

First report of Pseudomonas aeruginosa isolates harboring the CTX-M2 and PER genes in Algeria.



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Background

Despite significant improvements in burn care, multidrug-resistant (MDR) Pseudomonas aeruginosa (PA) remains one of the most common causes of life-threatening infections in patients suffering from thermal injuries. The objective of this study is to investigate the prevalence of MDR PA producing Extended-Spectrum Beta-lactamases (ESBLs) and Metallo-Beta-Lactamases (MBLs) in burn patients in Algeria.

Methods

Between April 2016 and October 2019, 47 non-redundant isolates of PA were collected from 47 burn patients admitted to the Department of Burns at the Military Hospital of Algiers in Algeria. Antibiotic susceptibility testing was performed by agar diffusion and the Phoenix automated method. Resistance genes were identified by PCR, and molecular typing of isolates was carried out by enterobacterial repetitive intergenic consensus (ERIC) sequences-polymerase chain reaction (PCR).

Results

Figure 1: Phenotypically ESBL-positive and MBL-positive isolates.

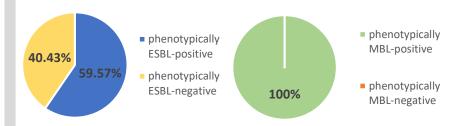


Figure 2: World map with countries where PER- and CTX-M2-postive Pseudomonas aeruginosa isolates have been reported.

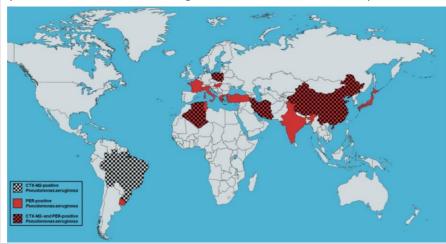


Table 1: Occurrence of beta-lactamase genes in the ESBL-positive isolates in relation to their antimicrobial susceptibility profiles.

Antibiotic Susceptibility Profile (n)	CTX-M-2 alone (n=3)	PER alone (n=1)	TEM alone (n=0)	CTX-M2, PER (no TEM) (n=4)	CTX-M2, TEM (no PER) (n=3)	PER, TEM (no CTX-M2) (n=0)	CTX-M2, PER, TEM (n=13)
AN, GM, CL (n=2)	0	1	0	1	0	0	0
CIP, LVX, CL (n=4)	1	0	0	3	0	0	0
AN, CL	0	0	0	0	0	0	5
(n=5) CL (n=13)	2	0	0	0	3	0	8

AN: Amikacin; GM: Gentamicin; CL: Colistin; CIP: Ciprofloxacin; LVX: Levofloxacin

Conclusions

- First report of CTX-M2-producing PA in the North Africa region.
- First report of CTX-M2- positive and PER-positive PA clinical isolates in Algeria.
- These results demonstrate the spread of these MDR PA strains in this part of the world.
- Identification of genotypic alterations that confer antibiotic resistance is critical in determining effective antimicrobial strategies. Hence, these findings could potentially guide antibiotic choice decisions.