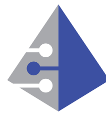
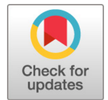
AMERICAN SOCIETY FOR MICROBIOLOGY



Microbiology Resource Announcements

GENOME SEQUENCES



Complete Genome Sequence of *Serratia marcescens* Siphophage Scapp

Brian T. Koehler,[a] Helena Hopson,[a] Rohit Kongari,[a] Rachele Bonasera,[a] Adriana C. Hernandez-Morales,[a] Mei Liu[a]

[a]Center for Phage Technology, Texas A&M University, College Station, Texas, USA

ABSTRACT *Serratia marcescens* is an opportunistic pathogen that typically infects the respiratory and urinary tract, with the majority of cases being hospital acquired. The study of *S. marcescens* phages may help control drug-resistant *S. marcescens* strains. In this study, we announce the complete genome sequence and the features of *S. marcescens* siphophage Scapp.

Serratia marcescens is an opportunistic pathogen that typically infects the respiratory and urinary tract, with the majority of cases being hospital acquired (1–3). Many strains of *S. marcescens* identified in intensive care unit patients in U.S. hospitals possess resistance to most available antibiotics (4). The study of *S. marcescens* phages may help control drug-resistant *S. marcescens* strains.

The siphophage Scapp was isolated using an *S. marcescens* strain from activated sludge collected from the water treatment plant in College Station, TX. Host bacteria were cultured on nutrient broth or agar (Difco) at 37°C with aeration. Phages were isolated and propagated by the soft agar overlay method (5). Phage genomic DNA was prepared using a modified Promega Wizard DNA cleanup kit protocol, as described previously (6). Pooled indexed DNA libraries were prepared using the Illumina TruSeq Nano low-throughput (LT) kit, and the sequence was obtained by the Illumina MiSeq platform using the MiSeq v2 500-cycle reagent kit, following the manufacturer's instructions, producing 447,621 paired-end reads for the index containing the phage genome. The quality of the reads was checked in FastQC 0.11.5 (https://www.bioinformatics.babraham.ac.uk/projects/fastqc/), and reads were trimmed with the FastX-Toolkit 0.0.14 (http://hannonlab.cshl.edu/fastx_toolkit/) and assembled in SPAdes 3.5.0 (7). The assembled genome was closed by PCR using primers 5′-AAACAACGGAGTGGGAAGAG-3′ and 5′-CAGGGTCTATCACGCAGTAAAT-3′ facing away from the center of the assembled contig and by Sanger sequencing of the resulting product, with the contig sequence manually corrected to match the resulting Sanger sequencing read. Protein-coding genes were predicted using Glimmer 3.0 (8) and MetaGeneAnnotator 1.0 (9) and corrected manually if needed. The tRNA genes were predicted using ARAGORN 2.36 (10). Protein functions were predicted by comparing sequence homology to proteins found using BLASTp 2.2.28 (11), and conserved domains were analyzed using InterProScan 5.15-5.40 (12). All analyses were performed under default settings using the CPT Galaxy (13) and WebApollo (14) interfaces (cpt.tamu.edu).

The complete 42,969-bp Scapp genome was assembled at 192.1-fold coverage. It has 59 protein-coding genes, an overall coding density of 93%, and a GC content of 56%. Using the progressiveMAUVE algorithm (v2.4.0) (15), Scapp shows less than 20% DNA sequence similarity to any other phage in the NCBI nucleotide (nt) database. The Scapp genome begins with an ~6,000-bp region that contains novel genes with no sequence similarity to other proteins in the NCBI nonredundant (nr) database. At the protein level, phage Scapp is most closely related to phages APSE-2 (GenBank accession number EU794049) and a prophage-like element (GenBank accession number

Citation Koehler BT, Hopson H, Kongari R, Bonasera R, Hernandez-Morales AC, Liu M. 2019. Complete genome sequence of *Serratia marcescens* siphophage Scapp. Microbiol Resour Announc 8:e00417-19. https://doi.org/10.1128/MRA.00417-19.

Editor John J. Dennehy, Queens College

Copyright © 2019 Koehler et al. This is an open-access article distributed under the terms of the Creative Commons Attribution 4.0 International license.

Address correspondence to Mei Liu, meiliu@tamu.edu.

Received 8 April 2019
Accepted 15 April 2019
Published 9 May 2019

HQ377374) associated with insect symbionts. Some of the structural proteins of phage Scapp are related to common enterobacterial siphophage proteins (BLASTp E value, $\leq 10^{-3}$), such as those found in phages N15, T1, and Lambda. These genes include those encoding head assembly, major capsid, tape measure, major tail, tail tip, and four minor tail proteins. An endonuclease, a transcriptional regulator, and a transposase are located next to the lysis cassette but do not interrupt any genes. An adjacent holin-antiholin pair and an endolysin (D-alanyl-D-alanine carboxypeptidase) were identified. The o-spanin is embedded in the i-spanin, and this spanin complex is located separately from the other lysis genes.

