Distinct Genetic Diversity of Carbapenem-Resistant *Acinetobacter baumannii* from Colombian Hospitals

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The global success of multidrug-resistant *Acinetobacter baumannii* has been associated with the dissemination of a high-risk clone designated clonal complex (CC) 92^B (Bartual scheme)/CC2^P (Pasteur scheme), which is the most frequent genetic lineage in European, Asian, and North American carbapenem-resistant *Acinetobacter* isolates. In these isolates, carbapenem resistance is mainly mediated by β -lactamases encoded by *bla*_{OXA-23-like}, *bla*_{OXA-24-like}, *bla*_{OXA-51-like}, and/or *bla*_{OXA-58-like} genes. In this study, we characterized the population genetics of 121 carbapenem-resistant *A. baumannii* complex isolates recovered from 14 hospitals in seven cities in Colombia (2008–2010). Multiplex PCR was used to detect *bla*_{OXA-23-like}, *bla*_{OXA-24-like}, *bla*_{OXA-51-like}, and *bla*_{OXA-58-like} genes. Molecular typing was performed using pulsed-field gel electrophoresis (PFGE) and multilocus sequence typing (MLST). PCR showed that 118 (97.5%) of the isolates were positive for both *bla*_{OXA-23-like} and *bla*_{OXA-51-like} genes, and three other isolates were only positive for *bla*_{OXA-51-like}. PFGE identified 18 different pulsotypes, while MLST identified 11 different sequence types (STs), seven of which had not been previously described in *Acinetobacter*. None of the STs found in this study was associated with CC92^B/CC2^P. The most widespread STs in our isolates belonged to ST636 and their single-locus variants ST121/ST124/ST634 (CC636^B) followed by STs belonging to CC110^B. Our observations suggest a wide distribution of diverse *A. baumannii* complex clones containing *bla*_{OXA-23-like} in Colombian hospitals (especially CC636^B and CC110^B) that differ from the high-risk clones commonly found in other regions of the world, indicating a distinct molecular epidemiology of carbapenem-resistant *Acinetobacter* spp. in Colombia.

Keywords: *Acinetobacter baumannii*, antibiotic resistance, carbapenemase, OXA enzymes, multilocus sequence typing

Introduction

ACINETOBACTER BAUMANNII IS an opportunistic pathogen associated with hospital-acquired infections and outbreaks worldwide, especially in critically ill patients. *A. baumannii* is typically able to survive on inanimate and dry surfaces and to be multidrug resistant (MDR), even to carbapenems.¹ Carbapenem resistance has been associated with the presence of carbapenemase-type β -lactamases, par-

ticularly those encoded by the *bla*_{OXA-23-like}, *bla*_{OXA-24-like}, *bla*_{OXA-51-like}, and *bla*_{OXA-58-like} genes, and the presence of the insertion sequences *ISAbal*, *ISAb3*, or *ISAb4*.^{2,3}

Multilocus sequence typing (MLST) has been used worldwide to study the population structures of *A. baumannii*.⁴ Two different MLST systems with their own methodology and databases have been developed: one described by Bartual *et al.* (<http://pubmlst.org/abaumannii/>) and the other described by the Pasteur Institute (www.pasteur.fr/mlst).⁵ Although these

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schemes share three of the seven housekeeping genes they use, both tools are useful for characterization of *A. baumannii* in population-based studies.⁶ The sequence types (STs) belonging to clonal complex (CC) 92^B (Bartual scheme)/CC2^P (Pasteur scheme) (also designated international clonal lineage II) have been reported as the most widespread in Europe, Asia, and the United States.⁷ Given its epidemiological success and its frequent association with carbapenem resistance, this CC has been designated a high-risk clone of MDR *A. baumannii*.^{8,9}

In South America, namely in Brazil and Argentina, CC79^P/CC113^B and CC15^P/CC104^B have been the predominant clones responsible for the dissemination of OXA-23-like-producing carbapenem-resistant *A. baumannii* (CRAB).^{10–20}

We aimed to characterize the population structure of CRAB isolates recovered from hospitals in Colombia and to identify possible high-risk clones responsible for dissemination of these organisms.

Materials and Methods

Bacterial isolates

A total of 121 carbapenem-resistant *A. calcoaceticus*–*A. baumannii* complex isolates obtained from the same number of patients were recovered from the isolate collection of the Colombian Nosocomial Resistance Study Group housed at the International Center for Medical Research and Training (CIDEIM) in Cali, Colombia. Bacterial identification was performed by the VITEK 2® automated system (bioMérieux, Marcy-l'Étoile, France), and *in vitro* antimicrobial susceptibility testing was performed by broth microdilution (Sensititre panels; Trek Diagnostic Systems, Westlake, OH) according

to the Clinical and Laboratory Standards Institute (CLSI).²¹ Clinical interpretation of susceptibility to tigecycline was based on breakpoints suggested previously by Jones *et al.*²²

The isolates were collected between 2008 and 2010 from 14 tertiary care hospitals in seven cities (Bogotá, Medellín, Cali, Pereira, Bucaramanga, Barranquilla, and Ibagué). This collection period was chosen as part of the surveillance of MDR organisms made by CIDEIM in Colombia, and corresponds to the time in which emergence and widespread dissemination of carbapenemase-producing *Enterobacteriaceae* occurred. The most common sample source was the respiratory tract ($n=40$, 33%), followed by blood ($n=35$, 29%) and skin and soft tissues ($n=33$, 27%). The majority of isolates were recovered from patients hospitalized in intensive care units (87, 72%).

