

Prediction and analysis of plasmids from multidrug-resistant *Klebsiella pneumoniae* and *Enterobacter aerogenes* clinical isolates

¹Hemanoel Passarelli Araujo, ¹Filipe Pereira Matteoli, ²Jussara Kasuko Palmeiro,
²Líbera Dalla-Costa, ¹Thiago Motta Venancio

¹Universidade Estadual do Norte Fluminense, ²Universidade Federal do Paraná

Bacteria typically carry extrachromosomal, self-replicating genetic elements known as plasmids. Hospital outbreaks have become increasingly prevalent due to the evolution and spread of multidrug resistance, particularly in the presence of selective antibiotic pressure, which is a permanent public health concern. Here we report a comparative genomic analysis of southern Brazilian nosocomial *Klebsiella pneumoniae* and *Enterobacter aerogenes* isolates representing different resistance profiles. We sequenced four *E. aerogenes* and six *K. pneumoniae* strains, isolated from hospital patients, through Illumina HiSeq 2000 platform. Plasmids were predicted using PlasmidSPAdes and genes annotated with RAST, Prokka, BLAST and srst2 servers. We integrated our computational analysis with results from *in vitro* antibiotic resistance tests. The results show that resistance genes *bla*CTX-M15, *bla*OXA-2, *bla*TEM, *bla*KPC-2, *bla*OXY, *bla*SHV, *aac*(6')-Ib-cr, *sul1* and *qnrB1* were variedly distributed among the isolates and presumably contributed to the diverse multidrug-resistance profiles. The *bla*KPC-2 genes were found to be located within Tn4401b and associated with plasmids of similar Inc groups in *K. pneumoniae*. Overall, our detailed analysis not only allowed the identification of the genetic basis of the observed antibiotic resistance phenotypes of these ten strains, but also revealed potential novel resistance to antibiotics that have not been tested yet.