

TITLE: *qnrVC* IS CARRIED BY DIFFERENT MOBILE GENETIC ELEMENTS IN CARBAPENEMASE-PRODUCING GRAM-NEGATIVE BACILLI ISOLATED FROM AQUATIC MATRICES

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ABSTRACT: Qnr proteins reduce bacterial susceptibility to quinolones. Unlike other widespread *qnr* families, *qnrVC* has been reported mainly in *Vibrio* spp. In a previous study, 22 *qnrVC*-carrying strains belonging to *Enterobacter* (17), *Klebsiella* (3), or *Pseudomonas* (2) were identified among 111 gram-negative carbapenemase-producing bacteria (*bla*_{KPC-2} in *Enterobacteriales* and *bla*_{VIM-2} in *Pseudomonas*) isolated from coastal water samples in the city of Rio de Janeiro. This study aimed to characterize the *qnrVC*-carrying isolates, emphasizing their identification, as well as *qnrVC* genetic context and transfer capacity. Representatives of strains' clonal diversity were selected by PFGE and subjected to later characterization, including antimicrobial susceptibility tests, conjugation assays, and whole-genome sequencing (WGS). Typification revealed 12 clonal profiles of *Enterobacter* and one of *Klebsiella*. Transconjugants (Tcs) were obtained from 5 *Enterobacter* isolates. Parental strains were resistant to several classes of antimicrobial agents, while Tcs were resistant to ampicillin and amoxicillin-clavulanate, with reduced susceptibility to extended-spectrum cephalosporins, meropenem, and ciprofloxacin. WGS analysis allowed the identification of *E. coli* (1), *E. kobei* (4), and a new *Enterobacter* species (Taxon 3) (7). The *Pseudomonas* strains were identified as related to *P. monteilii*. The *Klebsiella* isolate was identified as *K. quasipneumoniae* subsp. *similipneumoniae*, which belonged to the new ST5440. Resistance genes to different classes of antimicrobial agents and to various plasmid incompatibility groups (Inc) were identified in *Enterobacteriales*. However, no Inc groups were found in *P. monteilii*, which carried the *qnrVC6* and *bla*_{VIM-2} genes at the chromosome. *qnrVC1* or *qnrVC4* were identified together with *bla*_{KPC-2} in high molecular weight plasmids with different Inc in *Enterobacter*. In *K. quasipneumoniae*, *qnrVC1* was identified in association with *bla*_{KPC-2} in a low molecular weight plasmid. *qnrVC* variants were identified in different genetic contexts not previously described, and the *bla*_{KPC-2} gene in NTE_{KPC-II} type elements. As far as we know, this is the first description of *qnrVC* and *bla*_{KPC-2} carried by the same replicon in Brazil or environmental samples, as well as of NTE_{KPC-II} in Brazilian non-clinical isolates. Here, we highlight that *qnrVC* dissemination in aquatic matrices in Brazil is probably associated with several events of genetic recombination.

Keywords: *qnrVC*, *qnrVC* genetic context, *qnrVC* in aquatic matrices, *qnrVC* and carbapenemases association, *qnrVC* in gram-negative bacilli

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