

Genotyping and Antimicrobial Susceptibility of Carbapenem-resistant *Acinetobacter baumannii*: ISAb-1-bla_{OXA-23} association and plasmid analysis

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Abstract

The objective of this study was to characterize the molecular mechanisms responsible for carbapenem resistance among a collection of *Acinetobacter baumannii* isolates recovered at Taher Sfar University Hospital in Tunisia.

Antimicrobial susceptibility testing was performed on Mueller Hinton agar plates. Southern blot analysis and PCR-based replicon typing (PBRT) were conducted. β -lactamase genes were screened by PCR and sequencing. Conjugation experiments were carried out to determine the transferability of resistance determinants. Clonal relatedness was assessed by pulsed-field gel electrophoresis (PFGE). Sixteen carbapenem-resistant *Acinetobacter baumannii* strains were collected over a 3-year period from patient hospitalized in different wards of the Tahar Sfar University hospital. Resistance to carbapenems was mostly due to the expression of the acquired bla_{OXA-23} and the intrinsic bla_{OXA-66} genes, both genes being associated with the ISAb-1 insertion sequence. Mating-out assays showed that all carbapenem-resistant isolates carried the bla_{OXA-23} gene on plasmids that all belonged to the GR6 replicase group.

This study reports the molecular characterization of carbapenem resistance determinants in *A. baumannii* isolates from a single Tunisian hospital and highlights the potential for plasmid-mediated dissemination of resistance determinants at the local level.

Keywords: *Acinetobacter baumannii*, OXA-23, OXA-66, ISAb-1, imipenem, Tunisia

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1. Introduction

Acinetobacter baumannii, found ubiquitously in the environment, is an aerobic Gram-negative rod which is a non-fermenter of glucose [1]. It is recognized as one of the most problematic nosocomial pathogens, because of its intrinsic resistance to many antimicrobial molecules. Its clinical significance is controversial because the issue of attribute mortality frequently remains unsettled [2]. In fact, *A. baumannii* is often resistant to various antimicrobials, including β -lactams and especially carbapenems [3]. Resistance to these antibiotics may arise: (i) from upregulation of the chromosomal gene encoding a class D carbapenemase, namely OXA-51-like, thanks to efficient promoter sequences provided by insertion sequence ISAb-1 [4]; (ii) through the acquisition of genes encoding other class D carbapenemases such as OXA-23, -40, -58 and OXA-143-like enzymes; or (iii) less often, by acquisition of metallo- β -lactamases (MBLs) [5, 6].

The objective of this study was to investigate the molecular epidemiology and resistance mechanisms of carbapenem-resistant *A. baumannii* isolated at Taher Sfar University Hospital in Mahdia, Tunisia, with a particular focus on carbapenemase genes, their genetic environment, plasmid localization, and clonal relatedness.

2. Materials and methods

Strains, identification and susceptibility testing

Strain identification was performed by using the API20NE system (bioMérieux, Marcy l'Etoile) and 16S rRNA gene sequencing, as described previously [7]. The rifampin-resistant *A. baumannii* BM4547 was used as host in conjugation assays. *Escherichia coli* NCTC50192 harbouring four plasmids of 154, 66, 48 and 7 kb was used as a size marker.

The antibiotic susceptibility of the *A. baumannii* isolates was determined by the disk diffusion method on Muller-Hinton agar plates with β -lactam and non- β -lactam antibiotic-containing disks (Sanofi Diagnostics Pasteur,

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France). Minimum inhibitory concentrations (MICs) of ticarcillin, aztreonam, ceftazidime, imipenem, meropenem, and colistin were determined using Etest strips (AB bioMerieux, La Balme-les- Grottes, France) and interpreted according to the guidelines of the Clinical and Laboratory Standards Institute (2012) [8].

