

Draft genome sequence of multi-drug resistant *Klebsiella quasipneumoniae* subsp. *similipneumoniae* isolated from a teaching hospital wastewater in South West, Nigeria

Omowumi T. Akinola,¹ Samuel O. Dahunsi,^{1,2} Anthony Okoh³

AUTHOR AFFILIATIONS See affiliation list on p. 2.

ABSTRACT This broadcast is about the whole genome sequence of *Klebsiella quasipneumoniae* subsp. *similipneumoniae* (ST 1422) isolated from a teaching hospital wastewater in South West, Nigeria, in May 2022. This data set compiles information on the DNA size (5,332,183 bp) and GC content (57.91%) in its genome.

KEYWORDS antibiotic resistance

Klebsiella genus members are Gram-negative encapsulated non-motile bacteria that can acquire antibiotic resistance genes, causing mortality and morbidity (1). They cause both community- and hospital-acquired infections in humans. Pneumonia, upper respiratory tract infections, bacteremia, are some of these infections that affect people (2).

Klebsiella quasipneumoniae subsp. *similipneumoniae* is one of the member of the *Klebsiella pneumoniae* species complex (KpsC), identified on the basis of *gyrA* sequences and labeled as phylogroups of *K. pneumonia* (3). Due to the biochemical assays for *K. quasipneumoniae* and other *Klebsiella* spp. are identical, it is difficult to identify this organism using conventional laboratory techniques, which may result in misidentification and incorrect reporting (4), but whole-genome sequencing analysis can correctly identify it.

The sample was collected with a sterile bottle placed at hospital wastewater drain pool in Ogbomoso, Nigeria (8°08'02.5" N and 4°14'00.8".23 E). The sample was filtered using the membrane filtering technique (Millipore, Merck, South Africa) via a 0.45-μm nitrocellulose filter membrane. The filter was placed on MacConkey agar plate and incubated at 37°C for 24 h, after which pink mucoid colonies were subcultured to get a pure isolate. Biochemical test (5) results of indole negative, methyl red negative, and Voges-Proskauer positive revealed B105 to be *Klebsiella pneumonia*.

Genomic DNA was isolated from a pure culture plate using ZymoBIOMICS DNA Miniprep Kit (Zymo Research), following the manufacturers' instructions. Using the custom-built IDT 10 bp unique dual indices with a desired insert size of 320 bp, Illumina sequencing libraries were created by means of the tagmentation- and PCR-based Illumina DNA Prep kit. In one or more multiplexed shared-flow-cell runs, the DNA was sequenced by Illumina on an Illumina NovaSeq 6000 sequencer, yielding 2 × 151 bp paired-end reads. The reads were trimmed for quality using Trimmomatic v0.36 (6).

De novo assembly of cleaned reads was performed with Read Annotation Assembly Pipeline Tool (RAPT v0.55teamcity CI) (<https://github.com/ncbi/rapt>). The assembled genome was annotated via Prokaryotic Genome Annotation Pipeline (PGAP) Table 1 (7). The assembled genome was submitted to the *Klebsiella* multilocus sequence type (MLST 2.0) database at the Center for Genomic Epidemiology using seven housekeeping genes (8).

Editor Catherine Putonti, Loyola University Chicago, Chicago, Illinois, USA

Address correspondence to Omowumi T. Akinola, omowumi.akinola@bowen.edu.ng.

The authors declare a conflict of interest.

Received 6 August 2023

Accepted 15 December 2023

Published 25 January 2024

Copyright © 2024 Akinola et al. This is an open-access article distributed under the terms of the [Creative Commons Attribution 4.0 International license](https://creativecommons.org/licenses/by/4.0/).

TABLE 1 Features of B105 *Klebsiella quasipneumoniae* subsp. *similipneumoniae*

Features	Facts for B105: <i>Klebsiella quasipneumoniae</i> subsp. <i>similipneumoniae</i>
Sequence reads	
Total reads (bp)	1,462,203
Total length (bp)	5,332,183
Assembly	
DNA genome size (bp)	5,332,183
Contigs	96
Coverage (×)	81
G+C content (%)	57.91
Protein-coding genes	5,231
rRNA genes	8
tRNA genes	76
Contigs N50 (bp)	182,922
Contigs L50	10

K-mer inbuilt tool on the National Center for Biotechnology Information (NCBI) was employed to map sequence reads with the available sequences in database (9, 10). In the annotated result, strain B105 had an average nucleotide identity (ANI) of 99.185% with strain GCA_000613225.1, the type strain of *Klebsiella quasipneumoniae* subsp. *similipneumoniae* in the database.

ACKNOWLEDGMENTS

The authors thank Helix Biogen Institute, Ogbomoso, Oyo State, for their technical support.

