12-1-2022

Draft Genome Sequence of Staphylococcus epidermidis UMB7543, Isolated from a Female Patient with Recurrent Urinary Tract Infections

Sandra Jablonska
Loyola University Chicago

Alan J. Wolfe
Loyola University Chicago

Catherine Putonti
Loyola University Chicago

Recommended Citation

Jablonska, Sandra; Wolfe, Alan J.; and Putonti, Catherine. Draft Genome Sequence of Staphylococcus epidermidis UMB7543, Isolated from a Female Patient with Recurrent Urinary Tract Infections. Microbiology Resource Announcements, 11, 12: 1-2, 2022. Retrieved from Loyola eCommons, Biology: Faculty Publications and Other Works, http://dx.doi.org/10.1128/mra.00962-22

AMERICAN SOCIETY FOR MICROBIOLOGY | Microbiology Resource Announcements

GENOME SEQUENCES

Draft Genome Sequence of *Staphylococcus epidermidis* UMB7543, Isolated from a Female Patient with Recurrent Urinary Tract Infections

Sandra Jablonska,[a,b] Alan J. Wolfe,[c] Catherine Putonti[a,b,c]

[a]Department of Biology, Loyola University Chicago, Chicago, Illinois, USA
[b]Bioinformatics Program, Loyola University Chicago, Chicago, Illinois, USA
[c]Department of Microbiology and Immunology, Loyola University Chicago, Maywood, Illinois, USA

ABSTRACT *Staphylococcus epidermidis* is a Gram-positive bacterium that is part of the normal human flora, found in multiple anatomical sites. Here, we present the 2.6-Mbp draft genome sequence of *S. epidermidis* UMB7543, isolated from a catheterized urine sample from a female patient with a documented diagnosis of recurrent urinary tract infection.

Staphylococcus epidermidis is the most common source of infections from medical devices, including indwelling catheters (1, 2). These infections can be chronic and persistent due to the production of biofilms, which often confer antibiotic resistance (3, 4). Much more frequently, *S. epidermidis* is a benign member of the human epithelia. While it predominantly colonizes the skin, it can also be found in other organs, e.g., the urinary and gastrointestinal tracts. Here, we present the draft genome sequence of *S. epidermidis* UMB7543, isolated from a catheterized urine sample from a postmenopausal female patient with a recurrent urinary tract infection (rUTI). Although *S. epidermidis* has previously been associated with UTIs in children (5), this strain is not believed to be the cause of UTI symptoms for this individual.

S. epidermidis UMB7543 was isolated using the expanded quantitative urine culture (EQUC) method (6), as part of a prior institutional review board (IRB)-approved study (University of California, San Diego; IRB no. 170077AW). The genus and species for this isolate were determined by matrix-assisted laser desorption ionization–time of flight (MALDI-TOF) mass spectrometry following protocols detailed previously (7). The isolate was stored at −80°C until sequencing. The freezer stock was streaked onto a Columbia nalidixic acid (CNA) agar plate and incubated at 35°C with 5% CO_2 for 24 h. Tryptone soy liquid medium was inoculated with a single colony from the plate and incubated overnight at 37°C. DNA extraction was done using the Qiagen DNeasy blood and tissue kit; the manufacturer's Gram-positive protocol was followed with an altered prelysis step (previously described) (8). The purified DNA was quantified using a Qubit fluorometer. DNA sequencing was performed by SeqCenter (Pittsburgh, PA). There, sample libraries were prepared using the Illumina DNA prep kit and IDT 10-bp unique dual indices (UDI) and sequenced on the Illumina NextSeq 2000 platform. Sequencing yielded 1,167,425 pairs of 150-bp reads. Unless otherwise noted, default parameters were used for all software tools. The reads were trimmed using BBDuk v37.36, which is part of the BBTools suite (https://jgi.doe.gov/data-and-tools/software-tools/bbtools/). The reads were assembled using SPAdes v3.15.4 with the "only-assembler" option for k values of 55, 77, and 99 (9). The genome coverage was calculated using BBMap v38.47, also part of the BBTools suite. NCBI's Prokaryotic Genome Annotation Pipeline (PGAP) v6.2 was used to annotate the publicly available genome assembly (10).

The draft genome sequence is 2,527,127 bp long, assembled into 57 contigs, with an N_{50} value of 98,169 bp and 66.75× coverage. The GC content of the assembled genome is 32.1%, which is consistent with that of other publicly available *S. epidermidis* genomes. PGAP

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

Address correspondence to Catherine Putonti, cputonti@luc.edu.

The authors declare a conflict of interest.

