9-7-2017

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Comments

This is an article published by American Society for Microbiology in Genome Announcements in 2017, available online: https://dx.doi.org/10.1128/genomeA.00954-17

Recommended Citation

MacLea, K.S. and Trachtenberg, A.M. Complete Genome Sequence of Staphylococcus epidermidis ATCC 12228 Chromosome and Plasmids Generated by Long-Read Sequencing. Genome Announc, 5:e00954-17; doi:10.1128/genomeA.00954-17, 2017.

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PROKARYOTES

Complete Genome Sequence of *Staphylococcus epidermidis* ATCC 12228 Chromosome and Plasmids, Generated by Long-Read Sequencing

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ABSTRACT *Staphylococcus epidermidis* ATCC 12228 was sequenced using a long-read method to generate a complete genome sequence, including some plasmid sequences. Some differences from the previously generated short-read sequence of this nonpathogenic and non-biofilm-forming strain were noted. The assembly size was 2,570,371 bp with a total G+C% content of 32.08%.

Received 28 July 2017 **Accepted** 7 August 2017 **Published** 7 September 2017

Citation MacLea KS, Trachtenberg AM. 2017. Complete genome sequence of *Staphylococcus epidermidis* ATCC 12228 chromosome and plasmids, generated by long-read sequencing. Genome Announc 5: e00954-17. https://doi.org/10.1128/genomeA.00954-17.

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Among the Gram-positive staphylococci, *Staphylococcus aureus* is the most well-known pathogen, contributing to dangerous human and animal infections, including septicemia, as well as foodborne intoxication. Among other members of the genus, some strains of the common human skin bacterium *Staphylococcus epidermidis* are associated with serious nosocomial infections (1), and others, such as *S. epidermidis* ATCC 12228, are common commensals not associated with pathogenicity (2). Many genome sequences are available for *S. epidermidis*, with 389 previously reported in GenBank, of which 11 were complete genome sequences generated with short-read methods, such as the Illumina platform, or long-read sequencing methodologies, such as the PacBio platform (3–5). Here, we report the first sequence generated for *S. epidermidis* ATCC 12228 using long-read technology after its initial report using a short-read method in 2003 (2).

S. epidermidis 12228 was obtained from Thermo Fisher Scientific in lyophilized form and rehydrated, and a culture was grown from an isolated colony on a tryptic soy agar plate in tryptic soy broth at 30°C for 72 h. The Genomic-tip 500/G kit (Qiagen, Valencia, CA, USA) was used according to the manufacturer's instructions to isolate genomic DNA (gDNA). Purified gDNA of *S. epidermidis* 12228 was sequenced at the Institute for Genome Studies, University of Maryland, on a single PacBio (Pacific Biosciences, Menlo Park, CA, USA) RS II P6-C4 single-molecule real-time (SMRT) cell using a PacBio long-insert library after size selection to capture both plasmid and main chromosome sequences. The sequencing run resulted in a total of 155,545 long reads with a mean length of 6,023 bp, which represented an approximately 25-fold sequence coverage after read assembly. The generated genome size was 2,570,371 bp split into 6 contigs: the main chromosome of 2,497,508 bp and plasmids of 37,770 bp (pAMT1), 23,530 bp (pAMT2), 7,554 bp (pAMT3), 2,390 bp (pAMT4), and 1,619 bp (pAMT5). The G+C content of 32.08% was very close to the 32.1% determined by Illumina sequencing of the *S. epidermidis* 12228 genome (2).

Assembly of the genome was undertaken using the Celera version 8.1 assembler. Annotation of the genome used the NCBI Prokaryotic Genome Annotation Pipeline process (6), identifying a total of 2,545 genes, 2,462 coding sequences, 83 RNA genes (7 copies of 5S rRNAs, 6 of 16S rRNAs, 6 of 23S rRNAs, 60 tRNAs, and 4 noncoding RNAs),

and 85 pseudogenes. Although this new assembly did not capture as many plasmids (5 versus 6) and generated a slightly smaller main chromosome (2,497,508 versus 2,564,615 bp) than the original Illumina assembly of *S. epidermidis* ATCC 12228 (2), it did reveal more of each of the categories of genes described above. This new long-read complete sequence provides an additional high-quality closed genome sequence for *S. epidermidis* ATCC 12228 that should be useful for better understanding the ability of some strains of *S. epidermidis* to cause disease in humans and animals or to adapt as commensal organisms.

Accession number(s). This whole-genome project has been deposited at DDBJ/ENA/GenBank under the accession numbers CP022247 to CP022252.

ACKNOWLEDGMENTS

Sequencing was undertaken at the Institute for Genome Studies at the University of Maryland (http://www.igs.umaryland.edu) with the assistance of Luke Tallon and Lisa Sadzewicz. K.S.M. kindly thanks Holly MacLea for her efforts in 2017 to further this research. 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 sequencing. The funders played no role in study design, data collection, or interpretation or the decision to submit the work for publication.

REFERENCES

1. Rupp ME. 2014. Clinical characteristics of infections in humans due to *Staphylococcus epidermidis*. Methods Mol Biol 1106:1–16. https://doi.org/10.1007/978-1-62703-736-5_1.
2. Zhang YQ, Ren SX, Li HL, Wang YX, Fu G, Yang J, Qin ZQ, Miao YG, Wang WY, Chen RS, Shen Y, Chen Z, Yuan ZH, Zhao GP, Qu D, Danchin A, Wen YM. 2003. Genome-based analysis of virulence genes in a non-biofilm-forming *Staphylococcus epidermidis* strain (ATCC 12228). Mol Microbiol 49:1577–1593. https://doi.org/10.1046/j.1365-2958.2003.03671.x.
3. Christensen GJM, Scholz CFP, Enghild J, Rohde H, Kilian M, Thürmer A, Brzuszkiewicz E, Lomholt HB, Brüggemann H. 2016. Antagonism between *Staphylococcus epidermidis* and *Propionibacterium acnes* and its genomic basis. BMC Genomics 17:152. https://doi.org/10.1186/s12864-016-2489-5.
4. Gill SR, Fouts DE, Archer GL, Mongodin EF, DeBoy RT, Ravel J, Paulsen IT, Kolonay JF, Brinkac L, Beanan M, Dodson RJ, Daugherty SC, Madupu R, Angiuoli SV, Durkin AS, Haft DH, Vamathevan J, Khouri H, Utterback T, Lee C, Dimitrov G, Jiang L, Qin H, Weidman J, Tran K, Kang K, Hance IR, Nelson KE, Fraser CM. 2005. Insights on evolution of virulence and resistance from the complete genome analysis of an early methicillin-resistant *Staphylococcus aureus* strain and a biofilm-producing methicillin-resistant *Staphylococcus epidermidis* strain. J Bacteriol 187:2426–2438. https://doi.org/10.1128/JB.187.7.2426-2438.2005.
5. Galac MR, Stam J, Maybank R, Hinkle M, Mack D, Rohde H, Roth AL, Fey PD. 2017. Complete genome sequence of *Staphylococcus epidermidis* 1457. Genome Announc 5(22):e00450-17. https://doi.org/10.1128/genomeA.00450-17.
6. Tatusova T, DiCuccio M, Badretdin A, Chetvernin V, Ciufo S, Li W. 2013. Prokaryotic genome annotation pipeline. *In* The NCBI handbook, 2nd ed. National Center for Biotechnology Information, Bethesda, MD.