



Genome Sequence of *Kurthia* Type Species *Kurthia zopfii* Strain ATCC 33403^T

Abigail E. Goen,^a  Kyle S. MacLea^{a,b,c}

^aBiology Program, University of New Hampshire, Manchester, New Hampshire, USA

^bBiotechnology Program, University of New Hampshire, Manchester, New Hampshire, USA

^cDepartment of Life Sciences, University of New Hampshire, Manchester, New Hampshire, USA

ABSTRACT The genome of the type strain of the *Kurthia* genus, *Kurthia zopfii* ATCC 33403, was sequenced. Nonpathogenic *K. zopfii* has been isolated from intestinal contents, fecal material, meats, meat products, milk, water, and air, including air at high altitudes. The predicted genome size is 2,878,279 bp, with 37.05% G+C content.

Characteristically, the phylum *Firmicutes* consists of Gram-positive bacteria with low G+C content. In class *Bacilli* and order *Bacillales*, the family *Planococcaceae* includes the genus *Kurthia*, of which *Kurthia zopfii* is the type species and strain ATCC 33403 (= BARNES F64/100; DSM 20580; NCIB 9878; and NCTC 10597) is the type strain, which was first isolated in 1883. *K. zopfii* is a motile, saprophytic, Gram-positive firmicute of regular, unbranched rods that fragment into a coccoid morphology in older cultures (1–4). The type strain of *K. zopfii* was isolated from intestinal contents of poultry (5) as “*Bacterium zopfii*,” and many strains have since been found in meats, meat products, and milk, air from abattoirs, and also environments as diverse as wastewater and air samples collected above 3,000 m in altitude (1–4, 6–10). Although some members of the genus *Kurthia* are pathogens (11–13), no reports of pathogenicity have been made for *K. zopfii*.

The type strain of *K. zopfii*, ATCC 33403 (Kurth 1883) Trevisan 1885, was ordered (ATCC, Manassas, VA, USA) and rehydrated. Reconstituted bacteria were spread on tryptic soy agar (TSA) incubated at 26°C and then streaked onto brain heart infusion (BHI) agar for isolates. A single colony was then used to inoculate BHI broth, which was used to generate genomic DNA (gDNA) with a DNA minikit (Qiagen, Valencia, CA, USA). The double-stranded DNA (dsDNA) broad-range assay kit (DeNovix, Wilmington, DE, USA) was used to check DNA quality and quantity. One nanogram of clean gDNA was fragmented and tagged with adapters with the HyperPlus kit (KAPA, Wilmington, MA, USA), and ~5% of the total lane yield of 11 pM of a gDNA library was loaded on an Illumina HiSeq 2500 instrument by the Hubbard Center for Genome Studies (Durham, NH, USA) for sequencing. Prior to genome assembly, 250-bp paired-end reads were trimmed using Trimmomatic (14). We used SPAdes v. 3.11.1 (15) to assemble the genome using default settings. After removal of small contigs, the genome was submitted for annotation via the NCBI Prokaryotic Genome Annotation Pipeline (PGAP) process (16). The *K. zopfii* genome-sequencing project produced 110 contigs with a total length of 2,878,279 bp. The largest contig was 204,291 bp, with an N_{50} value of 59,099 bp and a G+C content of 37.05%. PGAP predicted 2,925 genes, of which 2,825 were protein coding genes, along with 13 rRNAs, 53 tRNAs, 5 other RNA genes, and 29 pseudogenes. The genome size is smaller than that of *Kurthia sibirica*, at 3.5 Mbp and 3,400 total genes (17). Although we achieved 344× genome coverage, it is possible that the *K. zopfii* draft genome is incomplete, resulting in an undercount of genes versus that of other members of the genus. Alternatively, these species may be quite different given their reportedly low DNA-DNA hybridization results (~20%) (18). Aver-

Received 7 June 2018 Accepted 20 June 2018
Published 12 July 2018

Citation Goen AE, MacLea KS. 2018. Genome sequence of *Kurthia* type species *Kurthia zopfii* strain ATCC 33403^T. *Microbiol Resour Announc* 7:e00833-18. <https://doi.org/10.1128/MRA.00833-18>.

Editor Julia Maresca, University of Delaware

Copyright © 2018 Goen and MacLea. 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/).

Address correspondence to Kyle S. MacLea, kyle.maclea@unh.edu.

age nucleotide identity (ANI) scoring using the EzBioCloud portal (19) generated 74.5% ANI, consistent with assignment to the same genus, although *K. zopfii* and *K. sibirica* are clearly quite different members of the *Kurthia* genus.

Data availability. The *Kurthia zopfii* ATCC 33403^T whole-genome shotgun sequence (WGS) project has been deposited in DDBJ/ENA/GenBank under accession number [QFVS00000000](https://www.ncbi.nlm.nih.gov/nuccore/QFVS00000000). The version described in this paper is the first version, QFVS01000000.

ACKNOWLEDGMENTS

Sequencing and bioinformatics analysis were undertaken at the Hubbard Center for Genome Studies at UNH, supported by NH-INBRE, with the kind assistance of Kelley Thomas, Toni Westbrook, and Stephen Simpson. K.S.M. acknowledges Thomas Kulik, UNH Manchester, for his very useful translation from the original Russian of Belikova et al., *Mikrobiologiya*, 1986 (18), which was used for comparative reading on the genus. This translation (20) has been deposited in GitHub to allow other scientists to access it (<https://github.com/KyleMacLea/Kurthia-sibirica>). K.S.M. further acknowledges the hard work of lab associate Patrick MacLea, UNH class of 2018. This work was a project of the Microbiology Education through Genome Annotation-New Hampshire (MEGA-NH) program.

