used to 42 construct 11 single *bla*_{KPC-2} mutants and one single *bla*_{KPC-3} mutant using the QuikChange II Site-43 Directed Mutagenesis Kit (Agilent Technologies, Les Ulis, France) (Table 1). Thus among the 44 12 generated mutants (Figure S1A), four were natural variants of KPC-2 [KPC-5 (P104R)⁶, KPC-45 6 (V240G)⁷, KPC-12 (L168M), and KPC-33 (D179Y)] and one of KPC-3 [KPC-31 (D179Y)]. Six 46 substitutions correspond to natural substitutions that occurred in KPC-2, but that were not 47 reported alone: V240A, G147K, A120L, D92G, W105A and W105G. Finally, the last mutant has 48 a substitution C238S, which is a conserved residue that establishes a di-sulfide bridge with the 49 C68. MICs were performed using the Etest (bioMérieux, Marcy-l'Etoile, France) and detection 50 tests were performed according to manufacturers' recommendations. Phenotypic profiles 51 and diagnostic testing results are summarized in Table 1. Increased MICs for aztreonam and 52 cephalosporins without any modification of those for carbapenems have been observed with 53 mutants in position 240. On the opposite substitutions at positions 168 and 92 led to low 54 carbapenem MICs, but yet detectable carbapenem hydrolysis (as evidenced using biochemical 55 tests, see Table 1). The mutants P104R and G147K led to increased MICs for aztreonam and 56 cephalosporins, with slight decreased MICs for carbapenems. The mutations on residues 105 57 and 238 resulted in a global decrease in MICs for all β -lactams except amoxicillin, with a 58 stronger impact observed for the C238S mutant. With all of these mutants (including those 59 with highly increased MICs for ceftazidime, such as P104R, V240G and V240A) avibactam was 60 able to restore ceftazidime susceptibility. Interestingly, KPC-31 and KPC-33 with a D179Y 61 substitution, exhibit reduced MICs for all β -lactams, including aztreonam and amoxicillin, 62 except for ceftazidime, for which increased MICs were observed. In addition, these two 63 mutants led to MICs for the combination of ceftazidime/avibactam, that were limit to 64 resistance according to CLSI and EUCAST. These results suggest that avibactam is not capable 65 of inhibiting KPC-31 and KPC-33 efficiently. In order to confirm this hypothesis IC50s were measured with purified proteins.⁵ The IC50 values for KPC-31 (20µM) and KPC-33 (42µM) were 66 67 ~100 fold higher than those of KPC-2 (230nM) and KPC-3 (350nM), further supporting that the residue D179 is important in the binding of avibactam.^{8,9,5} 68

69 Overall, all tested residues, except A120, have a direct impact on the phenotypic 70 expression profile of KPC enzymes. Residues 168 and 179 are located on the Ω loop, which is 71 known to play a crucial role in the substrate selectivity of the enzyme.⁹ Residues 105, 104 and 72 240 delimit the cavity of the active site. Accordingly, hydrolysis spectrum is influenced by the 73 nature of the residues at these positions. Since the two cysteines C238 and C68 (adjacent to 74 the S70) form a disulfide bridge that stabilizes the KPC folding, it was expected to identify a 75 dramatic impact of the C238S substitution on the catalytic activity of the enzyme, as shown for other class A carbapenemases such as SME and GES-5.^{10,11} Finally, although located at the 76 77 opposite of the active site, residues 92 and 147 have also a crucial impact on KPC activity. 78 Molecular modeling of the G147K mutant, performed with UCSF Chimera software,¹² shows a 79 clash with G143 located on the helix α 6, which is in vicinity of the active site (Figure S1B). This 80 clash might lead to a switch of this helix that subsequently impact on the shape of the active 81 site.

82 Several diagnostic tests based on imipenem hydrolysis (biochemical and MALDI-83 TOF-based), Lateral flow immunoassays and molecular techniques (PCR) were evaluated on 84 these different mutants. Unlike molecular tests that were able to detect all mutants, biochemical tests based on imipenem hydrolysi: Carba NP test¹³, Rapidec CARBA NP¹³ 85 86 (bioMérieux, Marcy l'Etoile, France) and β -CARBA¹⁴ (BioRad, Marnes la Coquette, France), and MALDI-TOF -based MBT STAR-Carba IVD¹⁵ (Bruker, Illkirch-Graffenstaden, France) were able 87 88 to distinguish between KPC variants with carbapenem hydrolytic capacities from those lacking 89 any carbapenemase activity (Table 1). Molecular assays, being an in-house KPC specific PCR 90 or a commercially-available PCR (Xpert Carba, Cepheid, Maurens-Scopont, France) detected 91 accurately all variants. NG-test Carba5 (NG Biotech, Guipry, France) and Resist-4 O.K.N.V. K-Set (Coris, Gembloux – Belgium) lateral flow immunoassays (LFIA)¹⁶ assays were also able to 92 93 detect all KPC variants except KPC-31 and KPC-33.⁴ As the two latter variants lack 94 carbapenemase activity, the non-detection does not lead to false negative results in terms of 95 true carbapenemase detection. As these 2 variants lead to avibactam resistance, it would be 96 nevertheless important that they are detected, but not classified as carbapenemases.

