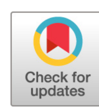
GENOME SEQUENCES



Draft Genome Sequence of Novel *Staphylococcus epidermidis* Strain EVL2000, Exhibiting Pathogenicity against *Caenorhabditis elegans*

Nathan Do,[a] Brian D. Ackley,[a] Patrick Lansdon[a]

[a]Department of Molecular Biosciences, University of Kansas, Lawrence, Kansas, USA

ABSTRACT *Staphylococcus epidermidis* is a frequent cause of nosocomial infections occurring after the insertion of indwelling medical devices. Here, we report the 2.5-Mb draft genome of *S. epidermidis* strain EVL2000, which was identified during an examination of nematode susceptibility to microbial pathogens.

Long considered a benign colonizer of skin and mucous membranes, *Staphylococcus epidermidis* is now one of the most frequent causes of nosocomial infections during the insertion of indwelling medical devices (1–6). *S. epidermidis* strains exhibit significant genomic diversity regarding virulence and host modulatory factors, allowing isolates to adapt to and persist in their ecological niches (7, 8). Thus, whole-genome sequencing, assembly, and annotation of novel *S. epidermidis* strains will improve our understanding of *S. epidermidis* as both a pathogen and a member of the microflora.

While examining *Caenorhabditis elegans* susceptibility to microbial pathogens, we serendipitously cultured a bacterial contaminant from nematode growth medium (NGM) plates that exhibited remarkable differences in nematocidal activity in two genetically diverged *C. elegans* wild isolates (9). The strain was streaked on a Luria-Bertani (LB) agar plate and incubated at 37°C for 24 h. A single colony was grown in low-salt LB medium at 37°C for 24 h with gentle shaking. DNA was extracted using a QIAquick miniprep column (Qiagen). Universal primers 27F and 1492R were used to amplify the 16S rRNA region, and the resulting Sanger sequencing product was aligned to *Staphylococcus epidermidis*. We provided the strain with the designation EVL2000.

For whole-genome sequencing, DNA was extracted from liquid culture using a DNeasy blood and tissue kit (Qiagen) following a modified manufacturer's protocol for Gram-positive microorganisms, with increases in lysozyme concentration (40 mg/mL) and incubation times for lysozyme (2 h) and proteinase K (3 h). The quantity and quality of extracted DNA were assessed using a Qubit 2.0 fluorometer (Invitrogen) and an Agilent TapeStation 2200 (Agilent), respectively. Library preparation and sequencing were performed by the Genome Sequencing Core at the University of Kansas (KU). The DNA library was prepared using Illumina Nextera chemistry following the manufacturer's instructions and was sequenced on the Illumina MiSeq platform with the Illumina v2 reagent kit using the paired-end protocol (2×150 bp). Sequencing yielded 1,398,550 reads with $85\times$ coverage.

Reads were quality checked with FastQC v0.11.9 (10). Trimming was performed using fastp v0.20.0 with the --correction flag enabled to remove Illumina adapter sequences and low-quality reads with Phred scores of <30 (11). Trimmed reads were *de novo* assembled using SPAdes v3.13.1 with kmers set to 21, 33, 55, and 77 and the --only-assembler and --careful flags enabled (12). Contigs of <200 bp were removed, and QUAST v5.0.2 was used to evaluate the genome assembly (13). The assembled genome contained 100 contigs (>200 bp), was 2,509,527 bp in size, and had a GC content of 31.96% and an N_{50} value of 105,624 bp. Annotation of the *S. epidermidis*

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

Copyright © 2022 Do et al. This is an open-access article distributed under the terms of the Creative Commons Attribution 4.0 International license.

Address correspondence to Patrick Lansdon, patrick_lansdon@ku.edu.

The authors declare no conflict of interest.

Received 28 December 2021
Accepted 26 February 2022
Published 14 March 2022

EVL2000 genome assembly using the NCBI Prokaryotic Genome Annotation Pipeline (PGAP) v6.0 identified 2,449 genes, with 2,313 protein-coding sequences, 68 pseudogenes, and 68 RNAs (7 rRNAs, 57 tRNAs, and 4 noncoding RNAs) (14).

Data availability. The whole-genome sequence of *S. epidermidis* EVL2000 has been deposited in DDBJ/ENA/GenBank under the accession number JAJSYT000000000. The version described in this paper is JAJSYT010000000. Raw reads have been deposited in the Sequence Read Archive (SRA) under the accession number SRR17282514.

ACKNOWLEDGMENTS

N.D. received support from a Kansas-INBRE semester scholar award (grant P20GM103418). B.D.A. was partially supported by an award from the KU Center for Chemical Biology of Infectious Diseases (grant P20GM113117). P.L. received grant support from an NIH IRACDA award (grant K12GM63651) and a Kansas-INBRE postdoctoral award (grant P20GM103418). The KU Genome Sequencing Core is partially supported by the KU Center for the Molecular Analysis of Disease Pathways (grant P20GM103638).

