Category (Complete): C2
Keyword (Complete): KPC; carbapenemase; *Enterobacteriaceae*

Diverse Genetic Background and clones of KPC Producing *Enterobacteriaceae*. First Detection of ST258 in South America.

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Background: KPC-producing *Enterobacteriaceae* (ETB) is an increasing therapeutic and infection control problem in the health care setting. KPC surveillance has been performed prospectively by WAN (70 hospitals) after the first occurrence of KPC in 2006.
Objective: To characterize KPC-producing ETB from Argentina.
Methods: From 2006-2009, all ETB clinical isolates with imipenem (IMP) inhibition zone ≤21 mm and synergism with boronic acid were submitted to the INEI. PCR and sequencing were used to detect the bla_{KPC} variant and the surrounding genetic structure. PFGE (n=28) and multilocus sequence typing (MLST) were done to stablish the genetic relatedness.
Results: Specific amplification for bla_{KPC} was obtained in 30 strains, isolated from Buenos Aires metropolitan area (BA) (10 hosp) and Neuquén (1 hosp) and Mendoza (1 hosp) provinces. Strains were as follows (n): *K. pneumoniae-Kpn* (22), *C.r freundii-Cfr-* (3), *E. cloacae-Ecl-* (3), *S. marcescens* (1), *E. coli* (1). Co-production of ESBL was detected in one *Cfr* (PER-2) and one *Ecl* (CTX-M). IMP MICs ranged from 2-64 μg/ml. Two distinctive groups were discrimintated based on the genetic platform: (i) 16 Kpn isolates from BA belonged to the same PFGE clonal type and to the ST258, and contained bla_{KPC-2} in Tn4401a; (ii) 14 ETB contained bla_{KPC-2} flanked by *ISKpn8*-Δbla_{TEM-1} and *ISKpn6-like.* Within group (ii), 3 Kpn from Mendoza were clonally indistinguishable and no genetic relationship was found between remaining isolates of the same specie (3 Kpn, 3 *Cfr*, 3 *Ecl).*
Conclusions: Rapid dissemination of bla_{KPC-2} in Argentina is caused by the clonal spread of Kpn-ST258 carrying Tn4401a and the horizontal interspecie dissemination platform (ii). This is the first report of the dissemination of ST258 in South America.