AMERICAN SOCIETY FOR MICROBIOLOGY | Microbiology Resource Announcements

GENOME SEQUENCES

Draft Genome Sequence of the Multidrug-Resistant Strain *Stenotrophomonas maltophilia* N0320, Isolated from a Commercial Nanoparticle Product

Miseon Park,[a] Christine V. Summage-West,[b] Lillie M. Sims,[b] Sung-Guk Kim[b]

[a]Division of Microbiology, National Center for Toxicological Research, U.S. Food and Drug Administration, Jefferson, Arkansas, USA

[b]Surveillance/Diagnostic Laboratory, Office of Scientific Coordination, National Center for Toxicological Research, U.S. Food and Drug Administration, Jefferson, Arkansas, USA

ABSTRACT *Stenotrophomonas maltophilia* is an emerging opportunistic pathogen that is frequently associated with hospital infections. We report the 4.8-Mbp draft genome sequence of the oxidase-positive *S. maltophilia* strain N0320, an isolate from a commercial hydroxyapatite nanoparticle product.

Stenotrophomonas maltophilia is a nonfermentative, obligate aerobic Gram-negative bacterium found in clinical and nonclinical environments (1). Although *S. maltophilia* is not considered to be a virulent pathogen, it has become one of the most common opportunistic nosocomial pathogens associated with significant mortality in immunocompromised or cystic fibrosis patients (2). *S. maltophilia* carries intrinsic and acquired multiple-drug-resistant genes among its clinical and nonclinical isolates (3).

Hydroxyapatite (HA) has been most extensively used as a synthetic bone graft substitute based on its functional property of encouraging bone growth (4). However, bacterial adherence to the surface of HA in dental and orthopedic applications consequently leads to serious medical complications, including implant failure, hospitalization, and surgical intervention (5). A commercial HA product was gently mixed by inversion, and 100 ml of the dispersed suspension was spread onto tryptic soy agar (TSA) supplemented with 5% sheep blood (Remel) and aerobically cultured at 37°C for 24 h. A single colony was selected from a blood agar plate, and repeated subculturing was performed to obtain a pure culture. The isolate, a Gram-negative rod-shaped aerobic bacterium, was identified as *S. maltophilia* using matrix-assisted laser desorption ionization–time of flight (MALDI-TOF) mass spectrometry (Bruker). The multidrug resistance and cytochrome oxidase expression of this isolate were determined as previously reported (6).

DNA was extracted from several colonies grown overnight on a TSA blood agar plate at 37°C using the DNeasy blood and tissue kit, following the manufacturer's instructions (Qiagen). The DNA was quantified using a Qubit fluorometer (Thermo Fisher Scientific). Libraries were prepared using the Nextera XT library prep kit, and sequencing was performed using the MiSeq v2 reagent kit in 250-bp paired-end mode on a MiSeq instrument (Illumina). Default parameters were used for all software unless otherwise noted. A total of 1.97 million raw reads were obtained; the reads were quality checked, and low-quality reads and adapter sequences were trimmed using the Fastq Utilities Service in PATRIC (6). The filtered reads were assembled using SPAdes v3.12.0 in PATRIC (7). The draft genome sequence of strain N0320 is 4,814,846 bp long with an N_{50} value of 108,307 bp, a G+C content of 66.35%, and 57× coverage in 79 contigs. The *S. maltophilia* N0320 genome sequence was annotated using the NCBI Prokaryotic Genome Pipeline (PGAP) v4.11 (8). The annotated genome sequence contains 4,328 proteins with functional assignments, 64 hypothetical proteins, 71 tRNAs, and 7 rRNAs. The genome of *S. maltophilia* N0320 shares an average nucleotide

Citation Park M, Summage-West CV, Sims LM, Kim S-G. 2021. Draft genome sequence of the multidrug-resistant strain *Stenotrophomonas maltophilia* N0320, isolated from a commercial nanoparticle product. Microbiol Resour Announc 10:e00914-21. https://doi.org/10.1128/MRA.00914-21.

Editor Steven R. Gill, University of Rochester School of Medicine and Dentistry

Address correspondence to Sung-Guk Kim, SungGuk.Kim@fda.hhs.gov.

