



Letter to the Editor

Carbapenemase-producing *Acinetobacter* spp. from environmental sources in a hospital in French Polynesia



Sir,

Multidrug-resistant (MDR) *Acinetobacter* spp. are now recognised as major pathogens in healthcare facilities. Carbapenem-resistant isolates are among the priority list of pathogens for which urgent novel therapeutics are mandatory. Carbapenem resistance in *Acinetobacter* spp. is mainly mediated by the production of carbapenem-hydrolysing class D β -lactamases (CHDLs) and, to a lesser extent, Ambler class B metallo- β -lactamases. Five main groups of CHDLs have been described in *Acinetobacter*, namely OXA-23, -24/-40, -58, -143 and -235 [1]. The most prevalent CHDL is OXA-23 that has been described worldwide, carried either by conjugative plasmids or on the chromosome and associated with different transposons involving either insertion sequence IS*Aba1* or IS*Aba4* [1]. The *bla*_{NDM-1} gene was described in *Acinetobacter* as part of composite transposon Tn125 bracketed by two copies of IS*Aba125* [1]. In 2003–2004, an outbreak of OXA-23-producing carbapenem-resistant *Acinetobacter baumannii* was observed at the Centre Hospitalier de Polynésie Française, the main hospital of Papeete, Tahiti, French Polynesia, located in the middle of the Pacific Ocean [2]. Here we describe the occurrence of carbapenemase-producing *Acinetobacter* spp. in the hospital environment in Tahiti Island, French Polynesia.

Four carbapenem-resistant *Acinetobacter* isolates were recovered over a 6-month period from 1 January 2017 to 30 June 2017 in Papeete Hospital, Tahiti Island, during routine screening for MDR bacteria. This screening aims to detect MDR isolates both in clinical samples and in the environment by targeting room sinks performed every week. Among the isolates, one isolate was recovered from a urine sample and the remaining three isolates were recovered in the showers of two hospital rooms (Table 1). Susceptibility testing revealed that all of the isolates were resistant to carbapenems. Isolates R10 and R11 were resistant to all β -lactams, whereas isolates R34 and TUM remained susceptible to ceftazidime. These isolates were positive for detection of carbapenemase activity using the CarbAcineto NP test. Detection of carbapenemase genes was performed by conventional PCR using primers targeting the most common carbapenemases identified in *Acinetobacter* spp. (*bla*_{OXA-23}, *bla*_{OXA-24/-40}, *bla*_{OXA-58} and *bla*_{NDM-1}) as described previously [3]. Isolates R10 and R11 harboured *bla*_{NDM-1}, whereas isolates R34 and TUM harboured *bla*_{OXA-23}. To assess the clonal relationship between the four isolates and to determine the full resistome of the isolates, whole-genome sequencing was performed (Table 1). The isolates were sequenced using Illumina technology as described previously [3]. The sequencing results are

summarised in Supplementary Table S1 in the online version at DOI: [10.1016/j.jgar.2018.11.001](https://doi.org/10.1016/j.jgar.2018.11.001). The genomes were assembled using CLC Genomic Workbench v.10.1 (QIAGEN, Courtabouef, France). Analysis of the genomes revealed that they belonged to the *Acinetobacter calcoaceticus*–*baumannii* complex, however isolates R10, R11 and TUM corresponded to *A. baumannii* whereas isolate R34 actually belonged to *Acinetobacter nosocomialis*. No additional acquired β -lactamases were detected. Only naturally occurring *bla*_{OXA-51-like} and *bla*_{ADC-like} were identified in the *A. baumannii* isolates (Table 1). The resistomes of the isolates (Table 1) were obtained using ResFinder 3.0 (<https://cge.cbs.dtu.dk/services/ResFinder/>). To investigate whether the three *A. baumannii* isolates were clonally related, multilocus sequence typing (MLST) was performed according to the Institut Pasteur MLST scheme [4]. MLST revealed that the isolates were not related, belonging to unrelated sequence types (STs). It should be noted that carbapenem-resistant *A. baumannii* isolate TUM from urine was not related to the previous outbreak in this hospital from 2003–2015 (M. Levy, personal communication). Interestingly, NDM-producing isolate R11 belonged to ST85. This particular clone was responsible for dissemination of the *bla*_{NDM-1} gene in France and recently in North Africa [3,5]. Single nucleotide polymorphism (SNP) analysis performed using CSI Phylogeny (<https://cge.cbs.dtu.dk/services/CSIPhylogeny/>) revealed that isolate R11 was more closely related to French isolates isolated in 2013–2015 than isolates recovered from North Africa (see Supplementary Fig. S1 in the online version at DOI: [10.1016/j.jgar.2018.11.001](https://doi.org/10.1016/j.jgar.2018.11.001)). However, this isolate clearly belonged to the same clone spreading in North Africa and France. Its presence in this healthcare setting is most likely due to frequent exchange of patients with hospitals in France. In addition, it possesses the same resistance phenotype and resistome. Whereas the *bla*_{NDM-1} gene is chromosomally located in isolate R10 and other ST85 and NDM-1-producing isolates, this gene was identified on a plasmid in isolate R11. The *bla*_{NDM-1} gene was carried by a conjugative plasmid identical to pNDM-BJ02 described in China (GenBank accession no. [JQ060896](https://www.ncbi.nlm.nih.gov/nuccore/JQ060896)). In both cases, *bla*_{NDM-1} was associated with one copy of IS*Aba125* upstream of the carbapenemase gene. In isolate TUM, the *bla*_{OXA-23} gene was part of transposon Tn2008. Regarding *A. nosocomialis* R34, the *bla*_{OXA-23} gene was identified on a plasmid previously identified in Portugal with only two SNP differences (GenBank accession no. [MF078634](https://www.ncbi.nlm.nih.gov/nuccore/MF078634)). No IS elements were identified upstream of the naturally occurring cephalosporinase and oxacillinase genes in these isolates.

