27th ECCMID Vienna, Austria 22 – 25 April 2017

The congress of ESCMID

Session: EV021 Nosocomial infection surveillance & epidemiology

Category: 8d. Nosocomial infection surveillance & epidemiology

22 April 2017, 08:45 - 15:30
EV0320

Interhospital spread of a multidrug-resistant Acinetobacter baumannii strain: phenotypic and molecular characterization of an outbreak

Juan Manuel Sanchez Calvo*[1], Fatima Galan-Sanchez[2], Eva Torres Martos[1], Lorena Lopez Cerero[3], Felipe Fernández-Cuenca[4], Juan Carlos Alados Arboledas[1], Manuel Rodriguez-Iglesias[2], María Dolores López Prieto[5]

[1]*Ags Norte de Cádiz. Hospital Sas de Jerez; Ugc Infectious Diseases and Microbiology*

[2]*Puerta del Mar Univ Hosp*

[3]*University Hospital Virgen Macarena; Microbiology*

[4]*University Hospital Virgen Macarena; Ugc Intercentros de Enfermedades Infecciosas, Microbiología Y Medicina Preventiva,*

[5]*Ags Norte de Cádiz. Hospital Sas de Jerez*

Background: Outbreaks of multidrug-resistant bacteria are a severe problem of health public. *Acinetobacter baumannii* is an emerging nosocomial pathogen which could colonize and produce nosocomial infections. The aim of this study is to describe the phenotypic and molecular characteristics of a multidrug-resistant *A. baumannii* (MDRAB) outbreak in an Spanish hospital.

Material/methods: We describe a MDRAB outbreak that occurred in an intensive care unit (ICU) at the Hospital SAS Jerez between July and October 2016. Matrix-assisted laser desorption/ionization time-of-flight (MALDI- TOF) mass spectrometry was used to identify the microorganisms. Antimicrobial susceptibility screening was carried out using the Vitex-2 system according to recommendations of EUCAST. The presence of bla_{OXA} genes encoding OXA-type carbapenemases (OXA-23, OXA-24, OXA-51, and OXA-58) was confirmed by multiplex PCR. Initial clonal relatedness among *A. baumannii* isolates from the ICU at Hospital SAS Jerez and two strains previously isolated from other two ICUs from two different hospitals of the same region was determined by repetitive-sequence-based PCR (REP-PCR) and confirmed by pulsed-field gel electrophoresis (PFGE), using the restriction enzyme *ApaI*. In addition, multilocus sequence typing (MLST) was performed on a selected subset of isolates. A series of enhanced strategies were implemented to control the outbreak.

Results: In May 2016, the index patient was interhospital transferred to other ICU for transjugular intrahepatic portosystemic shunt (TIPS) placement during only 24 hours. Outbreak started 2 months after his discharge. A total of 33 MDRAB strains were isolated of 16 patients and 17 environmental samples between May and October 2016. Only 6 patients were considered infected (respiratory infection (n=6) and bacteremia (n=1)). All isolates were resistant to piperacillin/tazobactam, ceftazidime, cefepime, carbapenems, ciprofloxacin, trimethoprim-sulphamethoxazole, and susceptible to colistin and minocycline, and showed variable susceptibility to aminoglycosides. Six patients received intravenous and/or inhaled colistin and one patient, who died, was treated with meropenem. Multiplex PCR for OXA group enzymes yielded a positive result for *bla*OXA-58-like and *bla*OXA-51-like genes. REP-PCR results revealed that all *A. baumannii* strains were genetically related. MLST showed that the strains belonged to ST745. PFGE demonstrated that clinical isolates were highly related (>95%). In fact, *A. baumannii* isolates from the index patient and environmental samples had an identical PFGE fingerprint pattern (96-100% similarity) that an isolate from the ICU where the index patient was admitted and an isolate detected in other nearby hospital one year ago.

Conclusions: All MDRAB strains isolated from the ICU were OXA-58-producers and were assigned to ST745. Interhospital spread was associated with patients transfer. Strict infection control measures are needed to limit the spread of organisms such as *Acinetobacter* among hospitals, as epidemiological studies for a better approach.