TITLE: MOBILIZABLE IncQ PLASMIDS HARBORING blages IN HUMAN AND ENVIRONMENTAL INTERFACE

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ABSTRACT: The spread of antibiotic resistance genes in Gram-negative bacteria occurs through several mechanisms, such as plasmid transfer (via transformation, conjugation, or mobilization). In this context, IncQ-type plasmid has shown a significant role in disseminating *bla*GES between clinical and environmental species. We compare the genetic context of two plasmids harboring different GES-type from Aeromonas veronii recovery from hospital effluent and Klebsiella variicola isolated from a rectal swab of a patient admitted to the cardiovascular intensive care unit. We performed hybrid assemblies by whole-genome sequencing using Illumina and Nanopore platforms. Plasmids sequence analysis revealed IncQ1 plasmid with almost identical backbones (100% coverage and 99.94% identity) and sizes of 9,413 kb (pAero28) and 9,526 kb (pKlebAC). A. veronii harbored blaGES-7 within a novel class 1 integron (In2061), and K. variicola carried blages-s within a class 1 integron (In2005) previously described in Enterobacter roggenkampii plasmid recovered from hospital sewage in Japan. In addition to blages, both integrons showed a fused gene cassette that encodes resistance to aminoglycosides and fluoroquinolones (aac(6')-Ib-cr/aac(6')-Ib-Hangzhou); and an IS6100 truncating the 3'-CS segment. Both plasmids have a similar mobilization system but did not show significant homology with other IncQ-type plasmids carrying *bla*GES previously reported. The similarity between environmental and clinical plasmids suggests the dispersion of blaGES. This highlights the ability of IncQ-like plasmids to spread from aquatic environment to hospital and the likelihood of their presence in the community.

Keywords: Aeromonas veronii; Klebsiella variicola; IncQ1; class 1 integron.

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