

Title: Draft genome of KPC-2-producing *Klebsiella pneumoniae* belonging to ST437 from Brazil.

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Abstract: Multiresistant *Klebsiella pneumoniae* producing KPC-type carbapenemases are spread worldwide, carrying other resistance genes associated to mobile genetic elements. Since its first description in Brazil (2006), KPC-producing *K.pneumoniae* strains have been found in several Brazilian states. The most important clones described worldwide, and also in Brazil, belongs to the clonal complex 11, being the ST437 the most detect sequence type in our country. Here we aim to announce the draft genome of a KPC-2-producing *K.pneumoniae* strain (CCBH5623) belonging to ST437 from Santa Catarina, Brazil. This isolate was recovered from a catheter tip in 2010. The strain had a multidrug resistant profile, being susceptible only to amikacin and polymyxin B. Whole genome shotgun libraries was prepared with the Nextera XT kit (Illumina) and sequenced on an Illumina MiSeq system. The software Geneious version 6.1.7 (Biomatters) was used to perform *de novo* assembling. Rapid Annotation using System Technology (RAST) server was used for genome annotation. Acquired resistance genes were analyzed using the ResFinder platform (available at: <http://www.genomicepidemiology.org>). Analysis of capsular typing, antimicrobial resistance genes and virulence genes were performed using BIGSdb-Kp databank (<http://bigsdb.web.pasteur.fr/klebsiella/klebsiella.html>). We obtained 196.857 reads, comprising 121.933.012 base pairs. N50 was 412,797 and the estimated genome size was 5,576,605 bp. The *bla*_{KPC-2} gene was found in a 54.6kb IncN plasmid associated to Tn4401 isoform b. This plasmid has been detected in other Brazilian states. This isolate carried other resistance genes: *bla*_{SHV-11}, *bla*_{TEM-1B}, *bla*_{TEM-163}, *bla*_{CTX-M-15}, *bla*_{OXA-1}, *qnrB1*, *oqxA* *oqxB*, *aac(3)-II*, *aac(6')Ib-cr*, *catB3*; *sul1*; *tet(A)*; *tet(D)*; *aph(3')-Ia*; *dfrA30*; *mph(A)*. The *bla*_{CTX-M-15}, *bla*_{OXA-1}, *aac(6')Ib-cr*, *tetA* genes were found on the same genetic structure, associated to IS26. The virulence genes found were *entB* (siderophore), *mrk*, *ycfM* and *fimH* (fimbriae and adhesins). Capsular typing analysis (*wzc* gene) characterized the strain as capsular type K36. The announcement of the whole-genome sequence of KPC-2-producing *K.pneumoniae* also provides basis for other studies, which will certainly increase our understanding of the role of this species in the drug resistance scenario.

Keywords: *K. pneumoniae*, KPC, ST437, genome

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