Molecular characterization of antimicrobial resistance determinants and plasmid typing

DNA extraction was performed as described previously [7]. A series of PCR reactions were performed to detect the different β -lactamase genes and their associated mobile genetic elements. Primers were designed to amplify the following genes: class A, *bla_{VEB}*, *bla_{PER}*, and *bla_{GES}*; class B, *bla_{IMP}*, *bla_{VIM}*, *bla_{GIM}*, *bla_{SPM}*, *bla_{SIM}*, and *bla_{NDM}*; and class D, *bla_{OXA-23}*-like, *bla_{OXA-40}*-like, *bla_{OXA-51}*-like, and *bla_{OXA-58}*-like [7]. PCR mapping experiments using combinations of the *ISAbal* specific primers and the OXA-51-like and OXA-23-like reverse primers were carried out [8]. In addition, isolates resistant to aminoglycosides were also screened for 16S rRNA methylase encoding genes production (*armA*, *rmtA*, *rmtB*, *rmtC*, *rmtD*, and *npmA*), as described [9]. All PCR products fragments were purified with QIAquick column (Qiagen, Courtaboeuf, France) and sequenced with an Applied Biosystems sequencer (ABI 377). The nucleotide and deduced amino acid sequences were analysed and compared to sequences available over the Internet on the National Center for Biotechnology Information website (<http://www.ncbi.nlm.nih.gov/BLAST/>).

Resistance gene transfer and plasmid analysis

Conjugation assays were carried out in trypticase soy broth agar with *A. baumannii* BM4547 (rifampicin resistant) as recipient strain. Mating broths were incubated at 37°C for 3 hours. The *A. baumannii* transconjugants were selected on trypticase soy agar plates containing ticarcillin (60 μ g/ml) and rifampicin (50 μ g/ml). Plasmid DNA was extracted using the Kieser method [10] and analyzed by electrophoresis on a 0.7% agarose gel. Plasmid typing was performed using the *A. baumannii* PCR based replicon typing [AB-PBRT] method as described previously [11].

Hybridization

Southern blot transfer of plasmid DNA was performed onto a nylon membrane (Hybond N+; Amersham Pharmacia Biotech, Orsay, France) as described previously [7]. The membrane was hybridized with a digoxigenin-labeled probe specific for *bla_{OXA-23}* (840 bp). Detection was carried out using the ECL non-radioactive labeling and detection system (Amersham Pharmacia Biotech), according to the manufacturer's instructions.

PFGE

A. baumannii strains were typed by using *Apal* macro restriction analyses and pulsed-field gel electrophoresis (PFGE) according to the manufacturer's recommendations (Bio-Rad, Marnes-la-Coquette, France). Samples were subjected to electrophoresis at 14°C, 6 volts/cm, and a switch angle with 1 linear switch ramp of 3–8 s for 10.5 h,

and then for 12–20 s for 10.5 h on an agarose gel using a CHEF-DR II apparatus [6]. Dendograms were generated using BioNumerics software (Applied Maths, Belgium) based on the Dice similarity coefficient, with clustering performed by the UPGMA method. Pulsotypes were defined using a similarity cutoff in accordance with Tenover et al. commonly accepted PFGE interpretation criteria [12]. Isolates showing DNA smearing after repeated attempts were considered non-typable.

3. Results

Strains

A total of 16 imipenem-resistant *A. baumannii* isolates were collected over a 37-month period (November 2008 to December 2011) from patient hospitalized at the Taher Sfar Hospital in Mahdia. Clinical data for these isolates are listed in Table 1.

Susceptibility testing

Carbapenem resistant isolates displayed various resistance profiles (11 antibiotypes for 16 isolates). All strains were resistant to β -lactams (ticarcillin, ticarcillin/clavulanic acid, cefotaxime, ceftazidime, cefepime, aztreonam, and carbapenems), to fluoroquinolones (norfloxacin, ofloxacin and ciprofloxacin), to nitrofurantoin, to chloramphenicol, to aminoglycosides (tobramycin, amikacin and gentamicin) but remained susceptible to colistin and rifampin. Resistance to aminoglycosides was heterogeneous. The most efficient aminoglycoside was tobramycin (resistance rate R=25%, n=4). Ten strains were resistant to amikacin whereas seven were resistant to gentamicin and three were resistant to netilmicin. Notably, three strains were highly resistant to all aminoglycosides (netilmicin, tobramycin, gentamicin and amikacin).

