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Journal

Microbiology Resource Announcements, 3(3)

ISSN

2576-098X

Authors

Greninger, Alexander L

Chorny, Ilya

Knowles, Susan

et al.

Publication Date

2015-06-25

DOI

10.1128/genomea.00421-15

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Peer reviewed

Draft Genome Sequences of Four NDM-1-Producing *Klebsiella pneumoniae* Strains from a Health Care Facility in Northern California

Alexander L. Greninger,^{a*} Ilya Chorny,^b Susan Knowles,^b Valerie L. Ng,^c Vishnu Chaturvedi^a

Microbial Diseases Laboratory, California Department of Public Health, Richmond, California, USA^a; Illumina, Inc., San Diego, California, USA^b; Department of Laboratory Medicine and Pathology, Alameda County Medical Center, Oakland, California, USA^c

* Present address: Alexander L. Greninger, University of California San Francisco School of Medicine, San Francisco, California, USA.

We report the draft genome sequences of *Klebsiella pneumoniae* strains from four patients at a northern California health care facility. All strains contained the New Delhi metallo- β -lactamase (NDM1) carbapenemase with extended antibiotic resistance, including resistance to expanded-spectrum cephalosporins, imipenem, ertapenem, and meropenem. NDM gene alignments revealed that the resistance was plasmid encoded.

Received 26 March 2015 Accepted 30 March 2015 Published 14 May 2015

Citation Greninger AL, Chorny I, Knowles S, Ng VL, Chaturvedi V. 2015. Draft genome sequences of four NDM-1-producing *Klebsiella pneumoniae* strains from a health care facility in northern California. *Genome Announc* 3(3):e00421-15. doi:10.1128/genomeA.00421-15.

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Address correspondence to Vishnu Chaturvedi, vishnu.chaturvedi@cdph.ca.gov.

Klebsiella pneumoniae is a Gram-negative bacterium that is part of the normal flora of the gastrointestinal tract but can cause serious community- and hospital-acquired infections. Due to the recent evolution of multiple antibiotic resistance genes, *K. pneumoniae* has been denoted as a microbial threat to human health (1, 2). New Delhi metallo- β -lactamase (NDM1) carbapenemase-producing *K. pneumoniae*, originally reported from India, have spread rapidly around the world with many imported strains reported from California (3, 4).

Four *K. pneumoniae* strains came from adult males at a northern California health care facility in summer/fall 2013 and were derived from urine, sputum, a rectal swab, and pigtail drain fluid. The California Department of Public Health initially performed PCR testing for *bla*_{KPC} and *bla*_{NDM}.

All four strains were sequenced using Nextera paired-end sequencing and Nextera gel-free mate-pair sequencing and assembly with SPAdes v3.0/v3.1 and annotation via PROKKA v1.10 and NCBI Prokaryotic Annotation Pipeline (5, 6). The Nextera paired-end draft genome assemblies for strains CPH3020, CPH3707, CPH3823, and CPH5262 include 93, 116, 112, and 102 contigs >200 nucleotides measuring a total of 5,468,355 bp, 5,359,393 bp, 5,360,573 bp, 5,351,951 bp, respectively. The *N*₅₀s of the strains measure 214,475 bp, 206,548 bp, 206,548 bp, and 172,934 bp with coverages of 70 \times , 147 \times , 124 \times , and 155 \times , and there are 5,275, 5,182, 5,187, and 5,178 predicted coding sequences (CDS), respectively. Assemblies from the Nextera gel-free mate-pair alone yielded 68, 58, 54, and 59 contigs >200 nucleotides measuring a total of 5,494,465, 5,368,188, 5,371,617, and 5,378,024 bp, respectively. The mate-pair kit had significantly higher *N*₅₀s to 2,988,282 bp, 2,989,016 bp, 2,989,036 bp, and 2,989,036 bp with coverages of 65 \times , 48 \times , 45 \times , and 69 \times , respectively.

Of predicted CDS, 16.2% in strain CPH3020 were annotated as

hypothetical proteins, while 15.2% were annotated as hypothetical proteins in the three other strains. GC content ranged from 57.1% for strain CPH3020 to 57.3% for the three other strains. The scaffolds for each genome demonstrated >99.9% nucleotide identity to each other and >99.5% nucleotide identity across >93% the bacterial chromosome of the reference genome *Klebsiella pneumoniae* MGH 78578. Less than 20% of the plasmid sequence of MGH 78578 was covered by scaffolds from these *Klebsiella* strains, with minimal contiguity. All four strains had *bla*_{NDM} resistance genes with 100% nucleotide identity to PMK1-NDM-1 and PittNDM01 NDM-1 genes, with the same flanking 10 kb, including the bleomycin resistance gene, phosphoribosyl anthranilate isomerase, Tn3 family transposase, and GroES/L (7–9). All strains contained *bla*_{OXA-1} and *bla*_{SHV} and/or *bla*_{TEM} beta-lactamases (10, 11). None of the strains contained the *bla*_{KPC}, *bla*_{VIM}, or *bla*_{OXA-48} and/or *bla*_{OXA-181} carbapenemase resistance genes nor the *bla*_{CTX-15} extended-spectrum beta-lactamase (12). The alignments of NDM and neighboring genes suggested that the resistance was plasmid encoded, with significant alignments spanning the entirety of the assembled contig to plasmids from NDM-containing strains of *Klebsiella pneumoniae*, *Escherichia coli*, and *Enterobacter hormaechei*. Additionally, the NDM locus had 2 \times to 3 \times the coverage of the bacterial chromosome in three of the four strains, suggesting it existed on a different element. The additional ~100 kb in the CDPH3020 genome not present in the other *Klebsiella* strains was entirely derived from the pPMK1-NDM plasmid (9).

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession numbers JQCW00000000 (3020), JQCX00000000 (3707), JQDX00000000 (3823), and JQDY00000000 (5262) for the paired-end assemblies. The mate-pair assemblies have been deposited at DDBJ/EMBL/GenBank under the accession numbers

LAFV00000000 (3020), LAFX00000000 (3707), LAFW00000000 (3823), and LAFU00000000 (5262).

ACKNOWLEDGMENTS

We thank William Probert and Janet Ely for assistance with NDM-1 test and DNA isolation.

No external funding was received for this study.

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