

P1446 Clonal diversity and detection of clonal complex 10 and 131 in carbapenemase-producing extraintestinal *Escherichia coli* from Argentina

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Background: The spread of extraintestinal *Escherichia coli* (ExPEC) was due to multiresistant clonal complex (CC)131 also disseminating KPC and NDM. Recently, the CC10 was recognized as a reservoir of *mcr-1*. Previously, we detected in Argentina 5 of 29 KPC producing ExPEC without epidemiological links belonging to ST131. Here, we aimed to characterize carbapenemase-producing ExPEC from Argentina.

Materials/methods: Between July 2008 and March 2017, 160 carbapenemase-producing ExPEC were referred to the Argentinean reference laboratory. 64 ExPEC from 41 institutions and 10 cities were selected for genome sequencing. Isolates were confirmed as KPC-2 (n=45), NDM-1 (n=16), IMP-8 (n=2) and VIM-2 (n=1) producers. XbaI-PFGE was performed. DNA was extracted with Qiagen Large-Construct kit (Qiagen) and sequenced using Illumina's HiSeq2000. Paired-end reads were assembled using Velvet-v2.2.5 and annotated with Prokka-v1.12. A pan-genome was created using Roary and core-genome alignment was generated. SNP-sites were used to identify the variable zones and a ML-tree was built with 100 bootstraps using RAxML. MLST, resistance and virulence genes were analyzed in Center for Genomic Epidemiology (<https://cge.cbs.dtu.dk/services/>). The serotypes were confirmed by serology.

Results: The 64 genomes were differentiated into 64 pulsotypes and 36 sequence types. The CC10 was identified in 5 cities and represented 24% (14/59) of the ExPECs (ST10, n=8, ST617, n=1, ST167, n=1, ST44, n=1; ST744, n=3). They were KPC producers (n = 8), NDM (n = 4), NDM-*mcr-1* (n=1), and IMP (n=1) and expressed diverse serotypes. The CC131 (ST131) identified in 6 cities, represented 13.5% (8/59). They were KPC producers (n = 7) (4 co-producers of *bla*_{CTXM}) or VIM (n = 1). In 5 ST131, O25:H4 was confirmed by serology and the major virulence genes detected (6/8) were *sat* (secreted autotransporter toxin) and *iss* (serum survival gene). The phylogenetic tree confirmed the great clonal diversity observed by PFGE and MLST results where CC10 and CC131 clustered each in separate branches of the tree.

Conclusions: We observed great clonal diversity among carbapenemase-producing ExPEC from Argentina being KPC the most abundant carbapenemase detected. However, hyperepidemic CC10 and CC131 are circulating and spreading carbapenemases in different geographical regions of the country.

