ICAAC 2014
54th Interscience Conference on Antimicrobial Agents and Chemotherapy
September 5 -9, 2014 | Washington, DC

Genetic diversity of clinical KPC-producing *Escherichia coli* from Argentina

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BACKGROUND: The global predominance of KPC has been associated to *Klebsiella pneumoniae* clonal type ST258 and increasingly among other *Enterobacteriaceae* and non-fermenters. The aim of this study was to analyze the ongoing situation of KPC-producing *E. coli* in Argentina.
METHODS: 20 non-duplicate nosocomial KPC-producing *E. coli* isolates were referred to the National Reference Laboratory from hospitals across Argentina between June 2008 to March 2013 for resistance and molecular characterization. The patients' clinical records were revised. The antibiotic susceptibility was studied by the disc diffusion method (CLSI 2013), the genetic relationship by *Xba*-I PFGE, the presence of other resistance determinants, KPC allele and genetic environment of bla_{KPC} by PCR and sequencing.
RESULTS: The isolates were recovered from 19 hospitals, 5 provinces and Bs. As. City. 42% were colonization samples, 19% urine, 14% abdominal drainage and 25% recovered from other sites. All isolates were not genetically related and harbored bla_{KPC-2} as the only allele. Three different genetic environments of bla_{KPC-2} were detected: 11/20 harbored tn*4401a* of which two isolates were PER-2 and CTX-M2 producers; 5/20 *ISKpn8*-bla_{KPC-2}-*ISKpn-6-like* and *4/20 ISKpn*8-Δbla_{TEM}-bla_{KPC-2}-*ISKpn*-6-like. The isolates harboring tn*4401a* were all in the resistant category for carbapenems and cephalosporins unlike the other isolates that fitted within the resistant and intermediate categories for the same antibiotics. All isolates remained susceptible to nitrofurantoin, minocycline, tigecycline, fosfomycin and colistin.
CONCLUSIONS: Our results indicate that the occurrence of KPC-producing *E. coli* in Argentina is associated with diverse genetic contexts but is still infrequent and not genetically related