presence of blaOXA-23 gene in all isolates. PFGE analysis showed that all the isolates were clonally related (>75% similarity); multiplex-PCR showed that isolates belonged to the sequence type Group 1, related to European clone II. Interestingly, the number of isolates from different settings varied significantly (ranging from 1 to 35) on the basis of infection control measures adopted.

Conclusions: Results showed an intra- and inter-hospital spread in different italian settings of an OXA-23 producing clone of *A. baumannii* and emphasize the ability of such pathogen to become epidemic/endemic acquiring resistance genes in the hospital environment if the diffusion is not promptly limited.

P1301 Clonal diversity of OXA-23 producing *Acinetobacter baumannii* isolates from Rio de Janeiro, Brazil

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Objectives: Multidrug-resistant (MDR) *Acinetobacter baumannii* (Ab) are a leading cause of nosocomial infections in Brazilian hospitals, being OXA-23 producers disseminated in several hospitals.

The aim of this study was to assess the diversity of OXA-23-producing Ab isolates disseminated throughout hospitals in Rio de Janeiro (2006–2007) and to analyse blaOXA-23 carrying genetic structure.

Methods: From a collection of 96 OXA-23 producing Ab recovered in 8 hospitals (January 2006 to September 2007) from Rio de Janeiro, Brazil, isolates representative of different pulsotypes (n = 5) were selected for further characterization. Susceptibility tests and identification by rDNA sequencing were performed. Pulsotypes were determined by PFGE with ApaI. The genomic location of the bla OXA-23 gene was determined by I-CeuI technique and with PCR using specific primers for the composite transposon Tn2006. MLST scheme was conducted according to the Ab MLST database (http://pubmlst.org/abaumannii/). The blaOXA-51 type was identified by PCR and sequencing.

Results: Ab isolates were resistant to several b-lactams, presenting variable susceptibility to amikacin (clones A and E were susceptible), kanamycin and sulfamethoxazole/trimethoprim (clone E was susceptible). In all isolates, the blaOXA-23 gene was inserted in Tn2006 and located on the chromosome. The 5 pulsotypes clustered in 4 different STs that presented 4 new allelic combinations and 2 new gpi alleles. These new allelic profiles were related to other STs found in Latin America, but not related with ST22, already described in several European countries and Korea which is also associated to OXA-23 producers. Genotype A (69% of the OXA-23 producing isolates), the most prevalent and found in seven hospitals, was assigned in the same ST of clone D (1%) both presenting blaOXA-66. Genotypes B (25%) C (4%) and E (1%) presented blaOXA-132, blaOXA-95 and blaOXA-69, respectively.

Conclusions: This is the first study describing the population structure of MDR OXA-23-producing Ab clones in Brazil. Our findings indicate an ongoing spread of blaOXA-23 associate to new and diverse ST of *A. baumannii* in hospitals of Rio de Janeiro. The identification of the blaOXA-66 as the predominant lineage confirms its ability to disseminate and establish in the hospital setting.

P1302 Analysis of carbapenem resistance genes in *Acinetobacter* baumannii isolates from Kuwait hospitals

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Objectives: This study was designed to investigate the molecular epidemiology and genetic basis of the carbapenem resistance in clinical isolates of *Acinetobacter baumannii* obtained from all government hospitals in Kuwait.

Methods: A total of 250 clinical isolates were collected from 8 hospitals. Their susceptibility to 18 antibiotics was determined by E test method. Carbapenems resistant isolates were screened for phenotypic MBL production by disk approximation test (DAT) and MBL E test. Genetic characterization of the resistant mechanisms was performed by PCR. Their clonal relatedness was assessed by PFGE. **Results:** All the isolates were multidrug resistant. Of the 250 isolates, 93 (37.2%) were resistant to carbapenems. The prevalence of MBL-producing isolates was 74.2% and 57% by DAT and MBL Etest, respectively. Sixty-five (69.9%) of the carbapenem-resistant isolates were positive for one or more resistance genes; 37 were positive for blaIMP-1, 17 blaVIM-1, 43 blaVIM2, 24 blaSPM-1, 32 blaOXA-23, 1 blaOXA-24. PFGE demonstrated widespread clones of similar strains in different hospitals and a cluster of 3 clones found only in one particular hospital. **Conclusion:** Resistance clinical isolates to carbapenem has reached unacceptable levels in Kuwait and MBLs, as well as oxacilinases, are highly prevalent among *A. baumannii* in our hospitals.

Acknowledgment: This work was supported by a Kuwait University Research Grant no. YM 01/08 which is gratefully acknowledged.

P1303 Genetic relatedness of *Acinetobacter baumannii* strains isolated from patients in a university hospital in Bialystok, Poland

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Objectives: Acinetobacter baumannii is an opportunistic pathogen that gives rise to nosocomial infections and outbreaks, in particular, in the intensive care unit. The increasing resistance to antibiotics leads to appearing of multi-drug resistant strains. Examining the genetic diversity of randomly chosen *A. baumannii* strains isolated in University Hospital in Bialystok and the examination of sensitivity to antibiotics were a purposes of the study.



Analysis of genetic relatedness of *Acinetobacter baumannii* strains. ICU, intensive care unit; SCH, surgery of the chest; RU, rescue unit; VS, vascular surgery; IC, invasive cardiology; H, haematology; G, gastroenterology; S, surgery; N, neurology.