Received 14 September 2021
Accepted 9 October 2021
Published 28 October 2021

identity of 98.1% with the reference genome of *S. maltophilia* K279a (GenBank accession number NC_010943.1), determined using the Similar Genome Finder in PATRIC (6). *S. maltophilia* N0320 does not harbor noticeable drug resistance genes, except multiple efflux pump-associated genes, though the strain is phenotypically multidrug resistant. The efflux pump genes (*smeABC*, *smeDEF*, *smeR*, and *smeS*) may be responsible for multidrug resistance in *S. maltophilia* N0320, as reported for other *S. maltophilia* strains (9, 10).

Data availability. The genome sequence has been deposited in GenBank under the accession number JABAGX000000000.1. The raw reads have been deposited in the Sequence Read Archive (SRA) under the accession number SRX11509207.

ACKNOWLEDGMENTS

We appreciate technical support from Alice R. Wattam at the University of Virginia and technical assistance from NCTR student interns Leah Rowe and Katelyn Mason.

This publication reflects the views of the authors and should not be construed to represent USFDA views or policies.

REFERENCES

1. An SQ, Berg G. 2018. Stenotrophomonas maltophilia. Trends Microbiol 26:637–638. https://doi.org/10.1016/j.tim.2018.04.006.
2. Brooke JS. 2012. Stenotrophomonas maltophilia: an emerging global opportunistic pathogen. Clin Microbiol Rev 25:2–41. https://doi.org/10.1128/CMR.00019-11.
3. Berg G, Roskot N, Smalla K. 1999. Genotypic and phenotypic relationships between clinical and environmental isolates of Stenotrophomonas maltophilia. J Clin Microbiol 37:3594–3600. https://doi.org/10.1128/JCM.37.11.3594-3600.1999.
4. Okada M, Furuzono T. 2012. Hydroxylapatite nanoparticles: fabrication methods and medical applications. Sci Technol Adv Mater 13:e064103. https://doi.org/10.1088/1468-6996/13/6/064103.
5. Coelho CC, Araújo R, Quadros PA, Sousa SR, Monteiro FJ. 2019. Antibacterial bone substitute of hydroxyapatite and magnesium oxide to prevent dental and orthopaedic infections. Mater Sci Eng C Mater Biol Appl 97:529–538. https://doi.org/10.1016/j.msec.2018.12.059.
6. Carmody LA, Spilker T, LiPuma JJ. 2011. Reassessment of Stenotrophomonas maltophilia phenotype. J Clin Microbiol 49:1101–1103. https://doi.org/10.1128/JCM.02204-10.
7. Wattam AR, Davis JJ, Assaf R, Boisvert S, Brettin T, Bun C, Conrad N, Dietrich EM, Disz T, Gabbard JL, Gerdes S, Henry CS, Kenyon RW, Machi D, Mao C, Nordberg EK, Olsen GJ, Murphy-Olson DE, Olson R, Overbeek R, Parrello B, Pusch GD, Shukla M, Vonstein V, Warren A, Xia F, Yoo H, Stevens RL. 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. Haft DH, DiCuccio M, Badretdin A, Brover V, Chetvernin V, O'Neill K, Li W, Chitsaz F, Derbyshire MK, Gonzales NR, Gwadz M, Lu F, Marchler GH, Song JS, Thanki N, Yamashita RA, Zheng C, Thibaud-Nissen F, Geer LY, Marchler-Bauer A, Pruitt KD. 2018. RefSeq: an update on prokaryotic genome annotation and curation. Nucleic Acids Res 46:D851–D860. https://doi.org/10.1093/nar/gkx1068.
9. Sanchez MB, Hernandez A, Martinez JL. 2009. Stenotrophomonas maltophilia drug resistance. Future Microbiol 4:655–660. https://doi.org/10.2217/fmb.09.45.
10. Rizek CF, Jonas D, Garcia Paez JI, Rosa JF, Perdigão Neto LV, Martins RR, Moreno LZ, Rossi Junior A, Levin AS, Costa SF. 2018. Multidrug-resistant Stenotrophomonas maltophilia: description of new MLST profiles and resistance and virulence genes using whole-genome sequencing. J Glob Antimicrob Resist 15:212–214. https://doi.org/10.1016/j.jgar.2018.07.009.