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Letter

New sequence types of *Acinetobacter baumannii* in two emergency hospitals in the Central-West region of Brazil

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Dear Editor:

Acinetobacter baumannii, a common causal agent of ventilator-associated pneumonia, is related with high hospital costs and mortality[1]. The 2016 surveillance report of the European Centre for Disease Prevention and Control reported that 49% of *A. baumannii* isolates were carbapenem resistant[2]. In Brazil, the percentage of this species with resistance to carbapenems is approximately 71%, with similar data for Chile and Argentina[3]. The genes $bla_{\text{OXA-23}}$, $bla_{\text{OXA-24}}$ (and its variants $bla_{\text{OXA-40}}$ and $bla_{\text{OXA-72}}$), $bla_{\text{OXA-58}}$, $bla_{\text{OXA-143}}$, and $bla_{\text{OXA-235}}$ of the Ambler class D β-lactamases are responsible for carbapenem resistance in *A. baumannii*[4]. Multilocus sequence typing (MLST) is used to determine the sequence type (ST) of isolates, with *A. baumannii* ST15, ST25, ST79, and ST1 being the most common in South America[5]. These clones are clustered in MLST clonal complexes (CC) CC15, CC25, CC79, and CC1, respectively[5]. In Brazil, *A. baumannii* ST15, ST79, and ST1 are also frequently found[6].

A total of nine *Acinetobacter* spp. isolates were extracted from rectal swab and wound secretion samples from nine patients hospitalized in intensive care units at two public emergency hospitals in Cuiaba and Varzea Grande, Mato Grosso State, Central Brazil: the Municipal Hospital and Emergency Room of Cuiaba, and the Municipal Hospital and Emergency Room of Varzea Grande. Rectal swabs and wound secretion samples were collected from the patients for routine surveillance by the hospital infection control committees between June 2012 and August 2012. Microorganism identification was performed, and drug resistance profiles based on the minimum inhibitory concentration were obtained using the Bact/Alert 3D and Vitek2 systems (BioMérieux, Marcy l'Etoile, France) in the Microbiology Laboratory of the Júlio Muller University Hospital, Cuiaba, Mato Grosso, Brazil. Isolates identified as *Acinetobacter* spp. were tested for their sensitivity to antimicrobials according to the 2017 Clinical and Laboratory Standards Institute Guidelines[7]. The genomic DNA extraction, polymerase chain reaction (PCR) for the detection of *A. baumannii* genes, and application of the MLST technique for genotypic analysis of the isolates were performed in the Laboratory of Veterinary Microbiology and Molecular Biology, College of Veterinary Medicine, Federal University of Mato Grosso, Mato Grosso, Brazil[8-10].

The research protocol (#850.791) was approved by the Ethics Research Committee of the Julio Muller Hospital, and was registered in the National System of the Ethical Evaluation of Human Research Projects (CAAE 28637414.0.0000.5541). The *A. baumannii* isolates were confirmed by the PCR-based amplification of the $bla_{\text{OXA-51}}$ gene. The patient demographics and the isolates' *in vitro* resistance to antimicrobials are detailed in **Table 1**.

The *A. baumannii* isolates analyzed in this study showed resistance to imipenem and other drugs, as well as sensitivity to polymyxin B, similar to the trends reported in other regions of Brazil and in other countries[2,3,9]. The $bla_{\text{OXA-23}}$ gene was most frequently found. These data are similar to those of other international and Brazilian studies[5,6,9,]. Other genes associated

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TABLE 1: Clinical characteristics of the nine hospitalized patients, and *in vitro* susceptibility to imipenem, resistance genes, sequence types, and clonal complexes of *Acinetobacter baumannii* isolates, from two emergency hospitals in the Center-West region of Brazil.

Patient	Age (year), Sex[a]	Sample[b]	Imipenem[c]	Time to isolation (day)	Hospital[d]	Prior treatment[e]	Outcome	*bla*$_{OXA-23}$/ IS*Aba1*	*bla*$_{OXA-24}$	*bla*$_{OXA-143}$	Sequence type (ST)	Clonal complex[f] (CC)
1	67, F	RS	R	20	A	IMP	Recovery	+	-	+	984	Singleton[g]
2	35, M	RS	R	19	A	PIPE/TAZ, IMP, VAN	Recovery	+	-	-	108	108
3	78, F	RS	R	05	A	CEFA	Death	+	+	-	1	1
4	41, F	RS	R	20	A	PIPE/TAZ, VAN	Recovery	+	+	-	108	108
5	45, M	RS	R	50	B	PIPE/TAZ, VAN	Recovery	+	+	-	162	162
6	23, M	WS	S	33	B	CEFE	Recovery	+	-	-	985	79
7	21, M	RS	R	14	B	CEFE, VAN	Recovery	+	+	-	409	1
8	23, M	RS	R	18	B	CEFI, CEFE, VAN	Recovery	+	+	+	987	987
9	42, F	RS	R	27	B	PIPE/TAZ	Recovery	+	+	+	NP[h]	NP

[a]**F:** female; **M:** male; [b]**RS:** rectal swab; **WS:** wound secretion; [c]**R:** resistant; **S:** sensitive; [d]**A:** Municipal Hospital and Emergency Room of Varzea Grande; **B:** Municipal Hospital and Emergency Room of Cuiaba; [e]**IMP:** imipenem; **PIPE/TAZ:** piperacillin/tazobactam; **CEFE:** cefepime; **CEFA:** cephalothin; **CEFI:** ceftriaxone; **VAN:** vancomycin; [f] Clonal complex according to the eBurst classification; [g]**ST984:** identified for the first time in this study and classified as a singleton by eBurst; [h]**NP:** not performed.

with carbapenem resistance were *bla*$_{OXA-24}$ and *bla*$_{OXA-143}$. The *bla*$_{OXA-24}$ gene is more prevalent in some countries, such as Ecuador and Mexico, and is uncommon in Brazil[5,6,11]. However, it was the second most prevalent carbapenem resistance gene found in another study conducted in the Center-West region of Brazil[9]. The *bla*$_{OXA-143}$ gene, which has been detected in southeastern, southern, and central Brazil, was again found in the Center-West region of the country[9,10]. The *bla*$_{OXA-58}$, *bla*$_{KPC}$, and *bla*$_{NDM}$ genes were not found. Phylogenetic classification by MLST revealed the presence of ST108, ST162, and ST1, which are commonly found in South American countries, including Brazil[5,6,9]. Interestingly, one of the isolates corresponded to ST409, a sequence type first described in Egypt, and was never described in Brazil until now[12]. Three new STs (ST984, ST985, and ST987) were found.

The isolates reported here were recovered form surveillance cultures, and only one patient evolved to death. However, the finding of isolates of different multidrug-resistant *A. baumannii* STs deserves the attention and concern of local health authorities owing to the extended antimicrobial resistance profile of this microorganism. More research is warranted to assess the impact of this multidrug-resistant bacterium on the generation of threatening infections in the study region.

Conflict of Interest

The authors declare that there is no conflict of interest.

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Accession numbers of new sequences reported in the article (https://pubmlst.org/abaumannii/): ST984, ST985, and ST987.

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