Carbapenem-resistant *Pseudomonas aeruginosa* disseminated in Centro Hospitalar do Baixo Vouga, Aveiro, Portugal

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Background

Polyclonal multidrug resistant (MDR) *Pseudomonas aeruginosa* (Pa) are usually associated to nosocomial infections and outbreaks worldwide, leading to high costs and mortality rates. Carbapenem resistance can be acquired through conjugative plasmids by horizontal gene transfer, or due to loss or modification of the OprD porins. Mobile genetic elements contribute to the quick dissemination of antibiotic resistance genes within the hospital environment. Treatment of Pa infections can be limited to colistin.

Aims

Characterization and evaluation of clonality of carbapenem-resistant Pa strains collected over a period of 2 years, from inpatients from different wards in Centro Hospitalar do Baixo Vouga (CHBV).

Conclusions

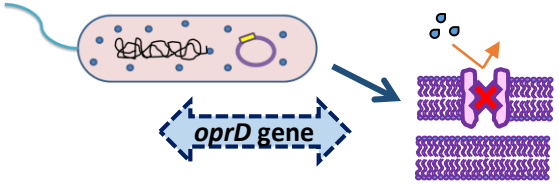
- ✓ Clonality suggests dissemination within the hospital.
- ✓ High percentage of carbapenem resistant Pa was found.
- ✓ Production of carbapenemases was not the only resistance mechanism to carbapenems.
- ✓ Control of Pa dissemination is required to avoid serious hospital outbreaks.

Results / Discussion

Table 1 – Distribution of Pa isolates.

Bacterial Isolates = 58 MDR	
Hospital ward	**Biological samples**
General medicine (40%) Emergency room (21%) Intensive care unit (16%) Urology (15%) Surgery / Orthopaedics (3%) Infectious diseases (2%)	Urine (59%) Sputum (22%) Pus (9%) Blood culture (7%) Catheter (3%)

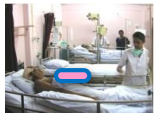
- Prevalence in male (81%) aged between 61-90 (83%).
- The same rep-PCR profile was obtained in isolates from different patients and from different wards.
- Imipenem and meropenem resistance was identified in 95% and 86% of the isolates, respectively
- New arrays were identified in class 1 integrons, some of which containing carbapenemases (OXA-2, VIM-2, GES-13). Other carbapenemases were found (GIM; DIM; SME, IMI).
- IS*CR*1 element and class 2 integrons were not detected.



Mutations observed
T103 → S103
D113 → P113

Fig.2 Schematic representation of mutations detected in oprD porin in the Pa isolates.

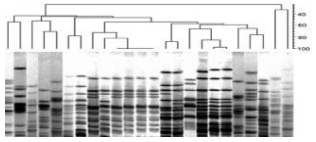
Methods

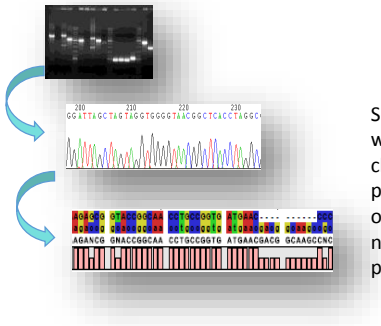


Pa isolated from inpatients biological samples

Antibiotic resistant profile was determined by VITEK2AES System (BioMérieux, Marcy L´Étoile, France), and confirmed by disk diffusion, using *P. aeruginosa* ATCC 27853 as control strain.

Clonal relationship was evaluated by rep-PCR, followed by GelCompar II 5.0 (Applied Maths, Kortrijk, Belgium) analyses.





Screening of integrons and IS*CR*1 element was performed by PCR. Molecular characterization of carbapenemases were performed by multiplex PCR.
oprD genes were amplified and their nucleotide sequences analyzed for the presence of mutations.

Acknowledgements

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