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Molecular Characterization of Enterobacteria from Argentina Producing blaKPC-2 Non-associated to Tn4401.

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Background: The surge of *Klebsiella pneumoniae* Carbapenemase (KPC) producers in Argentina was leaded by *K. pneumoniae* (KPN) ST258 harboring *bla*KPC-2 in Tn*4401a*. However, sporadic isolates of diverse enterobacterial (ETB) species (non-clonal relation among isolates of the same specie) without *bla*KPC-2 in Tn*4401a* were found in different regions.
Aim: to characterize *bla*KPC-2 strains non-associated to Tn*4401*.
Methods: We studied 16 *bla*KPC-2 clinical isolates: 6 KPN, 5 *Enterobacter cloacae*, 3 *Citrobacter freundii*, 1 *Serratia marcescens*, 1 *Escherichia coli*. MLST was done according to the MLST Database. PCR mapping, sequencing, southern blot (*bla*KPC probe) and conjugation were done by standard procedures. Plasmid content analysis was performed by phenol-chloroform extraction and PCR-based replicon typing (RepT) as reported by Carattoli et al.
Results: KPN *bla*KPC-2 belonged to 3 STs (n): ST11 (4); ST476 (1) ST526 (1).The new environment named Variants 1a/b, was found for *bla*KPC-2 in all isolates: flanked by Tn*801-like* element (upstream) and *IS*Kpn6-like (downstream). The *bla*TEM-1 of Tn*801-like* was 5'-deleted by *IS*Kpn8 and its tnpA was disrupted by a composite transposon found in the plasmid pFBAOT6 of *Aeromonas punctata*. Plasmid sizes ranged between 7-80 kb and some strains had more than 1 plasmid. The *bla*KPC probe hybridized with plasmids of different sizes. A single Inc group was detected in 11/16 isolates (n): IncHI2 (3), IncL/M (3), IncA/C (5). 3 Inc groups were found in 2 strains [E. coli, IncFIA-IncFIB-IncFrepB; KPN ST11, IncL/M-IncA/C-IncFIIS] and 3 strains were negative for all Inc groups. RepT allowed us to associate *bla*KPC-2 with IncL/M transferable plasmids in 2/3 transconjugants while the 3rd one was negative for all the Inc groups tested as the parental strain.
Conclusions: Our results suggest that not only conjugation but also *bla*KPC-2 mobilization among different plasmids could have had a major role in the Argentinean KPC emergence, leading to the dissemination of Variants 1a/b in diverse clones and ETB species.