

# Prevalence of Plasmid-Mediated Quinolone Resistance Genes in Clinical Enterobacteria from Argentina

Ezequiel Alborno<sup>1</sup>, Celeste Lucero<sup>1</sup>, Genara Romero<sup>1</sup>, María Paula Quiroga<sup>2</sup>, Melina Rapoport<sup>1</sup>,  
Leonor Guerriero<sup>1</sup>, Patricia Andres<sup>1</sup>, Cecilia Rodriguez<sup>2</sup>, WHONET-Argentina Group,<sup>\*</sup>  
Marcelo Galas<sup>3</sup>, Daniela Centrón<sup>2</sup>, Alejandra Corso<sup>1</sup>, and Alejandro Petroni<sup>1</sup>

This first nationwide study was conducted to analyze the prevalence of plasmid-mediated quinolone resistance (PMQR) genes in phenotypically unselected (consecutive) clinical enterobacteria. We studied 1,058 isolates that had been consecutively collected in 66 hospitals of the WHONET-Argentina Resistance Surveillance Network. Overall, 26% of isolates were nonsusceptible to at least one of the three quinolones tested (nalidixic acid, ciprofloxacin, and levofloxacin). The overall prevalence of PMQR genes was 8.1% (4.6% for *aac(6′)-Ib-cr*; 3.9% for *qnr* genes; and 0.4% for *oqxA* and *oqxB*, which were not previously reported in enterobacteria other than *Klebsiella* spp. from Argentina). The PMQR prevalence was highly variable among the enterobacterial species or when the different genes were considered. The prevalent PMQR genes were located in class 1 integrons [*qnrB2*, *qnrB10*, and *aac(6′)-Ib-cr*]; in the ColE1-type plasmid pPAB19-1 or Tn2012-like transposons (*qnrB19*); and in Tn6238 or bracketed by IS26 and *bla<sub>OXA-1</sub>* [*aac(6′)-Ib-cr*]. The mutations associated with quinolone resistance that were located in the quinolone resistance-determining region (QRDR mutations) of *gyrA*, *parC*, and *gyrB* were also investigated. The occurrence of QRDR mutations was significantly associated with the presence of PMQR genes: At least one QRDR mutation was present in 82% of the PMQR-harboring isolates but in only 23% of those without PMQR genes ( $p < 0.0001$ , Fisher's Test). To the best of our knowledge, this is the first report on the prevalence of PMQR genes in consecutive clinical enterobacteria where all the genes currently known have been screened.

---