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


Background

Pseudomonas aeruginosa is an opportunistic human pathogen responsible for nosocomial outbreaks, especially in Intensive Care Units (ICUs) and among the five most common bacteria in healthcare-associated infections in Europe. 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 clonal 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 pulse field gel electrophoresis (PFGE) and the obtained patterns were compared to identify epidemiological links. A Dce 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


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).

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.

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).

Table 1. Results of swabs at ICU admission

<table>
<thead>
<tr>
<th>Pattern</th>
<th>Positive</th>
<th>Negative</th>
<th>Total of patients (773)</th>
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<tbody>
<tr>
<td></td>
<td>N</td>
<td>%</td>
<td>%</td>
</tr>
<tr>
<td>Positive</td>
<td>34</td>
<td>44.73%</td>
<td>4.4%</td>
</tr>
<tr>
<td>Negative</td>
<td>42</td>
<td>55.27%</td>
<td>5.4%</td>
</tr>
<tr>
<td>Total</td>
<td>76</td>
<td>100%</td>
<td></td>
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</tbody>
</table>

References


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

Figure 2. Distribution of patients whose PFGE pattern belonged to P. aeruginosa isolates, generated from the PFGE profile.

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 isolates belonged to pattern A by PFGE.

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