The *bla*_{KPC-2} gene is plasmid located in the strain of *Pseudomonas aeruginosa* J5083553

^aAline Valério de Lima, ^aKeila de Oliveira Lima, Darlan Augusto da Costa Rocha, ^aSuely C F Sampaio, ^aJorge Luiz Mello Sampaio

^aUniversidade de São Paulo (USP), Faculdade de Ciências Farmacêuticas – Laboratório de Microbiologia Clínica - Avenida Professor Lineu Prestes, 580 Bloco 17 - Cidade Universitária – SP.

Pseudomonas aeruginosa is an important agent of healthcare-related infections worldwide, being related to high rates of antimicrobial resistance. Empirical treatment for resistant isolates is limited and usually includes the use of carbapenems. In Brazil, the main mechanisms of resistance to carbapenems in P. aeruginosa include loss of OprD porin, overexpression of efflux pumps and the production of SPM-1 type metallobetalactases. In this study, the *P. aeruginosa* strain J5083553 that caused a blood stream infection outbreak in a bone marrow transplant service in São Paulo in 2018 was found to be positive for KPC-2, an important endemic carbapenemase and associated with plasmids in *Klebsiella pneumoniae* in Brazil. The objective of the study was to define the location of the *bla*_{KPC} gene. The strain was subjected to genomic DNA sequencing by the MiSeq platform using Nextera XT libraries and assembly of contigs using the Geneious program. MLST was determined and the plasmid profile analysis was performed after digestion with the enzyme S1 nuclease and pulsed field gel electrophoresis (PFGE). Conjugation tests were also carried out. Sequencing analyzes showed the presence of the *bla*_{KPC-2} gene in a 128,487 bp contig, with 99.9% similarity to plasmid 1 of the P. aeruginosa strain RW109. PFGE analysis after digestion with S1 nuclease showed a plasmid of approximately 453 kbp; however, bacterial conjugation assays failed to obtain colonies of transconjugants. The *bla*_{KPC-2} gene was found flanked upstream by a truncated structure of a transposon of the Tn3 family and downstream by a truncated ISKpn6, a region often shared between plasmids of *P. aeruginosa* harboring the bla_{KPC-2} gene. This isolate belonged to ST446, considered an international high-risk clone. Considering the great similarity of the contig obtained with nucleotide sequences of plasmid deposited in GenBank, it is likely that the bla_{KPC-2} gene is located in the 453 kb plasmid.

Keywords: antimicrobial resistance; P. aeruginosa; KPC-2; plasmid

Author: Aline Valério de Lima; email address: aline_lima@usp.br