Draft Genome Sequence of a Polymyxin-Resistant Klebsiella pneumoniae Clinical Strain Carrying mcr-8.1 and blaNDM-5

Pei, Na; Jian, Zijuan; Liu, Yirui; Liang, Tianzhu; Liu, Wenen; Li, Junhua

Published in:
Microbiology resource announcements

DOI:
10.1128/MRA.01224-20

Publication date:
2021

Document version
Publisher's PDF, also known as Version of record

Document license:
CC BY

Citation for published version (APA):
Draft Genome Sequence of a Polymyxin-Resistant *Klebsiella pneumoniae* Clinical Strain Carrying *mcr*-8.1 and *bla*NDM-5

Na Pei,a,c Zijuan Jian,b Yirui Liu,a,d Tianzhu Liang,a Wenen Liu,b Junhua Li

aBGI-Shenzhen, Shenzhen, China
bDepartment of Clinical Laboratory, Xiangya Hospital, Central South University, Changsha, Hunan, China
cLaboratory of Genomics and Molecular Biomedicine, Department of Biology, University of Copenhagen, Copenhagen, Denmark
dSchool of Basic Medicine, Qingdao University, Qingdao, Shandong, China

**ABSTRACT** Carbapenem-resistant *Klebsiella pneumoniae* (CRKP) is a major threat to global health. Here, we report the draft genome sequence of a *Klebsiella pneumoniae* clinical strain carrying *mcr*-8.1 and *bla*NDM-5.

Infections caused by carbapenem-resistant *Klebsiella pneumoniae* (CRKP) have been increasing in recent years in hospitals and communities, which has attracted concern worldwide (1). Polymyxin is used as the last-resort antimicrobial drug for treating CRKP (2) infections. The *mcr* gene encodes the production of an enzyme which can alter the cell membrane of CRKP, enabling the bacteria to be resistant to polymyxin. However, a variety of *mcr* gene subtypes have been found since the first report of the plasmid-mediated colistin resistance gene *mcr-1* in 2015 (3–9). Studies show that the use of colistin has probably accelerated the dissemination of the *mcr* gene in animals and humans. *K. pneumoniae* strain 163109936 was recovered from the sputum sample of a 37-year-old male patient in the bone marrow transplantation department at a tertiary hospital in Hunan Province, China, in August 2016. The sputum was then plated and screened using sheep blood agar overnight. The MIC of colistin was determined using the broth microdilution method. The study was approved by the Human Ethics Committee of Xiangya Hospital of Central South University in Changsha, China (number 201806861).

Strain 163109936 is resistant to ertapenem (MIC, \(8\) mg/ml), imipenem (MIC, \(16\) mg/ml), meropenem (MIC, \(6\) mg/ml), and polymyxin B (MIC, \(8\) mg/ml). The extensive drug resistance caught our attention. Therefore, this isolate was subjected to whole-genome sequencing.

The isolate was grown on LB broth at 37°C and harvested by centrifugation at 10,000 rpm for 1 min. Genomic DNA from strain 163109936 was extracted from the sample using a TIANamp bacterial DNA kit (Tiangen Biotech Co. Ltd., Beijing, China). The library was generated using the MGIEasy universal DNA library prep set (item number 1000006985). Sequencing was performed on a BGISEQ-500 sequencing platform (MGI, Shenzhen, China) with the paired-end 150-bp strategy. A total of 0.811 Gb was generated, and raw reads were filtered using fastp v 0.18.0 (10) and SOAPnuke (11) v 2.1.2 with default settings. The clean reads were assembled using SPAdes v 3.10.1 (12) with default settings. A total of 163 contigs (\(N_{50}\), 346,937 bp; \(N_{90}\), 34,594 bp; total length, 5,813,626 bp) were generated with 56.64% G+C content. The genome with a size of 5.8 Mb was annotated using Prokka v 1.14 (13) with default settings. Multilocus sequence typing (MLST) of *K. pneumoniae* was performed according to the protocol described on the Pasteur Institute MLST website (https://bigdb.pasteur.fr/klebsiella/).

The strain belongs to sequence type 685 (ST685), which has been found in China, Italy, and Turkey (14, 15).

The *K. pneumoniae* strain 163109936 genome contains 5,426 coding sequences and 88 tRNA genes. Antimicrobial resistance genes were identified using Resistance Gene


Editor Irene L. G. Newton, Indiana University, Bloomington

Copyright © 2021 Pei et al. This is an open-access article distributed under the terms of the Creative Commons Attribution 4.0 International license.

Address correspondence to Wenen Liu, wenenliu@163.com, or Junhua Li, lijunhua@genomics.cn.

Received 8 November 2020
Accepted 6 March 2021
Published 25 March 2021
Identifiers v 4.0.3 (16) with default settings. According to our results, the strain was positive for several antimicrobial resistance genes, including blaNDM-5 (carbapenemase gene), blaTEM-1, and blaCTX-M-45. Most importantly, the colistin resistance gene mcr-8.1 was also found. The presence of these genes could confer polymyxin resistance, though this would need to be further validated. Plasmid replications were also predicted with the presence of 10 replicons, IncFIB, IncFII, CoIRN1, IncR, Col, IncFIA, IncX3, TrafA, IncHI2A, and IncHI2.

In conclusion, a polymyxin-resistant Klebsiella pneumoniae clinical strain carrying mcr-8.1 and blaNDM-5 was characterized. This reminds us that continuous monitoring of polymyxin resistance is urgent in clinical practice.

Data availability. This draft genome sequence has been deposited at GenBank under the accession number JACJVA000000000. The version described in this paper is version JACJVA010000000. The raw reads have been submitted to the Sequence Read Archive (SRA) database under the accession number SRR12995617.

ACKNOWLEDGMENTS

This work was supported by the Science, Technology, and Innovation Commission of Shenzhen Municipality under grant number JCYJ20170412153155228 and the National Natural Science Foundation of China (grant number 81672066). We are also grateful for the support by China National GeneBank (CNGB).

REFERENCES