

**P1127 Persistence of a multidrug-resistant *Pseudomonas aeruginosa* strain in an oncopaediatrics department**

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**Background:** *Pseudomonas aeruginosa* is an opportunistic pathogen commonly associated with nosocomial infections been among the five most common bacteria in healthcare-associated infections in Europe. A multidrug-resistant (MDR) *P. aeruginosa* isolate carbapenemase producer (IMP) that exhibited susceptibility to piperacillin-tazobactam, quinolones and colistine was detected from a bloodstream culture from an oncopediatrics patient in our hospital in 2017. The aim of this study was to investigate the outbreak of this MDR *P. aeruginosa* strain among the oncopediatrics patients since 2013 and carry out the molecular epidemiology.

**Materials/methods:** Clinical, microbiological and epidemiological data from patients entered in oncopediatrics department from January 2013 to October 2017 with a *P. aeruginosa* positive culture were reviewed. At least one isolate of all patients with this MDR *P. aeruginosa* were genotyped using pulsed field gel electrophoresis (PFGE) and the obtained profiles were compared by the software Bionumerics to identify epidemiological links. In addition, three representative isolates were also genotyped by MLST method at the National Reference Centre.

**Results:** Twenty patients have a *P. aeruginosa* positive culture. The MDR/carbapenemase producer phenotype was detected in 8 isolates from 5 patients. Using a similarity cut-off of 80%, the 8 isolates belonged to a single PFGE-cluster. MLST typing analysis of three isolates showed that belonged to ST446. Additionally, this cluster was different from the dominant profile in the adult Intensive Care Units of our hospital. These patients have had short and repeated stays over the years; all of them had overlapped, suggesting the person-to-person transmission. Following the outbreak definition, control measures like screening rectal swabs of all patients, standard precautions or the change of the therapy were taken. Subsequently, no further cases were detected.

**Conclusions:** The data obtained detected one cluster of MDR *P. aeruginosa* that belong to genotype ST446 over the period of observation in the oncopediatrics department. This PFGE-profile was unique for this department. Since the control measures were introduced there have been no further cases of this strain in the department. This study confirms the necessity of constant monitoring with local

molecular epidemiological data for the formulation of specific control measures aiming to limit the spread of clusters.