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Prevalence of Plasmid-Mediated Quinolone Resistance (PMQR) Genes in Clinical Isolates of *Escherichia coli*, *Shigella* spp. and *Salmonella* spp. from Argentina

E. Albornoz, C. Lucero, G. Romero, M. Rapoport, WHONET-Argentina Group, M. Galas, A. Corso, **A. Petroni**;
Serv Antimicrobianos, INEI-ANLIS Malbran, Bs As, ARGENTINA.

Background: we previously found a 19% overall prevalence of PMQR genes in *Klebsiella* spp, *Enterobacter* spp, *Citrobacter* spp and *Serratia* spp. Here we analyzed their prevalence in other enterobacteria commonly associated with community-acquired infections. **Methods:** We studied 748 isolates of *E. coli* (Eco, 673), *Shigella* spp (Shi, 66) and *Salmonella* spp (Sal, 9), consecutively collected over a 5-day period (2007) in 66 hospitals of WHONET-Argentina [Buenos Aires City (BAC) and all the 23 Provinces]. For the Eco subset, a representative sample of 98 isolates was analyzed [45 of 176 strains with resistance or decreased quinolone susceptibility (DQS) and 53 of 497 with full quinolone susceptibility were selected at random]. Antibiotic susceptibility tests were done under CLSI guidelines. Phenotypic detection of extended spectrum β-lactamases (ESBL) was done by disk diffusion test of the synergy between cefotaxime/ceftazidime and clavulanic acid. Detection of PMQR genes was done by PCR (*qnrA, -B, -C, -D, -S*; the genes found were sequenced), dot blot (*qepA*) or allele-specific PCR [*aac(6´)-Ib-cr*]. **Results:** 9 Eco isolates had unique PMQR genes: 2 *qnrB19*, 1 *qnrS1* and 6 *aac(6´)-Ib-cr*. The 9 isolates were from 8 hospitals (BAC and 6 provinces) and showed high resistance (MIC ranges, µg/ml) to nalidixic acid (NAL >128), ciprofloxacin (CIP 4->32) and levofloxacin (LVX 4->64). Therefore, the PMQR prevalence in Eco, calculated over the total sample of 673 isolates, was 5.2% [1.7% *qnr* genes, 3.5% *aac(6´)-Ib-cr*]. One of the 9 Sal isolates (11%) had *qnrB19* and showed DQS [MICs were (µg/ml): NAL 16, CIP 0.25 and LVX 1]. No PMQR genes were found in Shi. *aac(6´)-Ib-cr* was significantly associated with an ESBL phenotype (4/6, $p<0.001$, Fisher's Test). The 3 *qnrB19* genes were only found in ESBL negative isolates, located in the 2.7-kb plasmid pPAB19-1 previously described. **Conclusions:** This is the first study on PMQR prevalence in Eco, Sal and Shi from Argentina. Compared to the Sal isolate with *qnrB19*, all the PMQR-harboring Eco strains showed a phenotype compatible with the additional presence of mutations in topoisomerase II-enconding genes. The specific location of *qnrB19* was in agreement with the notion of its natural reservoir proposed for pPAB19-1.