

TITLE: GENETIC CONTEXT OF *bla*_{CTX-M-59} CARRIED BY A COMPLEX CLASS 1 INTEGRON

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ABSTRACT:

CTX-M-type β -lactamases are the most common extended-spectrum β -lactamases (ESBLs) spread worldwide and the CTX-M-2 group is frequently reported in Latin American countries. In South America and Europe, spread of *bla*_{CTX-M-2} is associated mainly with complex *sul1*-type integrons containing *ISCR1*, most carried on transferable plasmids. CTX-M-59 is a CTX-M-2 variant first described in a *K. pneumoniae* nosocomial outbreak in a neonatal intensive care unit in Brazil. The aim of this study was to describe the full genetic context of *bla*_{CTX-M-59} carried by a complex class 1 integron from a multidrug resistant *Klebsiella pneumoniae*. In a previously study, multidrug resistant *Klebsiella pneumoniae* 145/11 isolated from rectal swab in a Brazilian hospital was characterized as beta-lactamases KPC-2, CTX-M-59 and 16S rRNA methyltransferase RmtG producing. In this study, total genomic DNA of Kp145/11 was extracted to construct a Nextera XT DNA library. Sequencing was performed using MiSeq platform and *de novo* assembly was performed using A5-Miseq pipeline and Geneious v.R9. The genome was annotated using NCBI Prokaryotic Genome Annotation Pipeline v.3.2. EasyFig 2.0 was used to map region of interest containing the genetic context of *bla*_{CTX-M-59}. This Whole Genome Shotgun project has been deposited at DDBJ/ENA/GenBank under accession number MAOO00000000. Sequencing of genomic DNA of Kp145/11 produced 490,268 paired-end reads with a 30X total coverage. The genetic context of *bla*_{CTX-M-59} in Kp145/11 is composed by an *ISCR1*-type class 1 integron in association with a copy of the insertion sequence IS26. This integron carries trimethoprim resistance gene *dfrA15*, phenicol resistance gene *cmlA1*, spectinomycin and streptomycin O-nucleotidyltransferase gene *aadA2*, truncated ethidium bromide-methyl viologen resistance gene *qacEΔ1*, transposon gene *ISCR1*, an extended-spectrum β -lactamase gene *bla*_{CTX-M-59}, a second copy of *qacE*, and sulfonamide resistance gene *sul1*. The association of the insertion sequence *ISCR1* with a class 1 integrons is called "complex class 1 integrons" and may contribute to increase the mobilization of many antibiotic resistance genes. Genetic environment of *bla*_{CTX-M-59} is similar to the *bla*_{CTX-M-2-group} maintaining its *ISCR1*-associated class 1 integron arrangement. Genetic context characterization is important to elucidate the mechanism of capture and mobilization of resistance genes facilitating their dissemination.

Key words: genetic context, *ISCR1*-associated class 1 integron, *bla*_{CTX-M-59}

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