Whether, carbapenems might be used to treat infections with KPC-31 or KPC-33-producers, is
still debatable, but according to EUCAST guidelines the answer is Yes, as the MICs for
imipenem are in the susceptibility range.

Overall, our results demonstrate that KPC variants are nor equal, probably selected by different antibiotic usages. This is the case for KPC-5 that leads to high level cefixime resistance. Some KPC variants cannot be considered as carbapenemases anymore. This is the case for KPC-31 and KPC-33 that have lost their carbapenemase activity in a similar manner to KPC-14 and KPC-28 variants.⁵ These peculiar variants are challenging for their detection, and will require complementary approaches combining molecular or LFIA together with carbapenem hydrolysis detection systems.

107

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113 Transparency declarations

LD is co-inventor of the Carba NP Test, which patent has been licensed to bioMérieux (La
Balmes les Grottes, France). All other authors: none to declare.

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AA changes	ges Variant MICs (mg/L)								Carbapenem hydrolysis assays				PCR		LFIAª					
		AMX	ATM	CRO	CAZ	CAZ / AVI	CFX	СТХ	FEP	IMP	MEM	ERT	Carba NP test	RAPIDEC®	β- CARBA™	MBT STAR- Carba IVD	In house bla _{KPC} PCR	Xpert Carba-R	NG-Test CARBA 5	Coris Resist-4 O.K.N.V. K-Set
	KPC-2	>256	32	16	4	0.38	4	8	2	8	3	1	+	+	+	+	+	+	+	+
H272Y	KPC-3	>256	>256	48	>256	0.75	12	>32	6	8	3	1	+	+	+	+	+	+	+	+
P104R	KPC-5	>256	>256	>256	>256	0.5	>256	8	2	1	0.25	0.19	+	+	+	+	+	+	+	+
V240G	KPC-6	>256	>256	48	32	0.75	16	>32	4	4	3	1	+	+	+	+	+	+	+	+
L168M	KPC-12	>256	12	6	4	0.38	3	4	1	0.75	0.25	0.125	+	+	+	+	+	+	+	+
D179Y	KPC-33	12	0.75	1	>256	8	6	1.5	1	0.25	0.032	0.008	-	-	-	-	+	+	-	-
H272Y, D179Y	KPC-31	6	0.75	2	>256	12	4	1.5	1	0.25	0.032	0.008	-	-	-	-	+	+	-	-
D92G		>256	64	12	4	0.25	4	4	2	1.5	0.5	0.38	+	+	+	+	+	+	+	+
W105A		>256	32	1	1	0.25	3	1.5	0.75	0.75	0.125	0.094	+	+	+	+	+	+	+	+
W105G		>256	24	1	1	0.25	2	0.75	0.25	1	0.19	0.125	+	+	+	+	+	+	+	+
A120L		>256	32	16	3	0.38	3	6	2	6	1.5	1.5	+	+	+	+	+	+	+	+
G147K		>256	64	32	6	0.38	6	24	6	6	1	0.75	+	+	+	+	+	+	+	+
C238S		>256	2	0.25	2	0.38	1	0.25	0.19	0.25	0.047	0.008	-	-	-	-	+	+	+	+
V240A		>256	>256	64	12	0.38	12	>32	4	8	2	1.5	+	+	+	+	+	+	+	+
E. coli TOP10		6	0.047	0.032	0.012	0.012	0.38	0.064	0.064	0.25	0.032	0.004	-	-	-	-	-	-	-	-

Table 1. MIC profiles of *E. coli* TOP10 expressing single KPC mutants and performances of various diagnostic tests.

AMX: Amoxicillin, ATM: Aztreonam, CRO: Ceftriaxone, CAZ: Ceftazidime, AVI: Avibactam, CFX : Cefixime, CTX : Cefotaxime, FEP : Cefepime, IMP : Imipenem, MEM : Meropenem and ETP : Ertapenem Dark grey, light grey and white boxes represent MICs in the resistance, intermediate and susceptible range, respectively. Breakpoints were those of the European Committee on Antimicrobial Susceptibility Testing Breakpoint tables for interpretation of MICs and zone diameters Version 9.0, valid from 2019-01-01 (<u>http://www.eucast.org/fileadmin/src/media/PDFs/EUCAST_files/Breakpoint_tables/v_9.0_Breakpoint_Tables.pdf;</u> last accessed September 2019). Grey boxes represent negative test results. ^a LFIA: Lateral flow immunoassay

Supplementary data







Figure S1. A Positions of the substituted residues included in this study on the Crystal structure of KPC-2 (PDB code 5UJ3) complex with cefotaxime (green), **B.** Representation of the steric clashes (red lines) between the side chains of K147 and G143.