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LETTER TO THE EDITOR

PME-1-Producing *Pseudomonas aeruginosa* in Qatar

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The novel extended-spectrum β-lactamase (ESBL) PME-1 was first described in 2010 in an isolate from a *Pseudomonas aeruginosa* strain obtained from multiple clinical specimens from a single patient admitted to the University of Pittsburgh Medical Center in 2008. The patient had had a prolonged period of hospitalization in United Arab Emirates immediately before being transferred to the United States (1). We describe here the first case of *P. aeruginosa* carrying bla_{PME-1} isolated from Qatar and present the second report to date of this enzyme.

The *P. aeruginosa* HZ-QTR-51 isolate was sent to the reference laboratory at The University of Queensland Centre for Clinical Research (UQCCR) as part of a region-wide collaborative study on multidrug-resistant Gram-negative bacilli (2, 3). The Etest was used to measure the MIC of several antimicrobial compounds as listed in Table 1.

The bacterial genomic DNA was extracted using an UltraClean Microbial DNA isolation kit (Mo Bio Laboratories). Species identification was performed using the PAduplex assay as previously described (4). Paired-end libraries of whole genomic DNA of HZ-QTR-51 were prepared via the use of a Nextera XT DNA sample preparation kit and sequenced by the use of an Illumina HiSeq platform (Illumina, San Diego, CA, USA). The 100-bp-paired-end reads were *de novo* assembled using CLC Genomic Workbench with a minimum contig length of 200 bp. A total of 167 contigs were assembled with depth coverage of ca. 100×.

The sequence type (ST) of *P. aeruginosa* HZ-QTR-51 was confirmed as ST 654 by *in silico* multilocus sequence typing (MLST) (https://cge.cbs.dtu.dk/services/MLST/) (5). The ResFinder 2.1 platform (http://cge.cbs.dtu.dk/services/ResFinder/) (6) was also used to characterize acquired antimicrobial resistance mechanism genes among those in the draft genome. The isolate carried bla_{PME-1} as well as bla_{OXA-50}, bla_{GES-5}, and bla_{PAO} contributing to β-lactam resistance and *strA*, *aph(3′)-VIa*, *aph(3′)-IIb*, and *strB* for aminoglycoside resistance. The isolate also carried *fosA* for fosfomycin resistance, *catB7* for chloramphenicol resistance, *sul1* for sulfonamide resistance, and *tet*(A) and *tet*(G) for tetracycline resistance. For further confirmation, bla_{PME}-specific primers were used as previously described (1).

P. aeruginosa HZ-QTR-51 was phenotypically resistant to all tested antibiotics and was on the breakpoint border for amikacin (Table 1). The carbapenem resistance in this isolate might be due to the production of GES-5, which is a carbapenemase (7).

P. aeruginosa ST 654 is noteworthy for several reasons. VIM-2-producing *P. aeruginosa* ST 654 was isolated from a patient in Sweden following hospitalization in Tunisia (8). ST 654 was also associated with KPC-producing *P. aeruginosa* from Argentina (9). More recently, VIM-2-producing *P. aeruginosa* ST 654 was identified among the international "high-risk clones" in the United Kingdom (10). These reports highlight that *P. aeruginosa* ST 654 is an internationally disseminated clone with a multidrug-resistant phenotype, which might facilitate the rapid international spread of PME-1 (and GES-5)-producing *P. aeruginosa*.

TABLE 1 Antimicrobial MICs for PME-1-producing *P. aeruginosa* HZ-QTR-51

Antimicrobial category	Antimicrobial agent	MIC (mg/liter)	EUCAST interpretation[a]
Aminoglycosides	Gentamicin	>256	R
	Amikacin	16	NS
	Netilmicin	>8	R
Antipseudomonal penicillins and β-lactamase inhibitors	Ticarcillin/clavulanate	>256	R
	Piperacillin/tazobactam	>32	R
Carbapenems	Imipenem	>32	R
	Meropenem	>32	R
	Doripenem	>32	R
Extended-spectrum cephalosporins	Ceftazidime	32	R
	Cefepime	16	R
Fluoroquinolones	Ciprofloxacin	>32	R
Monobactams	Aztreonam	128	R

[a] R, resistant; NS, nonsusceptible.

In conclusion, this report presents the first description of PME-1-producing *P. aeruginosa* in Qatar and the second in the world (11). The currently described *P. aeruginosa* isolate belongs to successful international clone ST 654, which might contribute to the global spread of multiple antibiotic resistance mechanisms, including bla_{PME-1} and bla_{GES-5}. We suggest active surveillance for multidrug-resistant *P. aeruginosa* to assess the dissemination and prevalence of beta-lactamase-mediated antibiotic resistance in the Gulf region.

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