

TITLE: RESISTOME AND VIRULOME OF KPC-2 AND CTX-M-15-PRODUCING *KLEBSIELLA PNEUMONIAE* ST437 ISOLATED FROM A CLINICAL SAMPLE

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ABSTRACT:

KPC-producing *K. pneumoniae* isolates belonging to clonal complex 258 has contributed to the worldwide spread of resistance to carbapenems. In Brazil, KPC-2-producing *K. pneumoniae* are disseminated and ST11 and ST437 are the most frequently detected sequence types. Here, we report the whole genome sequence highlighting the resistome and virulome of *K. pneumoniae* 314/11 (Kp314/11) isolated from a clinical sample (blood) in Sao Paulo City, in 2011. This strain showed resistance to ceftazidime, cefotaxime, cefepime, aztreonam, ertapenem, imipenem, meropenem, tobramycin, ciprofloxacin, nalidixic acid, tetracyclin, ticarcilin-clavulanic acid, sulfamethoxazol-trimethoprim and piperacillin/tazobactam. Previously MLST analysis using conventional Sanger sequencing approaches determined Kp314/11 as belonging to ST437. Co-production of KPC-2 and CTX-M-15 were determined by PCR and DNA sequencing. Kp314/11 genomic DNA was extracted to construct Nextera XT DNA library sequenced using NextSeq platform (Illumina Inc, USA). *De novo* assembly was initially generated using Velvet v 1.2.10 pipeline that was further curated using Geneious v.R9 (Biomatters Ltd, New Zealand). For genome annotation NCBI Prokaryotic Genome Annotation Pipeline v.3.2 was used. Sequencing produced 11,865,174 paired-end reads with a 635.6X total coverage. 375 contigs were generated with a G+C content of 57.3% and an estimated size of 5,319,218 bp. Resistome *in silico* analysis using ResFinder 3.0 tool revealed the presence of the following resistance genes: *aac(6')Ib-cr*, *aadA2* (aminoglycoside resistance); *bla_{CTX-M-15}*, *bla_{SHV-11}*, *bla_{OXA-1}*, *bla_{KPC-2}* (beta-lactam resistance); *aac(6')Ib-cr*, *oqxA*, *oqxB* (fluoroquinolone resistance); *fosA* (fosfomicin resistance); *mphA* (macrolide resistance); *catB3* (phenicol resistance); *sul1* (sulphonamide resistance); *tetA* (tetracycline resistance) and *dfxA30* (trimethoprim resistance). Viruloma of Kp314 was determined using Pasteur Institute database revealing the presence of *mrk* cluster (*mrkACDFHIJ*) responsible for coding type 3 fimbriae. MLST 1.8 server of CGE confirm that Kp314/11 belongs to ST437 and PlasmidFinder analysis of Kp314/11 showed the presence of 4 plasmids belonging to incompatibility groups IncFII(K), IncFIB(K), IncFIB(pQil) and IncN. This draft genome sequence can provide useful information for comparative genomic analysis elucidating the dissemination and antimicrobial resistance gene acquisition of this clinically significant *K. pneumoniae* clone in Brazil.

Keywords: WGS, *Klebsiella pneumoniae*, KPC-2, CTX-15, ST437

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