Data availability. The genome sequence of phage Scapp was deposited under GenBank accession number MH553517. The associated BioProject, SRA, and BioSample accession numbers are PRJNA222858, SRR8788475, and SAMN11259833, respectively.

ACKNOWLEDGMENTS

This work was supported by funding from the National Science Foundation (awards EF-0949351 and DBI-1565146). Additional support came from the Center for Phage Technology (CPT), an Initial University Multidisciplinary Research Initiative supported by Texas A&M University and Texas AgriLife, and from the Department of Biochemistry and Biophysics at Texas A&M University.

We are grateful for the advice and support of the CPT staff.

This announcement was prepared in partial fulfillment of the requirements for BICH464 Phage Genomics, an undergraduate course at Texas A&M University.

REFERENCES

1. Khanna A, Khanna M, Aggarwal A. 2013. *Serratia marcescens*—a rare opportunistic nosocomial pathogen and measures to limit its spread in hospitalized patients. J Clin Diagn Res 7:243–246. https://doi.org/10.7860/JCDR/2013/5010.2737.
2. Jones RN. 2010. Microbial etiologies of hospital-acquired bacterial pneumonia and ventilator-associated bacterial pneumonia. Clin Infect Dis 51:S81–S87. https://doi.org/10.1086/653053.
3. Kawecki D, Kwiatkowski A, Sawicka-Grzelak A, Durlik M, Paczek L, Chmura A, Mlynarczyk G, Rowinski W, Luczak M. 2011. Urinary tract infections in the early posttransplant period after kidney transplantation: etiologic agents and their susceptibility. Transplant Proc 43:2991–2993. https://doi.org/10.1016/j.transproceed.2011.09.002.
4. Lockhart SR, Abramson MA, Beekmann SE, Gallagher G, Riedel S, Diekema DJ, Quinn JP, Doern GV. 2007. Antimicrobial resistance among Gram-negative bacilli causing infections in intensive care unit patients in the United States between 1993 and 2004. J Clin Microbiol 45:3352–3359. https://doi.org/10.1128/JCM.01284-07.
5. Adams MK. 1959. Bacteriophages. Interscience Publishers, Inc., New York, NY.
6. Summer EJ. 2009. Preparation of a phage DNA fragment library for whole genome shotgun sequencing. Methods Mol Biol 502:27–46. https://doi.org/10.1007/978-1-60327-565-1_4.
7. 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.
8. Delcher AL, Harmon D, Kasif S, White O, Salzberg SL. 1999. Improved microbial gene identification with GLIMMER. Nucleic Acids Res 27:4636–4641. https://doi.org/10.1093/nar/27.23.4636.
9. Noguchi H, Taniguchi T, Itoh T. 2008. MetaGeneAnnotator: detecting species-specific patterns of ribosomal binding site for precise gene prediction in anonymous prokaryotic and phage genomes. DNA Res 15:387–396. https://doi.org/10.1093/dnares/dsn027.
10. Laslett D, Canback B. 2004. ARAGORN, a program to detect tRNA genes and tmRNA genes in nucleotide sequences. Nucleic Acids Res 32:11–16. https://doi.org/10.1093/nar/gkh152.
11. Camacho C, Coulouris G, Avagyan V, Ma N, Papadopoulos J, Bealer K, Madden TL. 2009. BLAST+: architecture and applications. BMC Bioinformatics 10:421. https://doi.org/10.1186/1471-2105-10-421.
12. Jones P, Binns D, Chang HY, Fraser M, Li W, McAnulla C, McWilliam H, Maslen J, Mitchell A, Nuka G, Pesseat S, Quinn AF, Sangrador-Vegas A, Scheremetjew M, Yong SY, Lopez R, Hunter S. 2014. InterProScan 5: genome-scale protein function classification. Bioinformatics 30:1236–1240. https://doi.org/10.1093/bioinformatics/btu031.
13. Cock PJ, Gruning BA, Paszkiewicz K, Pritchard L. 2013. Galaxy tools and workflows for sequence analysis with applications in molecular plant pathology. PeerJ 1:e167. https://doi.org/10.7717/peerj.167.
14. Lee E, Helt GA, Reese JT, Munoz-Torres MC, Childers CP, Buels RM, Stein L, Holmes IH, Elsik CG, Lewis SE. 2013. Web Apollo: a web-based genomic annotation editing platform. Genome Biol 14:R93. https://doi.org/10.1186/gb-2013-14-8-r93.
15. Darling AE, Mau B, Perna NT. 2010. progressiveMauve: multiple genome alignment with gene gain, loss and rearrangement. PLoS One 5:e11147. https://doi.org/10.1371/journal.pone.0011147.