*Molecular screening and genetic background of the *bla_{OXA}* genes*

PCR experiments and sequencing showed that all strains harboured the CHDL OXA-23 encoding gene, along with the intrinsic gene *bla_{OXA-66}* (a variant of the *bla_{OXA-51}*-like gene). However, screening for 16S rRNA methylase production were negative for all three strains using PCR. The *ISAbal* element was found upstream to the corresponding genes *bla_{OXA-66}* and *bla_{OXA-23}*, in 100 % (16/16) and 43.75 % (7/16), respectively.

Genetic support characterisation

Mating-out assays with *A. baumannii* BM4547 followed by selection on ticarcillin plus rifampin containing plates showed that all carbapenem-resistant isolates carried their *bla_{OXA-23}* gene on plasmids. Kieser plasmid extraction of both parental strains and their respective transconjugants revealed one similar sized plasmid of ca. 90 kb.

Southern hybridization confirmed that the *bla_{OXA-23}* gene was located on a ca. 90 kb plasmid in all *A. baumannii* strains whereas the *bla_{OXA-66}* gene was chromosomally located.

Table 1. Clinical data of carbapenem resistant *Acinetobacter baumannii* clinical isolates

Isolate	Ward	Clinical data					MIC (µg/ml)	IS _{Aba-1} - bla _{OXA-23}	Pulsotype	
		Specimen	Date of isolation	Gender	Outcome	Antibiotic Treatment				
Ab 14	IC	TA	26/01/2009	M	dead	Ceftazidime, amikacin	>32	>32	+	S
Ab 19	G	CBEU	23/04/2009	F	improved	Amikacin, pipperacillin/tazobactam	>32	>32	-	S
Ab 20	IC	Central line	09/09/2009	F	dead	Ticarcillin/ clavulanate, amikacin	>32	>32	-	S
Ab 22	IC	TA	13/12/2009	F	Improved	Gentamicin, metronidazole pipperacillin/tazobactam,	>32	>32	-	III
Ab 32	IC	CBEU	02/08/2010	F	improved	Ceftazidime, amikacin	>32	>32	+	I
Ab 34	IC	CBEU	06/12/2010	M	improved	Ticarcillin/ clavulanate, amikacin	>32	>32	-	III
Ab 35	IC	CBEU	09/07/2011	M	improved	Amikacin, pipperacillin/tazobactam	>32	>32	+	II
Ab 36	IC	PTS	10/07/2011	M	improved	Imipenem, ciprofloxacin	>32	>32	+	II
Ab 37	IC	Urine	13/07/2011	M	dead	Amoxicilline/ clavulanate, imipenem	>32	>32	-	III
Ab 39	SU	ascitic fluid	11/08/2011	M	improved	Imipenem, ofloxacin	>32	>32	+	II
Ab 41	IC	PTS	03/09/2011	F	improved	Ticarcillin/ clavulanate, amikacin	>32	>32	-	V
Ab 43	IC	CBEU	21/11/2011	M	improved	Gentamicin, pipperacillin/tazobactam	>32	>32	+	II
Ab 44	IC	DPS	21/11/2011	F	dead	Imipenem, amikacin	>32	>32	-	IV
Ab 46	IC	TA	14/11/2011	M	improved	Amikacin, imipenem, levofloxacin	>32	>32	+	II
Ab 47	IC	Probe	10/12/2011	M	improved	Imipenem, colistin	>32	>32	-	IV
Ab 48	P	Probe	19/12/2011	M	improved	Ceftazidime, amikacin	>32	>32	+	I

Abbreviations: IC, Intensive care; SU, Surgical unit; TA, Tracheal aspiration; CBEU: cytobacteriological examination of urine; DPS, Distal protected specimen; P, Pediatric; G, genealogy; PTS, protected tracheal sampling; S, smears; M, male; F, Female.

Antibiogram performed for transconjugant revealed two antibiotypes. Transconjugants belonging to the antibiotic type I showed resistance to all β -lactam tested but ceftazidime and to amikacin (n=8) whereas transconjugants belonging to the antibiotic type II were also resistant to all β -lactams tested except ceftazidime and susceptible to aminoglycosides (n=8). Carbapenem MICs are listed in table 1. AB-PBRT PCR assigned all plasmids to GR6 replicase group.

