MOLECULAR CHARACTERIZATION OF MULTIDRUG-RESISTANT *PSEUDOMONAS AERUGINOSA* IN THE INTENSIVE CARE UNITS (ICUs) OF A TERTIARY-CARE UNIVERSITY HOSPITAL IN SPAIN

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Background

Pseudomonas aeruginosa is an opportunistic human pathogen responsible for nosocomial outbreaks, especially in Intensive Care Units (ICUs)[1] and among the five most common bacteria in healthcare-associated infections in Europe[2]. In 2015, 32.2% of *P. aeruginosa* isolates exhibited a multidrug-resistant (MDR) phenotype in ICUs in our hospital. Since considerable variation in pathogens and resistance trends exists between institutions, every centre should be familiar with its local trends in order to follow nosocomial pathogen spread and target appropriate empirical therapy.

The aim of this analysis was to describe molecular epidemiology of MDR *P. aeruginosa* in ICUs and know if epidemic or endemic clones were present.

Material/method

Between January to April 2016, the patients entered in ICUs were included in the study if they had at least one clinical or epidemiological specimen positive for MDR *P. aeruginosa*. We don't distinguish between colonization and infection by *P. aeruginosa*.

ICUs include four separate units (polyvalent, traumatology, coronary and cardiac); all patients were hospitalized in separate rooms. Epidemiological data of the patients including the unit and room of hospitalization were retrieved from the hospital information system.

The isolates of all patients were typed using pulsed field gel electrophoresis (PFGE) and the obtained patterns were compared to identify epidemiological links. A Dice coefficient of ≥0.80 was considered suggestive of possible clonal relatedness.

Conclusions

- The prevalence of *P. aeruginosa* in ICUs is 9.8% (76/773) and 3% (23/773) of MDR *P. aeruginosa.*
- MDR *P. aeruginosa* was detected in seven patients (0.9%) at ICU admission.
- Different clusters of MDR *P. aeruginosa* coexist in our ICUs.
- PFGE-type A was the largest clone that probably has a greater ability to spread in ICUs.
- A unique pattern of PFGE may show different resistance phenotypes.

These findings confirm the importance of local molecular epidemiological data for the formulation of specific control measures aiming to limit the unwanted nosocomial transmission.

References

1. Boers SA, Burggrave R, van Westreenen M, Goessens WH, Hays JP. Whole-genome mapping for high-resolution genotyping of Pseudomonas aeruginosa. *J Microbiol Methods*. 2014 Nov;106:19-22.
2. Horcajada JP, et al. Healthcare-associated, community-acquired and hospital-acquired bacteraemic urinary infections in hospitalized patients: a prospective multicentre cohort study in the era of antimicrobial resistance. *Clin Microbiol Infect*. 2013 Oct;19(10):962-8.

Results

During the study period, 773 patients were hospitalized on the ICUs. Seventy-six of them had a *P. aeruginosa*-positive sample. The prevalence was 9.8% (76/773) and 3% (23/773) of MDR *P. aeruginosa*. There were 34 (4.4%) patients with *P. aeruginosa*-positive epidemiological swabs and 7 (0.9%) of them had a MDR phenotype at ICU admission (Table 1).

Table 1. Results of swabs at ICU admission.

Swabs at ICU admission	Patients with positive isolates for PA N	%	Total of patients (773) %
Positive	34	44.73%	4.4%
Negative	42	55.27%	5.4%
Total	76	100%	

PA: *P. aeruginosa*

Thirty-nine isolates from twenty-three patients of *P. aeruginosa* were studied including three susceptible clinical isolates. Five of patients entered in the polyvalent ICU, thirteen in the traumatology ICU and five in the coronary ICU, whereas no patient was in the cardiac ICU (Figure 1). Of the 39, twenty isolates were epidemiological samples.

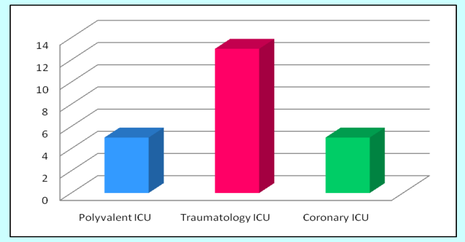

Figure 1. Distribution of the patients with MDR *P. aeruginosa* among the three ICUs.

Using a similarity cut-off of 80%, the 39 isolates produced 10 PFGE-patterns, designated from A to J (Figure 2, 3 and 4). In addition, the results revealed five clonal groups consisting of two or more isolates. Group A was the largest with 21 (53.8%) isolates in 13 (56.5%) patients and were observed in the three ICUs (Figure 5). Group A was also the majority with 6 (85.7%) of the 7 patients with MDR *P. aeruginosa*-positive swab at ICU admission. The remaining 5 unique PFGE-types were categorized as singletons. There were eleven patients with multiple isolates analyzed of which only in one patient multiple types were revealed (Figure 6).

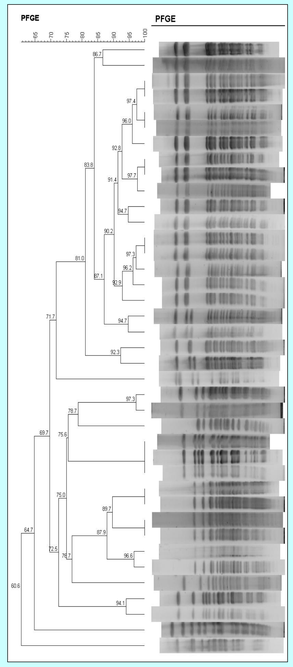

Figure 2. Dendrogram showing the clonal relationship of *P. aeruginosa* isolates, generated from the PFGE profiles.

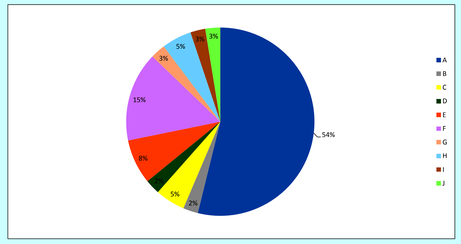

Figure 3. Distribution of the isolates by their PFGE-pattern (A to J).

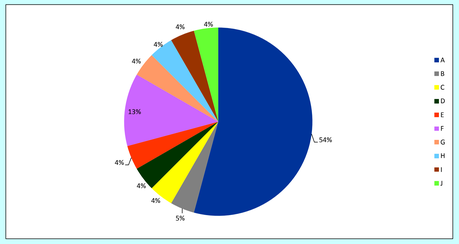

Figure 4. Distribution of the patients according to their PFGE-pattern isolate (A to J).

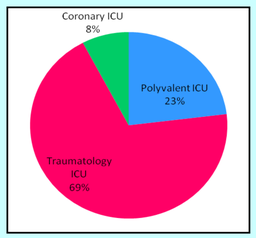

Figure 5. Distribution of patients whose isolate belonged to pattern A by PFGE.

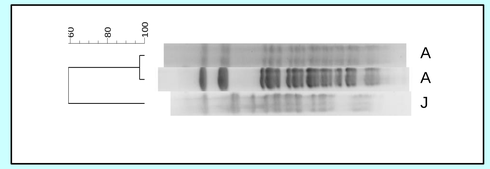

Figure 6. Dendrogram showing two PFGE profiles (A and J) of three isolates obtained of one patient.