Here we describe the occurrence of carbapenemase-producing *Acinetobacter* spp. in a hospital of French Polynesia. No genetic link was evidenced between the four isolates since they belonged to different STs and with a different genetic environment bracketing the carbapenemase gene. This is the first report of OXA-23-producing *A. nosocomialis* and NDM-1-producing ST85 *A. baumannii* isolates in a remote island of the South Pacific Ocean. This

Table 1
Features of carbapenemase-producing *Acinetobacter* spp. isolates in Tahiti island.

Isolate	Isolation source	Species	ST	Resistome ^a				MIC (mg/L)		
				β-Lactamase(s) [nucleotide percent identity]	Aminoglycoside resistance	QRDR mutation ^b	Other families	CAZ	IPM	MEM
TUM	Urine	<i>A. baumannii</i>	ST113	<u>bla_{OXA-23}</u> , <u>bla_{OXA-64}</u> , <u>bla_{ADC-25}</u> [97.22%]	None	None	<u>msr(E)</u> , <u>mph(E)</u>	1	32	32
R10	Shower drain room 10, visceral surgery ward	<i>A. baumannii</i>	ST37	<u>bla_{NDM-1}</u> , <u>bla_{OXA-51}</u> , <u>bla_{ADC-25}</u> [97.92%]	<u>aphA6</u> , <u>aadB</u>	None	None	>64	>32	>32
R11	Shower drain room 11, visceral surgery ward	<i>A. baumannii</i>	ST85	<u>bla_{NDM-1}</u> , <u>bla_{OXA-94}</u> , <u>bla_{ADC-25}</u> [95.97%]	<u>aphA6</u> , <u>aadB</u>	GyrA S81L; ParC S84L	<u>msr(E)</u> , <u>mph(E)</u> , <u>floR</u> , <u>sul2</u>	>64	>32	>32
R34	Shower drain room 34, pneumology ward	<i>A. nosocomialis</i>	ST71	<u>bla_{OXA-23}</u>	None	None	None	0.5	32	32

ST, sequence type; QRDR, quinolone resistance-determining region; MIC, minimum inhibitory concentration; CAZ, ceftazidime; IPM, imipenem; MEM, meropenem.

^a Acquired resistance determinants are underlined.

^b *Acinetobacter baumannii* ATCC 19606 (GenBank accession no. CZWC00000000) was used as wild-type strain for QRDR substitution.

widespread clone in North Africa could disseminate in French Polynesia and neighbouring countries, and surveillance is required in New Caledonia, New Zealand and Australia as patients between these countries/islands are frequently transferred.

This Whole Genome Shotgun project has been deposited at DDBJ/ENA/GenBank under the accession nos. QKWD00000000 for *A. nosocomialis* R34, QKWE00000000 for *A. baumannii* R11, QKWF00000000 for *A. baumannii* R10 and QKWG00000000 for *A. baumannii* TUM.

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Competing interests

None declared.

Ethical approval

Not required.

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