AUTHOR AFFILIATIONS

¹Microbiology Programme, College of Agriculture, Engineering, and Science, Bowen University Iwo, Iwo, Osun, Nigeria

²The Radcliffe Institute for Advanced Study, Harvard University, Cambridge, Massachusetts, USA

³SAMRC Microbial Water Quality Monitoring Centre, University of Fort Hare, Alice, South Africa

AUTHOR ORCIDS

Omowumi T. Akinola  <http://orcid.org/0000-0003-2155-4697>

Samuel O. Dahunsi  <http://orcid.org/0000-0003-3088-1577>

AUTHOR CONTRIBUTIONS

Omowumi T. Akinola, Conceptualization, Data curation, Methodology, Writing – original draft | Samuel O. Dahunsi, Project administration, Supervision, Writing – review and editing.

DATA AVAILABILITY

The BioProject accession number [SAMN36174866](https://www.ncbi.nlm.nih.gov/bioproject/544866) was used to store the sequencing data. The whole-genome shotgun of this project has been deposited at DDBJ/ENA/GenBank under the accession number [JAUHJP000000000](https://www.ncbi.nlm.nih.gov/nuccore/JAUHJP000000000). The raw sequence reads have been deposited in the Sequence Read Archive (SRA) under accession number [PRJNA989579](https://www.ncbi.nlm.nih.gov/sra/PRJNA989579).

REFERENCES

- Mathers AJ, Crook D, Vaughan A, Barry KE, Vegesana K, Stoesser N, Parikh HI, Sebra R, Kotay S, Walker AS, Sheppard AE. 2019. *Klebsiella quasipneumoniae* provides a window into carbapenemase gene transfer, plasmid rearrangements, and patient interactions with the hospital

- environment. *Antimicrob Agents Chemother* 63:e02513–e02518. <https://doi.org/10.1128/AAC.02513-18>
2. Navon-Venezia S, Kondratyeva K, Carattoli A. 2017. *Klebsiella pneumoniae*: a major worldwide source and shuttle for antibiotic resistance. *FEMS Microbiol Rev* 41:252–275. <https://doi.org/10.1093/femsre/fux013>
 3. Brisse S, Passet V, Grimont PAD. 2014. Description of *Klebsiella quasipneumoniae* sp., isolated from human infections, with two subspecies, *Klebsiella quasipneumoniae* subsp. *quasipneumoniae* subsp. nov. and *Klebsiella quasipneumoniae* subsp. *similipneumoniae* subsp. nov., and demonstration that *Klebsiella singaporensis* is a junior heterotypic synonym of *Klebsiella variicola*. *Int J Syst Evol Microbiol* 64:3146–3152. <https://doi.org/10.1099/ijs.0.062737-0>
 4. Chen M, Li Y, Li S, Tang L, Zheng J, An Q. 2016. Genomic identification of nitrogen-fixing *Klebsiella variicola*, *K. pneumoniae* and *K. quasipneumoniae*. *J Basic Microbiol* 56:78–84. <https://doi.org/10.1002/jobm.201500415>
 5. Arora B, Arora DR. 2007. Textbook of microbiology, p 41–42. CBS publishers and distributors, New Delhi.
 6. Bolger AM, Lohse M, Usadel B. 2014. Trimmomatic: a flexible trimmer for Illumina sequence data. *Bioinformatics* 30:2114–2120. <https://doi.org/10.1093/bioinformatics/btu170>
 7. Wattam AR, Davis JJ, Assaf R, Boisvert S, Brettin T, Bun C, Conrad N, Dietrich EM, Disz T, Gabbard JL, et al. 2017. Improvements to PATRIC, the all-bacterial bioinformatics database and analysis resource center. *Nucleic Acids Res* 45:D535–D542. <https://doi.org/10.1093/nar/gkw1017>
 8. Larsen MV, Cosentino S, Rasmussen S, Friis C, Hasman H, Marvig RL, Jelsbak L, Sicheritz-Pontén T, Ussery DW, Aarestrup FM, Lund O. 2012. Multilocus sequence typing of total genome sequenced bacteria. *J Clin Microbiol* 50:1355–1361. <https://doi.org/10.1128/JCM.06094-11>
 9. Ondov BD, Treangen TJ, Melsted P, Mallonee AB, Bergman NH, Koren S, Phillippy AM. 2016. Mash: fast genome and metagenome distance estimation using MinHash. *Genome Biol* 17:132. <https://doi.org/10.1186/s13059-016-0997-x>
 10. NCBI Taxonomy Browser. n.d. Taxonomy. Available from: <https://www.ncbi.nlm.nih.gov/taxonomy/>