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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) 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 endemic clones were present.

Material/methods: Between January to April 2016, the patients entered in ICUs were included in the study if they were hospitalized in one of ICUs and had at least one clinical 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.

Results: Seventy-six patients had a *P. aeruginosa*-positive sample at ICUs. Thirty-nine isolates from twenty-three patients including three susceptible clinical isolates of *P. aeruginosa* were studied. 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. Of the 39, twenty isolates were epidemiological samples. Fifteen (65.2%) patients with *P. aeruginosa*-positive sample had a MDR phenotype at ICU admission. Using a similarity cut-off of 80%, the 39 isolates produced 11 PFGE-types, designated from A to K. In addition, the results revealed six clonal groups consisting of two or more isolates. Group H was the largest with 19 (48.7%) isolates and were observed in the three ICUs. Group H was also the majority with 14 (35,9%) isolates in patients with MDR *P. aeruginosa*-positive sample 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.

Conclusions: Sum up, these data confirmed the fact that different clusters of MDR *P. aeruginosa* coexist in our ICUs, and PFGE H is the largest clone that probably has a greater ability to spread in ICUs. We conclude that these findings confirm the importance of local molecular epidemiological data for the formulation of specific control measures aiming to limit unwanted nosocomial transmission.