

# Cooperation between active efflux and porin alteration is sufficient to confer high-level resistance to meropenem in *Pseudomonas aeruginosa* clinical isolates

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## Introduction & Purpose

Carbapenems are used for treating infections caused by multidrug-resistant Gram-negative bacteria, which may promote the risk of emergence of high-level resistance usually ascribed to carbapenemase expression [1]. Upon screening of a collection of *Pseudomonas aeruginosa* (*Pa*) isolates from patients suffering of cystic fibrosis, MICs  $\geq 64$  mg/L for meropenem were observed in carbapenemase(s) - negative strains.

Our aim was to examine whether activity of efflux pumps, alterations of porins and expression of other  $\beta$ -lactamase(s) than carbapenemase(s) could explain the high-level resistance to meropenem in these strains.

## Methods

Six meropenem resistant (MEM-R) strains isolated from clinically-confirmed cystic fibrosis (CF) cases were compared to seven MEM-R strains collected from patients suffering from hospital-acquired pneumonia (HAP) (Table 1).

Meropenem (MEM) MICs were measured by microdilution in CA-MHB according to CLSI [2] in the absence or presence of the efflux pump inhibitor Phe-Arg- $\beta$ -naphthylamide (PA $\beta$ N; 20 mg/L [no toxicity at this concentration]).

Carbapenemases (VIM, IMP, NDM, OXA-48, KPC), ESBLs blaBEL (BEL-1 to 3), PER (PER-1 to 5, 7), GES (GES-1 to 18), VEB (VEB-1 to 7), CTX-M (1, 2, 9), blaTEM, blaSHV, and blaOXA (1, 2, 9, 10, 18, 20, 23, 24, 30, 58, 198), and AmpC expression was assessed by molecular techniques (PCR) and/or phenotypic tests (double disk for metallo- $\beta$ -lactamases; ESBL NDP and Carba NP tests [3]).

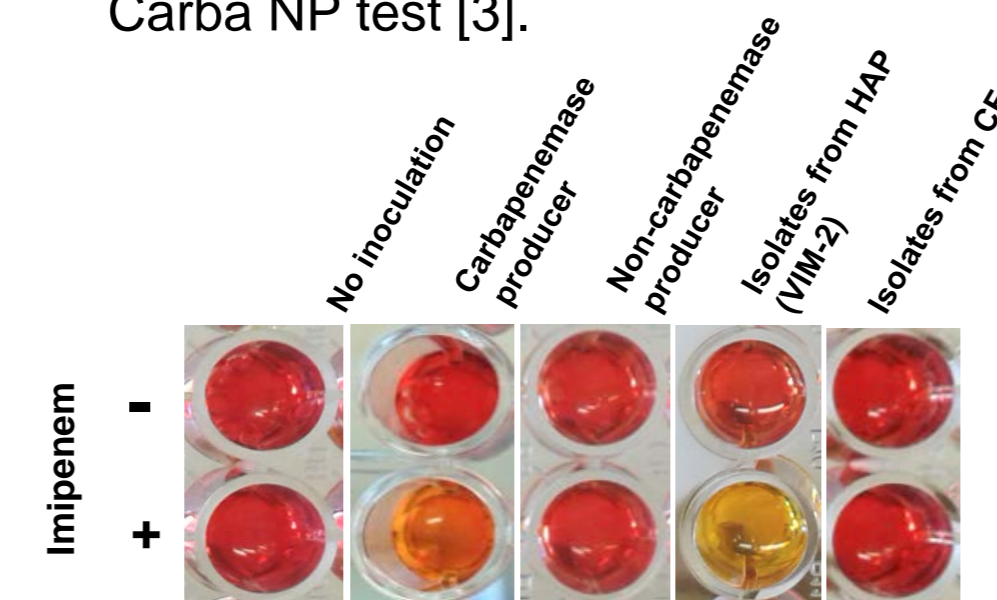
*oprD2* gene and its promoter were sequenced.

*mexA*, *mexX* and *mexC* transcripts were quantified by qPCR.

## References

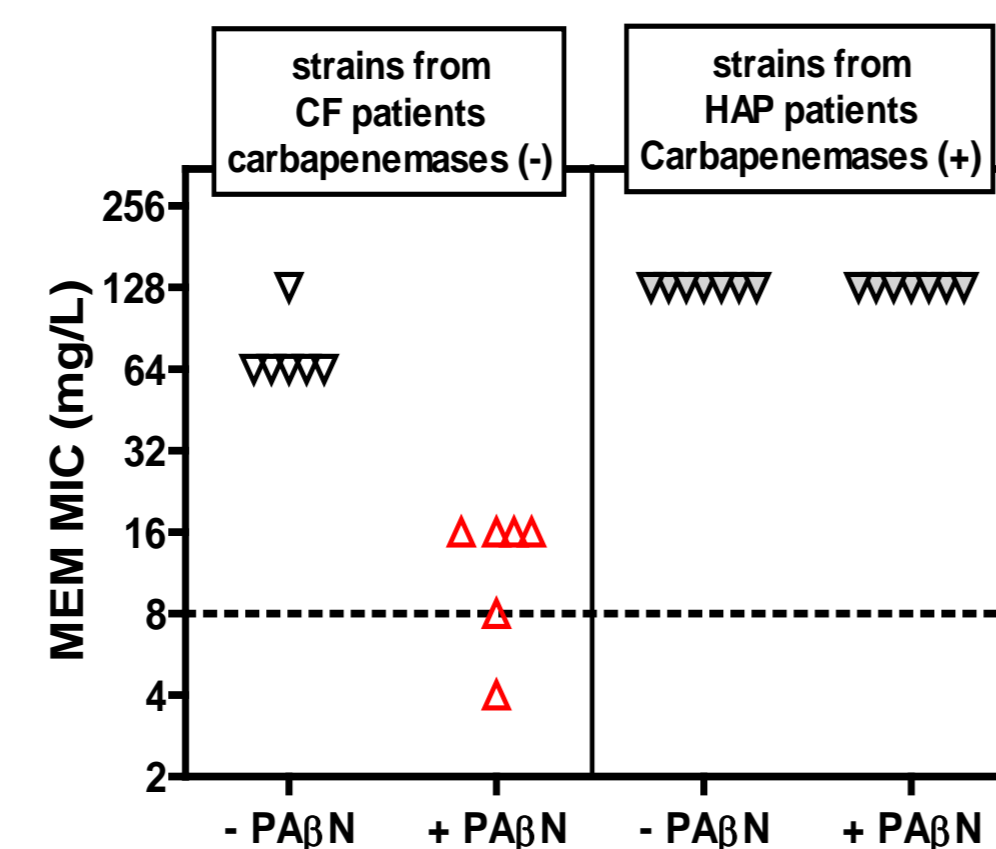
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**Figure 1:** Phenotypic screening of carbapenemases in meropenem-resistant strains using the Carba NP test [3].



