840. First Report of *Pseudomonas aeruginosa* Isolates Harboring the CTX-M2 and PER genes in Algeria.

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Session: P-36. HAI: Gram-negatives (MDR-GNR)

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. Among the 47 non-redundant MDR *PA* strains isolated, 59.57% were phenotypically ESBLs-positive, and 100% were phenotypically MBL-positive. The ESBL-positive isolates were subsequently screened for five groups of *bla* genes encoding ESBL-type enzymes, namely CTX-M2, PER, TEM, SHV, VEB, and GES. Out of the 28 ESBL-producing strains, 23 (82.14%) were CTX-M2 positive; 18 (38.29%) were PER positive, and 16 (34.04%) were TEM positive, while 5 (17.9%) were co-harboring CTX-M2, TEM, and PER genes. The SHV, VEB, and GES genes were not detected in any of the ESBL positive isolates. Since all isolates were MBL-positive, all 47 strains were screened for the NDM-1, IMP, VIM genes that produce MBLs; however, none of these genes were detected. Additional screening for the OprD gene demonstrated that 45 (95.74%) of the isolates were positive for this gene. Finally, ERIC PCR revealed 6 distinct *PA* clones among the CTX-M2 positive strains.

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

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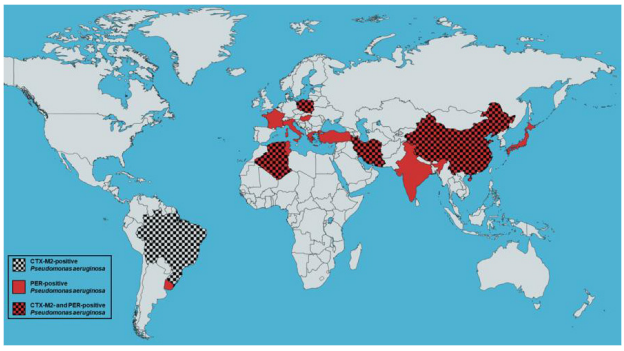
Antibiotic Susceptibility Profile (n)	CTX-M-2 alone (n=3)	PER alone (n=1)	TEM alone (n=0)	CTX-M2, PER (no TEM) (n=4)	CTX-M2, TEM (no PER) (n=3)	PER, TEM (no CTX-M2) (n=0)	CTX-M2, PER, TEM (n=13)
AN, GM, CL (n=2)	0	1	0	1	0	0	0
CIP, LVX, CL (n=4)	1	0	0	3	0	0	0
AN, CL (n=5)	0	0	0	0	0	0	5
CL (n=13)	2	0	0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

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

Conclusion. This is the first report of CTX-M2-producing *PA* in the North Africa region and the first to detect CTX-M2-positive and PER-positive *PA* clinical isolates in Algeria, therefore demonstrating the spread of such MDR 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.

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



Disclosures. **All Authors**: No reported disclosures

841. Frequency of carbapenemase-encoding genes among Imipenem-Resistant Gram-negative Bacilli isolated from Latin America: Is there a Role for Imipenem/Relebactam? Results from SMART 2017-2018

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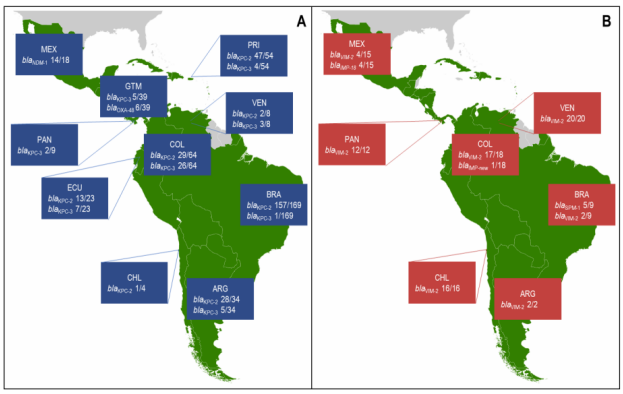
Session: P-36. HAI: Gram-negatives (MDR-GNR)

Background. New beta-lactamase inhibitors in combination with beta-lactams such as imipenem /relebactam (IMI/REL) were recently developed and approved for clinical use to overcome the emergence and spread of carbapenemase-producing Gram-negative bacilli (GNB). We evaluated the frequency of carbapenemase-encoding genes (CEG) among imipenem-resistant GNB isolated from Latin America through the SMART Program (2017-2018), in order to gain insight to the possible therapeutic role of IMI/REL in this region.

