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P1614 Diversity of genetic platforms in plasmids carrying the *bla*PER-2 gene in *Enterobacteriaceae* from Argentina

Melina Ruggiero[1], Florencia Brunetti[1], Marianlaura Dabos[2], José Di Conza[1], Pablo Power[1], Gabriel Gutkind*[1], Thierry Naas[2]

[1] Facultad de Farmacia y Bioquímica, Universidad de Buenos Aires, Buenos Aires, Argentina, [2] Service de Bactériologie - Hygiène, Université Paris Sud, Hôpital de Bicêtre, Le Kremlin-Bicêtre, France

Background: PER-2 has been the second most prevalent BLEE in *Enterobacteriaceae* in Argentina, responsible for 5-10% of oxyimino-cephalosporins resistance in *Klebsiella pneumoniae* and *Escherichia coli*. Recently, we reported the complete sequence of an IncA/C1 plasmid carrying *bla*PER-2, being the first study on genetic platforms carrying this gene. To clarify the low dissemination and evaluate the diversity of genetic platforms associated with blaPER-2 gene, plasmids from 12 enterobacteria isolates recovered from hospitalized patients in Buenos Aires and Santa Fe cities between 1997-2012 were sequenced and the *bla*PER-2 genetic environment compared.

Materials/methods: Plasmid DNA form each strain were transformed into *E. coli* TOP10 and the whole DNA sequenced by Illumina MiSeq. Reads' assembly was carried out by SPAdes with previous chromosomal DNA reads filtering against a reference genome. Gaps were closed by PCRs, annotations were made by RAST, detection of antibiotic resistance genes by ResFinder, determination of plasmid incompatibility groups by PlasmidFinder and genetic comparisons by MAUVE.

Results: *bla*PER-2 gene was encoded in a variety of plasmids of different incompatibility groups: IncN2 (4), IncA/C1 (1), IncA/C2 (2), IncA/C2-like (2) IncFIB(Mar)/HI1B (3). Other β-lactam antibiotic resistance genes detected in the plasmid set were: *bla*TEM-1, *bla*CTX-M-2, *bla*OXA-2, *bla*OXA-9 and *bla*SCO-1. The previously reported "IS*Pa*12-like/*bla*PER-2/*gst*-like/*abct*" structure was observed in all cases, associated either with the complete or partial IS. Flanking the immediate environment of this structure, the presence of one or two copies of the IS*Kox2*-like was evidenced. In several plasmids these larger structures were found next to a class 1 integron.

Conclusions: *bla*PER-2 gene can be associated with different plasmid incompatibility groups, either those frequently detected in *Enterobacteriaceae* (IncA/C2) or those that do not have a high prevalence (IncA/C1). These plasmids probably belong to lineages which are not so efficient for transmission or have not yet been transferred to successful clones for dissemination. Even so, their persistence over time indicates at least that they can be selected by antibiotic pressure and persist. In all cases, *bla*PER-2 is related to ISK*ox2*-like, suggesting that this IS would be responsible for its recruitment from the source of origin and the dissemination between different types of plasmids.