Clonal analysis

PFGE analysis divided the 16 *A. baumannii* isolates into five pulsotypes. Three isolates (Ab14, Ab19, and Ab20) produced DNA smears despite repeated attempts and were therefore considered non-typable.

The observed diversity of pulsotypes suggests genetic heterogeneity among the isolates rather than dissemination of a single dominant clone within the hospital (Table 1).

Isolates co-expressing *ISAbal*-*blaOXA-23* and *ISAbal*-*blaOXA-66* belonged to pulsotypes I and II whereas strains with *ISAbal*-*blaOXA-66* and *blaOXA-23* were distributed among pulsotypes III, IV and V (Table 1).

4. Discussion

This study provides insight into the molecular mechanisms underlying carbapenem resistance in *A. baumannii* isolates recovered from a single tertiary-care hospital in Tunisia (The Taher Sfar Hospital Mahdia, Tunisia) over a 37-month period.

The *blaOXA-23* gene was identified in all of the *A. baumannii* isolates in our collection. The first report of this enzyme in *A. baumannii* was ARI-1, which was identified in an isolate from United Kingdom collected in 1985 interestingly the same year that imipenem was approved for use [13]. In 2000, enzyme sequence analysis (re-named OXA-23) indicated that it was a member of the ambler class D group of β -lactamases [14]. Numerous international studies have found the *blaOXA-23* to be the most frequent acquired carbapenemase among carbapenem resistant *A. baumannii* [6, 15-22]. This dominance was also found in Tunisia. In fact, only few studies described the dissemination of OXA-23-producing carbapenem-resistant *A. baumannii* in Tunisia. The first description was reported in thirteen isolates during 2008. All the OXA-23-positive isolates were clonally related, and the *blaOXA-23* gene was found to be chromosomally located and associated with an upstream-located insertion sequence *ISAbal* [23]. In 2011, a second work was published reporting the presence of *blaOXA-23* gene among imipenem-resistant *A. baumannii* recovered from different wards at the Charles Nicolle Hospital [24]. Another work reported the production of OXA-23 in *A. baumannii* clinical isolates recovered in the Maternity and the Neonatology Center in Monastir, Tunisia [7]. Chihi et al. reported also the occurrence of the *blaOXA-23* gene in clinical isolates of *A. baumannii* recovered from two hospitals in Tunis, Tunisia [25], and more recently, Mathlouthi et al. reported the *blaOXA-23* as the most prevalent oxacillinase encoding gene among twenty-five imipenem-resistant *A. baumannii* clinical isolates isolated from Mohamed Kassab Orthopaedic Institute in Tunis, Tunisia [26].

The *blaOXA-23* gene was detected in all isolates and was consistently located on a ~90-kb plasmid belonging to the GR6 (repAci6) replicase group. This finding supports the important role of repAci6-type plasmids in the local dissemination of carbapenem resistance determinants, as previously reported in Tunisia and other regions. The repAci6 gene was identified as the unique rep gene that were successfully transferred in mating experiments, thereby confirming the association of the repAci6 gene with the self-transferability property of this *A. baumannii* plasmid group [27]. In fact, this group of plasmids has been shown to be highly prevalent in *A. baumannii* and was previously found to be associated with the *blaOXA-23*, *blaOXA-40*, and *blaOXA-58* CHDL genes and GES type β -lactamases [7, 25, 27-28].

Non-carbapenemase-mediated mechanisms such as efflux pump overexpression or reduced membrane permeability are discussed here as hypotheses only, as these mechanisms were not experimentally investigated in the present study.

In Tunisia, both plasmid and chromosomal location of the *blaOXA-23* were reported [7, 23]. Recently, Kessis-Charfi et al. reported the *blaOXA-23* gene in neonatal population; the gene was also located onto a 90 ca plasmid assigned to the GR6 [7], which suggest the circulation of a similar plasmid backbone.

Naturally occurring OXA carbapenemases are OXA-51-like enzymes. Until today, up to 95 variants of OXA-51 have been identified from medical centers worldwide [17, 29-30]. PCR performed showed that all 16 carbapenem-resistant *A. baumannii* clinical isolates harboured the variant *blaOXA-66*. Although the presence of *ISAbal* upstream of *blaOXA-51*-like genes has been associated with carbapenem resistance, some isolates harbouring this genetic configuration have been reported to remain susceptible to carbapenems. In our study, all isolates displayed high-level carbapenem resistance, suggesting that additional factors may contribute.