Received 11 September 2022
Accepted 28 October 2022
Published 10 November 2022

annotations included 2,296 genes total, 2,296 encoding proteins, and 56 tRNAs. No antibiotic resistance genes were found within the genome assembly using ResFinder v4.1 (11). PHASTER analysis of the draft genome found one incomplete and one intact prophage (12). When queried against the nonredundant/nucleotide (nr/nt) database via MegaBLAST, the intact prophage sequence, 55.1 kbp, most closely resembled metagenome assemblies of phages. Despite high percent identities (>90%), these hits often had low query coverage (10 to 63%). When queried against the refseq_genome database of viruses using MegaBLAST, the greatest sequence similarity was to the characterized *Staphylococcus* phage vB_SepiS-phiIPLA5 (GenBank accession no. NC_018281.1) (query coverage, 15%; identity, 93.62%).

Data availability. This whole-genome shotgun project has been deposited at GenBank under the accession no. JANRMH000000000. The version described in this paper is the first version, JANRMH010000000. The raw sequencing reads have been deposited in the SRA under the accession no. SRR21102740.

ACKNOWLEDGMENTS

For prior participant recruitment, we acknowledge the Loyola Urinary Education and Research Collaborative (LUEREC) and the participant who provided the sample for this study. S.J. is funded by the Carbon Research Fellowship (Loyola University Chicago).

REFERENCES

1. Otto M. 2009. *Staphylococcus epidermidis*—the "accidental" pathogen. Nat Rev Microbiol 7:555–567. https://doi.org/10.1038/nrmicro2182.
2. Walker JN, Flores-Mireles AL, Lynch AJL, Pinkner C, Caparon MG, Hultgren SJ, Desai A. 2020. High-resolution imaging reveals microbial biofilms on patient urinary catheters despite antibiotic administration. World J Urol 38:2237–2245. https://doi.org/10.1007/s00345-019-03027-8.
3. Fey PD, Olson ME. 2010. Current concepts in biofilm formation of *Staphylococcus epidermidis*. Future Microbiol 5:917–933. https://doi.org/10.2217/fmb.10.56.
4. O'Gara JP, Humphreys H. 2001. *Staphylococcus epidermidis* biofilms: importance and implications. J Med Microbiol 50:582–587. https://doi.org/10.1099/0022-1317-50-7-582.
5. Lozano V, Fernandez G, Spencer PL, Taylor SL, Hatch R. 2015. *Staphylococcus epidermidis* in urine is not always benign: a case report of pyelonephritis in a child. J Am Board Fam Med 28:151–153. https://doi.org/10.3122/jabfm.2015.01.140118.
6. Price TK, Dune T, Hilt EE, Thomas-White KJ, Kliethermes S, Brincat C, Brubaker L, Wolfe AJ, Mueller ER, Schreckenberger PC. 2016. The clinical urine culture: enhanced techniques improve detection of clinically relevant microorganisms. J Clin Microbiol 54:1216–1222. https://doi.org/10.1128/JCM.00044-16.
7. Hilt EE, McKinley K, Pearce MM, Rosenfeld AB, Zilliox MJ, Mueller ER, Brubaker L, Gai X, Wolfe AJ, Schreckenberger PC. 2014. Urine is not sterile: use of enhanced urine culture techniques to detect resident bacterial flora in the adult female bladder. J Clin Microbiol 52:871–876. https://doi.org/10.1128/JCM.02876-13.
8. Truckenbrod A, Miller-Ensminger T, Voukadinova A, Wolfe AJ, Putonti C. 2020. Draft genome sequence of *Staphylococcus epidermidis* UMB8493, isolated from the female urinary tract. Microbiol Resour Announc 9:e00419-20. https://doi.org/10.1128/MRA.00419-20.
9. Bankevich A, Nurk S, Antipov D, Gurevich AA, Dvorkin M, Kulikov AS, Lesin VM, Nikolenko SI, Pham S, Prjibelski 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.
10. Tatusova T, DiCuccio M, Badretdin A, Chetvernin V, Nawrocki EP, Zaslavsky L, Lomsadze A, Pruitt KD, Borodovsky M, Ostell J. 2016. NCBI Prokaryotic Genome Annotation Pipeline. Nucleic Acids Res 44:6614–6624. https://doi.org/10.1093/nar/gkw569.
11. Bortolaia V, Kaas RS, Ruppe E, Roberts MC, Schwarz S, Cattoir V, Philippon A, Allesoe RL, Rebelo AR, Florensa AF, Fagelhauer L, Chakraborty T, Neumann B, Werner G, Bender JK, Stingl K, Nguyen M, Coppens J, Xavier BB, Malhotra-Kumar S, Westh H, Pinholt M, Anjum MF, Duggett NA, Kempf I, Nykäsenoja S, Olkkola S, Wieczorek K, Amaro A, Clemente L, Mossong J, Losch S, Ragimbeau C, Lund O, Aarestrup FM. 2020. ResFinder 4.0 for predictions of phenotypes from genotypes. J Antimicrob Chemother 75:3491–3500. https://doi.org/10.1093/jac/dkaa345.
12. Arndt D, Grant JR, Marcu A, Sajed T, Pon A, Liang Y, Wishart DS. 2016. PHASTER: a better, faster version of the PHAST phage search tool. Nucleic Acids Res 44:W16–W21. https://doi.org/10.1093/nar/gkw387.