Carbapenemase phenotypic detection returned negative results for CF strains but positive results for HAP strains (Fig. 1), with presence of *bla*<sub>VIM-2</sub> [metallo- $\beta$ -lactamase gene] confirmed by PCR.

**Figure 2:** Influence of the efflux inhibitor (PA $\beta$ N) on meropenem MIC in CF vs. HAP strains (the horizontal dotted line shows the current meropenem EUCAST susceptibility breakpoint [4]).



Meropenem MICs were decreased of 2 to 4 log<sub>2</sub> dilutions in the presence of PA $\beta$ N for all CF strains but not for HAP strains (Fig. 2).

## Results

**Table 1:** Molecular characterization of CF and HAP clinical isolates: expression of efflux systems, porin alterations, expression of  $\beta$ -lactamases.

Clinical isolates (with patient's identification code and date of collection)	Expression of genes encoding efflux pumps (relative to PAO1)			OprD2 porin sequencing			$\beta$ -lactamase
	<i>mexA</i>	<i>mexX</i>	<i>mexC</i>	no amino acid (WT=443)	Amino acid changes in protein sequence	Loops affected	
CF (DAF69 - 09/09/10)	2.2	0.8	0.0	117	D43N, S57E, S59R, D118STOP	L1	Deletion of 2 nt (312-313)
CF (DAF69 - 04/10/10)	3.7	1.7	2.3				
CF (DAF69 - 19/10/10)	2.3	1.2	0.2	295	D43N, S57E, S59R, E202Q, I210A, E230K, S240T, N262T, A267S, A281G, K296STOP	L1, L4, L5, L6	-
CF (DAF69 - 26/10/10)	14.3	3.1	2.7				
CF (DAF69 - 09/11/10)	6.9	2.4	1.7	228	D43N, S57E, S59R, change in reading frame $\rightarrow$ 229STOP	L1	Deletion of 1 nt (410)
CF (132 - 08/07/12)	0.3	3.5	0.7				
HAP (DS - 26/12/05)	2.3	1.0	1.0	441	V127L, E185Q, P186G, V189T, E202Q, I210A, E230K, S240T, N262T, T276A, A281G, K296Q, Q301E, R310E, G312R, A315G, L347M, S403A, <b>R412P*</b> (new mutation in L8), Q424E	L2, L3, L4, L5, L6, L7, L8	Shortened loop 7
HAP (DS - 26/01/06)	4.3	2.8	1.4				
HAP (DS - 13/02/06)	6.5	4.3	13.6	276	V127L, E185Q, P186G, V189T, E202Q, I210A, E230K, S240T, N262T, T276A, W277STOP	L2, L3, L4, L5	-
HAP (OG - 08/04/06)	6.4	9.6	5.4				
HAP (OG - 02/05/06)	2.8	1.6	0.9	276	V127L, E185Q, P186G, V189T, E202Q, I210A, E230K, S240T, N262T, T276A, W277STOP	L2, L3, L4, L5	-
HAP (ND - 10/08/06)	3.4	7.5	1.2				
HAP (ND - 11/09/06)	3.7	4.8	1.3				

- All clinical isolates showed an increase in transcription levels of *mexA*, *mexX* and/or *mexC*, and mutations in *oprD2* gene leading to truncated OprD2 porins.
- All CF isolates were derepressed for AmpC cephalosporinases.
- All HAP isolates expressed VIM-2 metallo- $\beta$ -lactamase.

## Conclusions

- Antibiotic exclusion from bacteria by concomitant efflux and reduced uptake is as effective as carbapenemases to confer high level resistance to meropenem in strains expressing AmpC.
- Incomplete restoration of susceptibility upon PA $\beta$ N addition results from the coexistence of OprD2 mutations, AmpC production and/or possibly also incomplete inhibition of MEM efflux by PA $\beta$ N at the concentration used.
- As active efflux can confer cross-resistance to other antipseudomonal agents, i.e. other  $\beta$ -lactams or quinolones for example, determining the mechanism of resistance to meropenem is recommended in clinical settings in order to optimize the antibiotic therapy.

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