

TITLE: Genomic Features of *rmtB*-harboring Plasmids: Is there an intercontinental dissemination of a single plasmid?

AUTHORS: D. Cassu-Corsi¹, W.M.B.S. Martins¹, P. I. P. Ramos², A.C. Gales¹

INSTITUTIONS: ¹UNIFESP, São Paulo-SP, Brazil; ²IGM, FIOCRUZ-BA, Salvador-BA, Brazil

ABSTRACT:

RmtB-producing isolates is associated with high resistance rates to aminoglycosides. Usually, *rmtB* is carried by mobile genetic elements, including plasmids, which often carry other resistance encoding genes. It has been argued that pHN7A8-related plasmids, which harbors *rmtB*, could have potential for intercontinental dissemination. The objective of this study was to comparatively evaluate the genomic features of *rmtB*-harboring plasmids. Complete sequences of *rmtB* plasmids from distinct continents available in the GenBank were studied. General features, including %GC content, and size of plasmids were evaluated by SnapGene[®] tool. Integron content associated with *rmtB* genetic background was determined by INTEGRALL database. Investigation of Inc Group, and the distinct resistance genes associated with *rmtB* plasmids were evaluated by PlasmidFinder and ResFinder, respectively. Global similarity among all plasmids was determined by MAUVE. EasyFig was used for pair-to-pair comparison. ISFinder and EMBOSS were employed for validating all insertions sequences including their respective inverted repeats. Phylogeny studies were performed by PHYLIP package program. 21 fully sequenced *rmtB* plasmids were deposited in the GenBank until June, 2017. Most plasmids were recovered from *E. coli* (n=10) and *K. pneumoniae* (n=9). The size of plasmids ranged from 10 Kb (pCD4359) to 236 Kb (pKP64216a), with %GC ranging from 49% (pC629) to 59% (pCD4359). Ten plasmids possessed a class 1 integron within the *rmtB* genetic background, and nine of them belonged to In27. *rmtB* plasmids harbored distinct resistance genes, including aminoglycoside modifying enzymes (AMEs), OqxAB, QepA, and β -lactamases. *bla*_{NDM-1} and *bla*_{KPC-2} were observed in European and Chinese isolates, respectively. p397Kp, p477Kp and pHN7A8 plasmids showed high nucleotide sequence similarity, while others exhibited high genetic diversity. Five genetic backgrounds were associated with Tn2 in *rmtB* backbone. IS26 was detected in all analyzed plasmids. Interestingly, most plasmids belonged to the incompatibility group IncFII. Although most *rmtB* plasmids harbored similar resistance encoding genes, a high genetic

diversity was observed among *rmtB* plasmids, especially those belonging to the IncFII group. Our data also demonstrated that *rmtB* has always been associated with Tn2 and not with Tn3 as previously reported. In addition, IS26 may have played a role in the *rmtB* dissemination.

Key-words: aminoglycosides resistance, transposon and *rmtB*-harboring plasmids