The Department of Life Sciences at UNH Manchester provided funds for purchasing the bacterial strain. Sequencing costs were supported by New Hampshire-INBRE through an Institutional Development Award (IDeA) (P20GM103506), from the National Institute of General Medical Sciences of the NIH. The funders had no role in study design, data collection and interpretation, or the decision to submit the work for publication.

REFERENCES

- Gardner GA. 1969. Physiological and morphological characteristics of *Kurthia zopfii* isolated from meat products. *J Appl Bacteriol* 32:371–380. <https://doi.org/10.1111/j.1365-2672.1969.tb00986.x>.
- Belikova VL, Cherevach NV, Baryshnikova LM, Kalakutskii LV. 1980. Morphologic and physiologic-biochemical characteristics of *Kurthia zopfii*. *Mikrobiologiya* 49:64–69. (In Russian.)
- Shaw S, Keddie RM. 1983. A numerical taxonomic study of the genus *Kurthia* with a revised description of *Kurthia zopfii* and a description of *Kurthia gibsonii* sp. nov. *Syst Appl Microbiol* 4:253–276. [https://doi.org/10.1016/S0723-2020\(83\)80054-X](https://doi.org/10.1016/S0723-2020(83)80054-X).
- Stackebrandt E, Keddie RM, Jones D. 2006. The genus *Kurthia*, p. 519–529. *In* The prokaryotes. Springer, New York, NY.
- Kurth H. 1883. Über bacterium zopfii, eine neue bacterienart. *Ber Dtsch Bot Ges* 23:97–100. (In German.)
- Günther C. 1896. Bakteriologische untersuchungen in einem Falle von Fleischvergiftung. *Arch Hyg* 28:153–158. (In German.)
- Jacobsen HC. 1907. Ueber einen richtenden Einfluss beim Wachstum gewisser Bakterien in Gelatine. *Zbl Bakteriol Parasitenkd Infekt Hyg*, 2 Abt 17:53–64. (In German.)
- Wenner JJ, Rettger LF. 1919. A systematic study of the proteus group of bacteria. *J Bacteriol* 4:331–353.
- Holzappel WH. 1992. Culture media for non-sporulating Gram-positive food spoilage bacteria. *Int J Food Microbiol* 17:113–133. [https://doi.org/10.1016/0168-1605\(92\)90110-O](https://doi.org/10.1016/0168-1605(92)90110-O).
- Shabbir MZ, Park J, Muhammad K, Rabbani M, Rana MY, Harvill ET. 2014. Culture independent analysis of respiratory microbiome of houbara bustard (*Chlamydotis undulata*) revealed organisms of public health significance. *Int J Agric Biol* 16:222–226.
- Pancoast SJ, Ellner PD, Jahre JA, Neu HC. 1979. Endocarditis due to *Kurthia bessonii*. *Ann Intern Med* 90:936–937. <https://doi.org/10.7326/0003-4819-90-6-936>.
- Ongrádi J, Stercz B, Kövesdi V, Nagy K, Chatlyne L. 2014. Isolation of *Kurthia gibsonii* from non-gonorrheal urethritis: implications for the pathomechanism upon surveying the literature. *Acta Microbiol Immunol Hung* 61:79–87. <https://doi.org/10.1556/AMicr.61.2014.1.8>.
- Kövesdi V, Stercz B, Ongrádi J. 2016. *Kurthia gibsonii* as a sexually transmitted zoonosis: from a neglected condition during World War II to a recent warning for sexually transmitted disease units. *Indian J Sex Transm Dis* 37:68. <https://doi.org/10.4103/0253-7184.180296>.
- 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>.
- Bankevich A, Nurk S, Antipov D, Gurevich AA, Dvorkin M, Kulikov AS, Lesin VM, Nikolenko SI, Pham S, Pribelski AD, Pyshkin AV, Sirotkin AV, Vyahhi N, Tesler G, Alekseyev MA, Pevzner PA. 2012. SPAdes: a new genome assembly algorithm and its applications to single-cell sequencing. *J Comput Biol* 19:455–477. <https://doi.org/10.1089/cmb.2012.0021>.
- Tatusova T, DiCuccio M, Badretdin A, Chetvermin V, Ciufu S, Li W. 2013. NCBI prokaryotic genome annotation pipeline. *Nucleic Acids Res* 44:6614–6624. <https://doi.org/10.1093/nar/gkw569>.
- Goen et al. 2018. Microbiol Resour Announc, in press. <https://doi.org/10.1128/MRA00841-18>.
- Belikova VA, Cherevach NV, Kalakutskii LV. 1986. New species of bacteria in the genus *Kurthia*—*Kurthia sibirica* sp. nov. *Mikrobiologiya* 55:831–835. (In Russian.)
- Yoon S-H, Ha S-M, Kwon S, Lim J, Kim Y, Seo H, Chun J. 2017. Introducing EzBioCloud: a taxonomically united database of 16S rRNA gene sequences and whole-genome assemblies. *Int J Syst Evol Microbiol* 67:1613–1617. <https://doi.org/10.1099/ijsem.0.001755>.
- Kulik T, MacLea KS. 2017. Translation of *Kurthia sibirica*, a new bacterial species of the *Kurthia* genus, by V. A. Belikova, N. V. Cherevach, L. V. Kalakutski. *Mikrobiologiya* 55:831–835. Published in 1986.