B.D.A. and P.L. designed and conceived the project, N.D. and P.L. acquired data, and N.D., B.D.A., and P.L. analyzed and interpreted data and wrote the manuscript. All authors approved the manuscript.

REFERENCES

1. Byrd AL, Belkaid Y, Segre JA. 2018. The human skin microbiome. Nat Rev Microbiol 16:143–155. https://doi.org/10.1038/nrmicro.2017.157.
2. Chu VH, Miro JM, Hoen B, Cabell CH, Pappas PA, Jones P, Stryjewski ME, Anguera I, Braun S, Munoz P, Commerford P, Tornos P, Francis J, Oyonarte M, Selton-Suty C, Morris AJ, Habib G, Almirante B, Sexton DJ, Corey GR, Fowler VG, Jr. 2009. Coagulase-negative staphylococcal prosthetic valve endocarditis: a contemporary update based on the International Collaboration on Endocarditis: prospective cohort study. Heart 95:570–576. https://doi.org/10.1136/hrt.2008.152975.
3. Namvar AE, Bastarahang S, Abbasi N, Ghehi GS, Farhadbakhtiarian S, Arezi P, Hosseini M, Baravati SZ, Jokar Z, Chermahin SG. 2014. Clinical characteristics of *Staphylococcus epidermidis*: a systematic review. GMS Hyg Infect Control 9:Doc23. https://doi.org/10.3205/dgkh000243.
4. Oliveira WF, Silva PMS, Silva RCS, Silva GMM, Machado G, Coelho L, Correia MTS. 2018. *Staphylococcus aureus* and *Staphylococcus epidermidis* infections on implants. J Hosp Infect 98:111–117. https://doi.org/10.1016/j.jhin.2017.11.008.
5. Otto M. 2009. *Staphylococcus epidermidis*: the 'accidental' pathogen. Nat Rev Microbiol 7:555–567. https://doi.org/10.1038/nrmicro2182.
6. Santarpia L, Buonomo A, Pagano MC, Alfonsi L, Foggia M, Mottola M, Marinosci GZ, Contaldo F, Pasanisi F. 2016. Central venous catheter related bloodstream infections in adult patients on home parenteral nutrition: prevalence, predictive factors, therapeutic outcome. Clin Nutr 35:1394–1398. https://doi.org/10.1016/j.clnu.2016.03.009.
7. Zhou W, Spoto M, Hardy R, Guan C, Fleming E, Larson PJ, Brown JS, Oh J. 2020. Host-specific evolutionary and transmission dynamics shape the functional diversification of *Staphylococcus epidermidis* in human skin. Cell 180:454–470.e18. https://doi.org/10.1016/j.cell.2020.01.006.
8. Conlan S, Mijares LA, Program NCS, Becker J, Blakesley RW, Bouffard GG, Brooks S, Coleman H, Gupta J, Gurson N, Park M, Schmidt B, Thomas PJ, Otto M, Kong HH, Murray PR, Segre JA, NISC Comparative Sequencing Program. 2012. *Staphylococcus epidermidis* pan-genome sequence analysis reveals diversity of skin commensal and hospital infection-associated isolates. Genome Biol 13:R64. https://doi.org/10.1186/gb-2012-13-7-r64.
9. Lansdon P, Carlson M, Ackley BD. 2021. Wild-type *Caenorhabditis elegans* isolates exhibit distinct gene expression profiles in response to microbial infection. bioRxiv 2021.10.16.464663. https://doi.org/10.1101/2021.10.16.464663.
10. Andrews S. 2010. FastQC: a quality control tool for high throughput sequence data. https://www.bioinformatics.babraham.ac.uk/projects/fastqc.
11. Chen S, Zhou Y, Chen Y, Gu J. 2018. fastp: an ultra-fast all-in-one FASTQ preprocessor. Bioinformatics 34:i884–i890. https://doi.org/10.1093/bioinformatics/bty560.
12. 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.
13. Gurevich A, Saveliev V, Vyahhi N, Tesler G. 2013. QUAST: quality assessment tool for genome assemblies. Bioinformatics 29:1072–1075. https://doi.org/10.1093/bioinformatics/btt086.
14. Li W, O'Neill KR, Haft DH, DiCuccio M, Chetvernin V, Badretdin A, Coulouris G, Chitsaz F, Derbyshire MK, Durkin AS, Gonzales NR, Gwadz M, Lanczycki CJ, Song JS, Thanki N, Wang J, Yamashita RA, Yang M, Zheng C, Marchler-Bauer A, Thibaud-Nissen F. 2021. RefSeq: expanding the Prokaryotic Genome Annotation Pipeline reach with protein family model curation. Nucleic Acids Res 49:D1020–D1028. https://doi.org/10.1093/nar/gkaa1105.