AMERICAN SOCIETY FOR MICROBIOLOGY | genomeAnnouncements

Complete Genome Sequence of KPC-Producing *Klebsiella pneumoniae* Strain CAV1193

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Carbapenem resistance in *Klebsiella pneumoniae*, frequently conferred by the bla_{KPC} gene, is a major public health threat. We sequenced a bla_{KPC}-containing strain of *K. pneumoniae* belonging to the emergent lineage ST941, in order to better understand the evolution of bla_{KPC} within this species.

Received 4 December 2015 **Accepted** 7 December 2015 **Published** 28 January 2016

Citation Sheppard AE, Stoesser N, Sebra R, Kasarskis A, Deikus G, Anson L, Walker AS, Peto TE, Crook DW, Mathers AJ. 2016. Complete genome sequence of KPC-producing *Klebsiella pneumoniae* strain CAV1193. Genome Announc 4(1):e01649-15. doi:10.1128/genomeA.01649-15.

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Klebsiella pneumoniae carbapenemase (KPC) confers multidrug resistance, with KPC-producing *Enterobacteriaceae* becoming increasingly prevalent in nosocomial infections. The most commonly described lineage associated with KPC is *K. pneumoniae* multilocus sequence type ST258, which is found globally (1–4). We previously characterized 37 KPC-producing *K. pneumoniae* isolates from a single health care institution, revealing a high level of genetic diversity, with the most prevalent lineage being ST941 (5). Here, we describe the complete genome sequence of CAV1193, a KPC-producing ST941 isolate from this institution.

CAV1193 was isolated from the ventilated airway of a 46-year-old female on hospital day 31 following a severe trauma. A genetically similar isolate (CAV1199) had been isolated from her sputum on hospital day seven. The patient was given 14 days of intravenous trimethoprim-sulfamethoxazole to which CAV1199 was susceptible (MIC of 40 μg/mL, VITEK2). CAV1193 was isolated 24 days later and was phenotypically resistant to trimethoprim-sulfamethoxazole. The tigecycline zone size had also increased from 18 mm to 21 mm, but otherwise CAV1199 and CAV1193 had identical susceptibility patterns.

PacBio sequencing of CAV1193 and initial *de novo* assembly were performed as previously described (5). To refine the assembly, we also performed Illumina sequencing, as previously described (5). Illumina reads were then mapped to the PacBio assembly using bwa-mem version 0.7.5a-r405 (6) and visualized using Gap5 version 1.2.14-r (7). Unmapped reads were *de novo* assembled using a5-miseq version 20140401 (8) to identify small plasmids, as these were expected to be absent from the PacBio assembly due to size selection of the input DNA (i.e., <7-kb DNA fragments were removed). Plasmid and chromosome structures were closed by resolving repeats at the ends of contigs. As the repeats were generally imperfect, mapping information was used to determine the correct sequence in each case. To validate the final assembly structure, each replicon was relinearized in a non-repeat region, the Illumina reads were remapped, and Gap5 was used for visualization, confirming the absence of misassemblies. The consensus sequence from mapping was also used to correct minor errors in the assembly sequence (generally single-base indels in homopolymeric regions).

The initial PacBio assembly consisted of five contigs (one chromosomal, four plasmid), with Illumina sequencing identifying one additional small plasmid. The final closed assembly consisted of a chromosome of 5,319,154 bp and five plasmids of 3,741 bp, 49,565 bp, 77,808 bp, 166,486 bp, and 257,944 bp.

The bla_{KPC} gene was located on the 49,565-bp plasmid, named pKPC_CAV1193, which was related to the bla_{KPC} plasmid pKPC_UVA01, previously identified from another *K. pneumoniae* isolate at the same institution (5). pKPC_CAV1193 differs from pKPC_UVA01 by one single-nucleotide variant and two insertions of 4,878 bp and 1,066 bp, which interrupt genes encoding a resolvase and the conjugal transfer protein TrbI, respectively.

Nucleotide sequence accession numbers. The complete genome sequence of CAV1193 has been deposited in GenBank under the accession numbers CP013321 to CP013326.

ACKNOWLEDGMENTS

We thank Joanne Carroll and the microbiology staff from the University of Virginia Clinical Laboratory for assistance with susceptibility testing and shipping.

The research was supported by the National Institute for Health Research (NIHR) Oxford Biomedical Research Centre. D.W.C. and T.E.P. are NIHR Senior Investigators.

FUNDING INFORMATION

The National Institute for Health Research (NIHR) Oxford Biomedical Research Centre provided funding to Tim E. Peto and Derrick W. Crook.

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