Endemicity of *Pseudomonas aeruginosa* Producing IMP-18 and/or VIM-2 Metallo-β-Lactamases from the High-Risk Clone ST111 in Central America

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Objective

Pseudomonas aeruginosa is an important cause of serious nosocomial infections.

Despite the overall genetic diversity of *P. aeruginosa* isolates, highly conserved clonal complexes (CCs) have been observed among multidrug-resistant isolates.

P. aeruginosa that belong to ST235, ST357, and ST111 are common among MDR and metallo-beta-lactamase-producing (MBL) isolates.

We evaluated 5 *P. aeruginosa* isolates from Central America that carried IMP-18 and/or VIM-2 encoding genes from the SENTRY Antimicrobial Surveillance Program.

Methods

Five extensively drug resistant (XDR; CLSI/EUCAST) *P. aeruginosa* isolates collected in 2017-2018 were investigated.

Susceptibility testing was performed by CLSI broth microdilution.

Whole genome sequencing was performed using MiSeq (Illumina) and MinION (Oxford Nanopore).

- Assembled contigs from short and long reads were combined for *in silico* screening of resistance genes, multilocus sequence typing (MLST), core genome (cg)MLST, and SNP analysis using the 1928 Diagnostics platform.
- SENTRY isolates were compared at nucleotide level to a *P. aeruginosa* AG1 (PaeAG1) ST111 strain isolated from a Costa Rican hospital in 2010 which carried $bla_{\text{VIM-2}}$ and $bla_{\text{IMP-18}}$.

Results

The 5 *P. aeruginosa* isolates were recovered from patients with urinary tract infections or pneumonia.

Isolates were resistant to imipenem (MIC >8 mg/L), meropenem (>32 mg/L), ceftolozane-tazobactam (>32 mg/L), tobramycin (>16 mg/L), amikacin (4 of 5; >32 mg/L), and levofloxacin (>16 mg/L) and intermediate to colistin (CLSI; 1-2 mg/L).

When the consensus sequence of each isolate was individually compared against the published sequence of the ST111 isolate PaeAG1 (CP045739.1), between 101 and 1,124 differences were recorded (Table 1).

All isolates belonged to ST111 but carried different combinations of resistance encoding genes, mostly aminoglycoside-modifying, enzyme-encoding genes.

- Transposon-associated MBL genes, *bla*$_{VIM-2}$ and/or *bla*$_{IMP-18}$, were chromosomally located.
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