qnr are plasmid-mediated quinolone resistance (PMQR) genes, which encoding proteins act by protecting the target enzymes from fluoroquinolones action, moderately reducing the susceptibility to this class of antimicrobials. In a previous study, we identified 22 isolates carrying qnrVC gene family among 111 gram-negative carbapenemase-producing bacteria isolated from coastal waters of beaches located in Rio de Janeiro city. qnrVC was detected in Enterobacter spp. (17), Klebsiella pneumoniae (3) and Pseudomonas spp (2). Such dissemination of qnrVC in different bacterial genera in the same environment is unprecedented in the scientific literature. Thus, this project aims to study the diversity and genetic background of qnrVC detected in isolates recovered from Rio de Janeiro coastal waters. For this purpose, qnrVC variants were identified by PCR and sequencing. Representatives of the bacterial collection diversity were recognized by PFGE typing. Representatives of clonal profiles were submitted to complementary characterization, including potential of gene spreading by conjugation, and PCR for identification of plasmid incompatibility groups (Inc), co-transference of carbapenemase encoding genes, and presence of class 1 integron. Besides that, 3 Enterobacter spp. were submitted to whole genome sequence (WGS). qnrVC1 was detected in 18 samples (15 Enterobacter spp. and 3 K. pneumoniae), qnrVC4 in 2 Enterobacter spp. and qnrVC6 in both Pseudomonas spp. PFGE revealed 12 clonal profiles of Enterobacter spp. and one of K. pneumoniae. Transconjugants were obtained from 5 Enterobacter spp., in which qnrVC was transferred along with blaKPC, but not from K. pneumoniae and Pseudomonas spp. Of 29 Inc groups researched, five were identified on Enterobacter spp. donor and transconjugant strains (F, FIA, FIIA, ColRNA e U); six on K. pneumoniae (F, FIA, FIIA, L/M, K and ColRNA) and six on Pseudomonas spp. (F, FIB, FIIA, Q1, Q2, and R). intI1 was detected in both Pseudomonas spp., suggesting the presence of class 1 integron in these samples. WGS analysis evidenced different genetic contexts surrounding qnrVC genes compared to those previously described, and on isolate 221 qnrVC and blaKPC were detected on the same contig. Results indicate that the Enterobacter genus carries and may disseminate qnrVC and blaKPC in aquatic environment. Also, our data suggest that these genes are located in plasmids, inserted in new not conserved genetic contexts.

Keywords: qnrVC, carbapenemases, Enterobacter, coastal water, genetic context

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