OXA enzymes possess weak carbapenemase activity. However, the over-expression of *blaOXA* genes, driven mostly by promoters provided by their upstream ISs, is one of the means by which *A. baumannii* acquires a high level of carbapenem resistance. Insertion sequence *ISAbal*, which has 11-bp inverted repeat sequences (IRs) flanked by 9-bp direct repeats of the target sequence, has been identified in *A. baumannii* and as one of many IS elements contains promoters that play a role in the expression of antibiotic resistance genes [31]. Evans and Aymes reported that *ISAbal* provides a promoter for the *blaOXA-23*-like gene when it is inserted 25-bp upstream of the gene [17]. In addition, some studies have shown that transposons such as Tn2006 can be formed by two *ISAbal* elements bracketing the *blaOXA-23* gene, which in turn involves in the dissemination of resistance determinants [6]. Moreover, studies have reported that the presence of *ISAbal* upstream to the *blaOXA-51*-like genes can also provide a promoter that allows the hyper-production of these enzymes, resulting in carbapenem resistance [32]. Some isolates harboring the *blaOXA-51*-like gene with an upstream *ISAbal* are still susceptible to carbapenems [33]. In our case, all the carbapenem-resistant *A. baumannii* isolates had *ISAbal* element found upstream of the *blaOXA-66* gene. The *ISAbal* element was also detected upstream to the *blaOXA-23* in 43.75% (7/16).

However, all isolates displayed a high resistance level toward carbapenems (imipenem and meropenem MICs > 32 μ g/ml). Two hypotheses may be advanced as possible explanation for this high resistance: 1) The upregulated genes *blaOXA-23* and the *blaOXA-66* by the insertion of the *ISAbal* element may act in concert and increase the MICs of carbapenems to a high level [34,35]. 2) on-carbapenemase-mediated resistance mechanisms such as reduced membrane permeability due to porin changes and over expression of efflux pumps make a trivial contribution toward carbapenem resistance in *A. baumannii* [35]. Heritier et al. reported that the synergism between acquired oxacillinases and the RND efflux pump, AdeABC, was implicated in the increased levels of resistance toward carbapenems [36-38]. Therefore, synergism between oxacillinases and efflux pump may also explicate the high carbapenems resistance in our isolates. More studies on the role of non-carbapenemase-mediated mechanisms in *A. baumannii* are required. These kind of mechanisms such as efflux pump overexpression or reduced membrane permeability are discussed here as hypotheses only, as these mechanisms were not experimentally investigated in the present study.

Using PFGE typing, which is still considered a good typing method, our strains were assigned to three clusters (3 pulsotype for 11 strains) suggesting a non-clonal dissemination. In fact, carbapenem-resistant *A. baumannii* exhibiting different CHDL genes were also detected in the environment and in the community worldwide [39-42]. However, no investigation had been undertaken in this direction in our country.

Conclusion

This study characterizes the molecular features of carbapenem-resistant *A. baumannii* isolates recovered at Taher Sfar University Hospital in Mahdia, Tunisia. Our findings highlight the predominant role of *blaOXA-23*, carried on transferable GR6 plasmids, in mediating carbapenem resistance in this setting.

Although limited by the small sample size and single-center design, this work provides important baseline molecular data and emphasizes the need for continuous surveillance and robust infection control measures to prevent the dissemination of multidrug-resistant *A. baumannii*, thereby protecting patient safety and public health.

Author disclosure statement

None to declare.

Declaration of Competing of Interest

The authors declare that they have no conflicts of interest.

Author Contributions

WM: conceptualization, supervision, validation, project administration, formal analysis, writing, review and editing; KC: methodology, investigation, writing original draft

preparation; RG: methodology, investigation; AM: methodology, investigation; TBR: formal analysis, writing, review; IEA: methodology, investigation; ABHK: methodology, investigation; MA: conceptualization, project administration, supervision, validation, formal analysis, writing, review and editing. All authors approved the final manuscript.

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