Analysis of bla genes

Detection of OXA-type enzymes was performed by a multiplex PCR assay targeting *bla*_{OXA-23-like}, *bla*_{OXA-24-like}, *bla*_{OXA-51-like}, and *bla*_{OXA-58-like} genes, following protocols previously reported.²³ In addition, identification of IS*Aba1* and IS*Aba4* associated with *bla*_{OXA-23-like} gene was performed using PCR and sequencing in the isolates analyzed through MLST.²³

Molecular typing

Pulsed-field gel electrophoresis (PFGE) was performed in all 121 isolates studied, following the method described by Gautom²⁴ and using the *SmaI* restriction enzyme. Analysis of pulsotypes and construction of dendrograms were performed using Fingerprinting II software (Bio-Rad Laboratories,

FIG. 1. Dendrogram of genomic comparison for the 18 representative PTGs identified by pulsed-field gel electrophoresis in *Acinetobacter baumannii* complex isolates using the UPGMA based on Dice similarity. PTGs, pulsotype groups; ST, sequence type (Bartual scheme); UPGMA, unweighted pair group method with arithmetic mean.

TABLE 1. MOLECULAR CHARACTERIZATION AND ANTIMICROBIAL SUSCEPTIBILITY TESTING OF CARBAPENEM-RESISTANT *ACINETOBACTER BAUMANNII* COMPLEX FROM COLOMBIAN HOSPITALS

No.	City	PTG	ST ^B	bla _{OXA-23-like}	bla _{OXA-51-like}	ISAba1	Sample	Antibiotic MIC (µg/ml)									
								AMK	CEP	CEF/SUL	CIP	IMI	MEM	PIPTAZ	POLB	TIG	
1	CLO	PTG1	637	POS	POS	POS	Respiratory tract	>64	32	128/64	>8	64	64	>256/4	1	0.5	
2	BOG/CLO/MED/PEI	PTG2	637	POS	POS	POS	Respiratory tract	>64	16	64/32	>8	32	64	>256/4	2	0.25	
3	BOG/CLO/MED/PEI	PTG2	637	POS	POS	POS	Skin and soft tissues	>64	32	64/32	>8	32	64	>256/4	1	0.5	
4	BGA/CLO	PTG3	637	NEG	POS	POS	Respiratory tract	>64	32	128/64	>8	32	64	>128/4	1	0.5	
5	BGA/BOG/CLO	PTG4	637	POS	POS	POS	Respiratory tract	>64	32	64/32	>8	64	64	>256/4	1	0.5	
6	BGA/BOG/CLO	PTG4	637	POS	POS	POS	Gastrointestinal tract	>64	64	64/32	>8	32	64	>256/4	2	0.25	
7	BGA/BOG/CLO	PTG4	641	POS	POS	POS	Gastrointestinal tract	>64	64	64/32	>8	32	64	>256/4	2	0.25	
8	CLO/MED	PTG5	636	POS	POS	POS	Skin and soft tissues	>32	>16	64/32	>2	32	64	>64/4	1	0.25	
9	BOG/CLO/IBE/PEI	PTG6	640	POS	POS	POS	Respiratory tract	>64	32	32/16	>8	64	64	>256/4	2	0.5	
10	CLO/PEI	PTG7	174	POS	POS	POS	Respiratory tract	64	128	128/64	>8	32	64	>256/4	2	4	
11	BOG/CLO/IBE	PTG8	636	POS	POS	POS	Blood	>64	32	128/64	>8	64	64	>256/4	2	0.5	
12	BGA/BOG/BQA/IBE/MED	PTG9	518	POS	POS	POS	Blood	>64	>32	128/64	>8	128	128	>256/4	4	2	
13	BGA/BOG/BQA/IBE/MED	PTG10	121	POS	POS	POS	Blood	>64	64	64/32	>8	32	64	>256/4	2	0.25	
14	BOG/BQA	PTG11	638	POS	POS	POS	Urine	>64	32	32/16	>8	32	64	>128/4	<0.5	0.5	
15	BOG	PTG12	124	POS	POS	POS	Urine	64	>64	>128/64	>8	>64	>64	>128/4	1	0.5	
16	BOG	PTG13	634	POS	POS	POS	Respiratory tract	32	16	64/32	>8	32	64	>256/4	1	0.5	
17	BGA/BQA	PTG14	641	POS	POS	POS	Respiratory tract	>64	64	64/32	>8	64	128	>256/4	1	0.5	
18	BQA	PTG15	641	POS	POS	POS	Blood	64	32	64/32	8	32	64	>256/4	<0.5	1	
19	BGA	PTG16	637	NEG	POS	NEG	Gastrointestinal tract	>64	64	64/32	>8	32	64	>256/4	2	0.25	
20	BOG	PTG17	639	POS	NEG	POS	Blood	>64	32	64/32	<1	128	128	>256/4	1	1	
21	CLO	PTG18	636	POS	POS	POS	Blood	>64	32	64/32	<1	128	128	>256/4	1	1	

Isolates selected for multilocus sequence typing are presented.