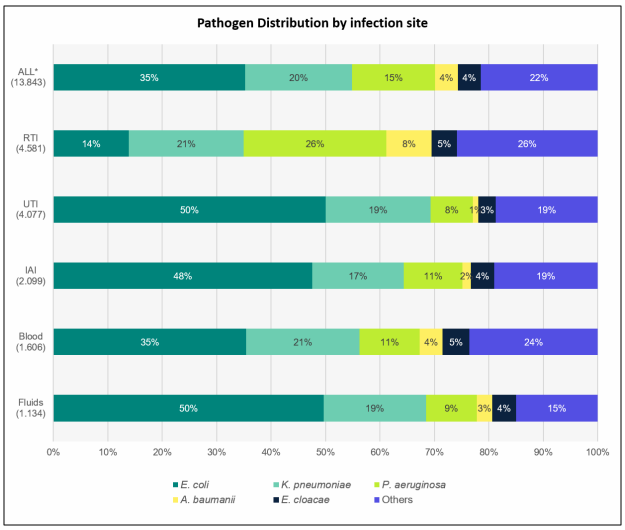
Methods. 13,843 GNB isolates including Enterobacterales (ENT) and *P. aeruginosa* (PSA), were collected consecutively from 10 Latin American countries during 2017-2018. GNB were recovered from patients diagnosed with distinct body site infections including bloodstream and respiratory tract infections. MICs were determined and interpreted according to CLSI broth microdilution recommendations. IMI-resistant isolates were selected for characterization of carbapenemase content by PCR followed by DNA sequencing.

Results. IMI resistance rates for *E. coli* (EC; N= 4,877), *K. pneumoniae* (KPN; N=2,718), *P. aeruginosa* (PSA; 2,108), *Acinetobacter* spp. (N=711), and *E. cloacae* (ECL; N=578) were 1.0%, 17.9%, 31.7%, 71.3% and 6.4%, respectively. These species accounted for 79.4% of all collected isolates. Detection of CEG was carried out in nearly 62.5% of the IMI-resistant ENT and PSA isolates. bla_{KPC-2} was the most common CEG found in IMI-resistant KPN, followed by bla_{KPC-3}, in most LATAM countries (Figure 1). MBL encoding genes were detected in 92/415 (22.2%) IMI-resistant PSA. bla_{VIM-2} was detected in 79.3% of these isolates, followed by IMP variants (20.6%). $bla_{GES-5, -19, -20, and -26}$ were only detected in PSA isolated from Mexico, while bla_{SPM-1} was only observed in five Brazilian PSA. IMI/REL showed excellent activity against EC [$MIC_{50/90}$, 0.12/0.5 µg/mL; 99.6% susceptible (S)], KPN ($MIC_{50/90}$, 0.25/.05 µg/mL; 96.5%, %S), and ECL ($MIC_{50/90}$, 0.25/0.5 µg/mL; 96.7%S).

Most frequent carbapenemase encoding genes detected among IMI-resistant Enterobacterales (Panel A) and P. aeruginosa (Panel B) in Latin American countries



Species distribution by infection site



Conclusion. Important local variations were observed for some CEG variants detected only in specific countries. IMI/REL showed relevant in vitro activity against IMI-resistant ENT and MBL-negative PSA; and seems to be an important option for treatment of infections in LATAM.

Disclosures. **Ana Cristina Gales, Medical Doctor, CRISTALIA** (Consultant)**EUROFARMA** (Consultant)**INFECTOPHARM** (Consultant)**MSD**