with a colorimetric substrate (NBT/BCIP). The transfer of resistance was evaluated by conjugation and electroporation using as recipient strain *E. coli* TOP10 the transconjugants and transformants were selected on Bertani Luria plates supplemented with streptomycin (50 mg/mL) and ampicillin (50 mg/mL).
Results: The isolate was resistant to meropenem, aztreonam and ceftriaxone with MIC > 32 mg/mL for each antimicrobial, showed intermediate resistance to imipenem with MIC 8 mg/mL and was sensitive to amikacin, ceftazidime, cefepime, ciprofloxacin, piperacillin/tazobactam, ampicillin/sulbactam, cefoperazone/sulbactam and colistin. PCR gene detection from OXA carbapenems gene suggested presence from gene blaOXA-51-like and blaOXA-24-like, and the sequencing amplification products confirmed the presence from OXA-72 carbapenemase in the isolate. In studies of location of the genomic DNA only hybridized with probe for the 16S rRNA gene, while the plasmid DNA gave three hybridization signals with the blaOXA24 probe, demonstrating that the OXA-72 gene is on plasmid. Attempts to transfer resistance by conjugation or transformation of plasmid DNA were unsuccessful.
Conclusions: In isolation analyzed the results suggest that blaOXA-72 gene is located on plasmid, however it is not possible to establish if in multiple plasmids or a plasmid present in different forms.

P792 Frequent occurrence of genomic resistance islands among *Acinetobacter* spp.

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Objectives: Genomic islands have been recently identified in *Acinetobacter baumannii* (AbaR) from diverse isolates being either multidrug resistant or not. In *A. baumannii* strain AYE, the AbaR1 island was 86-kb in size, and harbored 45 resistance genes. Whole genome sequencing of a couple of *A. baumannii* strains from diverse geographical origins and distinct clonal lineages identified other AbaR elements, varying in size and content. Analysis of the AbaR surrounding sequences identified an hotspot for integration, corresponding to the ATPase encoding gene. AbaR elements are often bracketed by 5-bp duplications suggesting their acquisition through a transposition-based event. Our objective was to evaluate the distribution of AbaR-like islands among a collection of *A. baumannii* isolates from worldwide origin, to identify their content and their integration site. Additionally, transposition experiments were attempted to evaluate the mobility of one AbaR element.
Methods: Forty-seven clinical *Acinetobacter* spp. isolates were collected from worldwide origin, including 41 *A. baumannii*, 3 *A. junii,* 2 *A. johnsonii,* and 1 *A. lwoffii.* Detection of the AbaR elements was performed by PCR mapping followed by sequence analysis. Transposition/conjugation assays have been conducted with *A. baumannii* BM4547 (Rif-R) as recipient and *A. baumannii* B1190 possessing an AbaR10 element and harbouring a conjugative plasmid used as donor.
Results: Our collection consisted of strains belonging to the three different European clonal lineages (I, II, and III). 36 out of the 47 isolates possessed a truncated ATPase gene, being all *A. baumannii*. 30 out of those 36 isolates possessed the same ATPase-AbaR left-junction than that originally identified with AbaRI, and 28 possessed the same ATPase-AbaR right-junction. PCR mapping revealed that all the AbaR elements identified were heterogeneous in size and genetic content. Attempts to demonstrate the transposition of one AbaR from its original host failed. Attemps to demonstrate a circular form of those AbaR elements using an inverse-PCR approach did not identify any circular intermediate for all these structures.
Conclusion: This study showed that dissemination of AbaR elements among *A. baumannii* is widely spread, being identified among isolates from distinct clonal lineages. The variety of those AbaR elements suggests a capacity to evoluate and accumulate foreign genes, including resistance genes.

P793 A 63-kb genomic resistance island in an *Acinetobacter baumannii* isolate from 1977

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Objective: Multidrug resistance in *Acinetobacter baumannii* has been significantly associated with a few international clonal lineages. Multidrug-resistant (MDR) strains of two of these lineages (EU clones I and II) have occurred in European hospitals since at least the 1980s. Three large (86 kb, 63 kb and 56 kb), stucturally related genomic resistance islands (AbaR1, AbaR3 and AbaR5, respectively) integrated into the ATPase gene were recently found in EU clone I strains isolated between 1997 and 2004. The aim of this study was to assess whether a MDR outbreak strain of EU clone I isolated in 1977 harbours an AbaR-like resistance island.
Methods: Strain HK302 was isolated during a hospital outbreak in Switzerland in 1977 (Antimicrob Agents Chemother 1982; 22: 323) and later was allocated to EU clone I. Strain AYE harbouring AbaR1 was used as a positive control for the detection of AbaR1-associated genes and PCR mapping. Disruption of the ATPase gene was determined using PCR with primers derived from both ends of the gene. The presence of 29 AbaR1-associated genes was investigated by PCR using primers inferred from the sequence of AbaR1. PCR mapping using the Long Range PCR kit (Qiagen) was performed, followed by RFLP analysis of amplicons. The regions different from those of AbaR1 were sequenced.
Results: A genomic region inserted into the ATPase gene at the same position as known for AbaR1 was found in HK302. In addition, 18 AbaR1-associated genes were identified in this strain. PCR mapping combined with RFLP analysis revealed that HK302 harboured a 63-kb resistance island which shared regions of a total size of 57 kb with AbaR1. Two segments (sized 4 kb and 2 kb) different from those of AbaR1 were sequenced and found to correspond to the regions described in AbaR3, i.e. one comprising the topoisomerase topA gene and the other a transposon carrying blaTEM-1.
Conclusion: An AbaR3-like resistance island was identified in HK302, which indicates that highly complex resistance islands existed in EU clone I strains already in the late 1970s.
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P794 Multidrug resistance phenotype associated with presence of integrons and specific clonal types of *Acinetobacter* spp.

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Objective: The main objective of this study was to determinate the presence of class 1, 2 and 3 integrons in *Acinetobacter* spp. and the association of these elements with multidrug resistance phenotype and with clonal profile of the strains.
Methods: Firstly, 63 *Acinetobacter* spp., isolated from inpatients of University Hospital of Juiz de Fora, Minas Gerais State, Brazil, from 2006 to 2007, were classified as multidrug resistant (MDR) or non-multidrug resistant (n-MDR). Class 1, 2 and 3 integrons were investigated by specific PCR amplification of intI1, 2 and 3 genes fragments and by RFLP obtained by RsaI and HinfI digestion of intI1, 2 and 3 fragments, amplified with consensus primers. The prevalence of integrons were compared among MDR and n-MDR groups, and statistical significance was estimated applying Fisher's exact. PFGE was performed and types were defined by clusters formed at 85% Dice similarity cutoff on a dendrogram constructed by UPGMA.
Results: 48 (76.1%) out of 63 *Acinetobacter* spp. were considered MDR isolates. Class 1 integrons were detected in 11 (17.5%) *Acinetobacter* spp. isolates, by specific PCR and by RFLP, all of them were MDR. Class 2 integrons were found in 30 (47.6%) *Acinetobacter* spp. isolates, by RFLP and, in 23 of them, by specific PCR. 96.7% (29) of these isolates were MDR. Class 1 and 2 integrons relationship with MDR *Acinetobacter* spp. isolates was statistically significant. No class 3 integrons was found. PFGE analysis revealed