AMK, amikacin; BGA, Bucaramanga; BOG, Bogotá; BQA, Barranquilla; CEF/SUL, cefoperazone/sulbactam; CEP, cefepime; CIP, ciprofloxacin; CLO, Cali; IBE, Ibagué; IMI, imipenem; MED, Medellín; MEM, meropenem; MIC, minimum inhibitory concentration; NEG, negative; PEI, Pereira; PIPTAZ, piperacillin/tazobactam; POLB, polymyxin B; POS, positive; PTG, pulsotype group; ST^B, sequence type (Bartual scheme); TIG, tigecycline.

panied one of them. These isolates exhibited an MDR phenotype that might be explained by mechanisms not examined in this study such as the loss or modification of the carbapenem-associated outer membrane protein CarO, or modification of penicillin-binding proteins as previously reported elsewhere.^{29,30} *bla*_{OXA-51-like} has only been found to lead to carbapenem resistance if *ISAbal* is located upstream of the gene.²

Analysis by PFGE showed the presence of 18 different band profiles (pulsotypes; Fig. 1); five of them represented by polyclonal isolates. Based on these results, 21 isolates (at least one isolate per pulsotype) were selected for MLST (Table 1). Results showed 11 different STs, seven of which had not been previously reported in *A. baumannii* (ST636, ST634, ST637, ST638, ST639, ST640, and ST641). These STs have been submitted in the MLST database (<http://pubmlst.org/abbaumanni/>). The diversity of STs in *A. baumannii* has been associated with the variability found in *gyrB* and *gpi* genes in the MLST scheme.³¹ However, in our study, the *cpn60* gene was the one that exhibited high sequence diversity among the Colombian *A. baumannii* complex isolates.

Overall, carbapenem resistance in *A. baumannii* complex from Colombian hospitals in this study was linked to the widespread dissemination of *bla*_{OXA-23-like} β-lactamase. Although the isolates were analyzed between 2008 and 2010, the resistance profile of *A. baumannii* in Colombia has likely not changed (based on our latest surveillance data), and as a result, the resistance mechanisms are expected to be similar to date.^{32–35}

The most common STs found within the isolate collection were the novel ST636 and its single-locus variants (SLVs) ST121 (Spain),⁷ ST124 (USA),⁷ and ST634 (novel in this study), all of these belonging to CC636^B (designated in this study) (Fig. 2). Other STs included ST637 and ST641 (SLVs of CC110^B), as well as ST518. CC636^B has been predominantly related to the spread of CRAB in Mexico.³⁶

Interestingly, ST637 and ST641 are SLVs of ST110, which is the founder of the CC110^B previously reported in Argentina, Korea, and the United States.⁷ The only other study of its kind in Colombia, recently reported the presence of ST229 (CC110^B) and ST758.³⁵ However, this study included 32 *A. baumannii* complex isolates collected from five hospitals in only one city (Medellín).

Of note, none of the STs found in this study was associated with CC92^B/CC2^P, which has been reported as the most prevalent *Acinetobacter* MDR lineage in 34 countries of the world.⁷ In Latin America, MLST allelic profiles for CRAB have seldom been reported related to CC92^B/CC2^P in Brazil and Mexico.^{7,14,36} It is also important to note that almost all STs described in this study were present in Bogotá, the capital and largest city of Colombia (Table 1). This phenomenon is likely explained by the fact that third-level hospitals in Bogotá are referral centers for the rest of the country and have high levels of complexity.

Conclusions

This study shows that *bla*_{OXA-23} was the most prevalent determinant of carbapenem resistance in *A. baumannii* complex strains collected from 14 Colombian hospitals between 2008 and 2010. The *bla*_{OXA-23} harboring *A. baumannii* complex isolates belonged to the MLST-defined CC110^B, previously reported in Argentina, Korea, and the United States, and the novel CC636^B, containing diverse STs, some of them previously found in Spain and the United States. Genetic lineages of CRAB reported to be widely distributed in all the continents, such as the high-risk clone CC92^B/CC2^P, were not found in our study.

Our observations serve as an initial characterization of the population structure of CRAB in Colombia during the same time in which dissemination of carbapenemases in *Enterobacteriaceae* occurred in our country and became epidemic. Molecular studies contribute to the understanding of the population genetic diversity and mechanisms of carbapenem resistance in *A. baumannii*.

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