

Complete genome sequence of strain SS-5, a magnetotactic gammaproteobacterium isolated from the Salton Sea, a shallow, saline, endorheic Rift Lake located on the San Andreas Fault in California

Denis Trubitsyn, Caroline Monteil, Corey Geurink, Viviana Morillo-Lopez, Luiz Gonzaga Paula de Almeida, Ana Tereza Ribeiro de Vasconcelos, Fernanda Abreu, Dennis Bazylinski, Christopher T. Lefèvre

▶ **To cite this version:**

Denis Trubitsyn, Caroline Monteil, Corey Geurink, Viviana Morillo-Lopez, Luiz Gonzaga Paula de Almeida, et al.. Complete genome sequence of strain SS-5, a magnetotactic gammaproteobacterium isolated from the Salton Sea, a shallow, saline, endorheic Rift Lake located on the San Andreas Fault in California. Microbiology Resource Announcements, 2021, 10 (1), pp.e00928-20. 10.1128/mra.00928-20 . hal-03336923

HAL Id: hal-03336923
https://hal.science/hal-03336923

Submitted on 9 Sep 2021

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.



Distributed under a Creative Commons Attribution 4.0 International License

AMERICAN SOCIETY FOR MICROBIOLOGY | Microbiology Resource Announcements

GENOME SEQUENCES

Complete Genome Sequence of Strain SS-5, a Magnetotactic Gammaproteobacterium Isolated from the Salton Sea, a Shallow, Saline, Endorheic Rift Lake Located on the San Andreas Fault in California

Denis Trubitsyn,[a] Caroline L. Monteil,[b] Corey Geurink,[c] Viviana Morillo-Lopez,[c] Luiz Gonzaga Paula de Almeida,[d] Ana Tereza Ribeiro de Vasconcelos,[d] Fernanda Abreu,[e] Dennis A. Bazylinski,[c] Christopher T. Lefevre[b]

[a]Department of Biological and Environmental Sciences, Longwood University, Farmville, Virginia, USA
[b]Aix-Marseille University, CNRS, CEA, UMR7265 Biosciences and Biotechnologies Institute of Aix-Marseille, Saint Paul lez Durance, France
[c]School of Life Sciences, University of Nevada Las Vegas, Las Vegas, Nevada, USA
[d]Laboratório Nacional de Computação Científica, Petrópolis, Brazil
[e]Instituto de Microbiologia Paulo de Goes, Universidade Federal do Rio de Janeiro-UFRJ, Rio de Janeiro, Brazil

ABSTRACT We report the 3.7-Mb genome sequence of strain SS-5, a magnetotactic, sulfur-oxidizing rod and member of the family *Chromatiaceae* of the class *Gammaproteobacteria*, which biomineralizes membrane-bound, elongated, prismatic octahedral, magnetite nanocrystals. This genome sequence brings further diversity for understanding the origin and evolution of magnetotaxis and magnetosome biomineralization.

Magnetotactic bacteria (MTB) biomineralize membrane-bound magnetic nanocrystals to form bacterial organelles, the so-called magnetosomes (1). The formation and arrangement of magnetosomes within these cells are genetically controlled (2, 3). The magnetosome chain allows MTB to passively align along geomagnetic field lines as they swim (4). MTB are not represented in a well-defined taxonomic group of prokaryotes but, instead, are distributed over several bacterial taxa (5, 6).

Here, we report the genome sequence of the magnetotactic gammaproteobacterium strain SS-5, isolated from a sediment sample of the Salton Sea in California (7). DNA was extracted from a 2-liter pure culture of cells grown autotrophically (7) using the standard phenol-chloroform assay. All kits were used according to the manufacturers' standard recommendations. A Clean & Concentrator (Zymo Research) kit was used for DNA purification. DNA quality was confirmed with the Agilent Bioanalyzer system, and samples were quantified with a Qubit v2.0 fluorometer. Libraries were prepared according to the manufacturer's standard protocol using a GS FLX Titanium 3-kb span paired-end library kit. 454 genome sequences were obtained in one run on the GS FLX system sequencer (Roche) with average read lengths of 216 bp. Sequence duplicates were removed using the cd-hit v4.6.1 algorithm (8). All remaining 595,403 reads (234,621,138 bp, 63× coverage) were used for assembly. The assembly performed with Newbler v2.6 (Roche) (9) using default parameters resulted in 9 scaffolds (N_{50}, 1,196,217 bp). Gap closure was completed using a previously published procedure (10). The genome was rotated, and the *dnaA* gene was positioned close to the beginning of the consensus sequence. The completed genome of SS-5 was annotated using PGAP (11) and consists of 3,729,439 bp with a G+C content of 61.6%: 3,223 predicted coding DNA sequences, 51 tRNAs, and two identical sets of 5S/16S/23S rRNAs.

Strain SS-5 is a member of the *Gammaproteobacteria* that was originally determined to belong to the order *Chromatiales* (7). The average amino acid identity (two-way AAI)

Citation Trubitsyn D, Monteil CL, Geurink C, Morillo-Lopez V, Gonzaga Paula de Almeida L, Ribeiro de Vasconcelos AT, Abreu F, Bazylinski DA, Lefevre CT. 2021. Complete genome sequence of strain SS-5, a magnetotactic gammaproteobacterium isolated from the Salton Sea, a shallow, saline, endorheic rift lake located on the San Andreas Fault in California. Microbiol Resour Announc 10:e00928-20. https://doi.org/10.1128/MRA.00928-20.

Editor J. Cameron Thrash, University of Southern California

Copyright © 2021 Trubitsyn et al. This is an open-access article distributed under the terms of the Creative Commons Attribution 4.0 International license.

Address correspondence to Christopher T. Lefevre, christopher.lefevre@cea.fr.

Received 5 August 2020
Accepted 20 November 2020
Published 7 January 2021

Downloaded from https://journals.asm.org/journal/mra on 09 September 2021 by 147.94.135.30.

between SS-5 and its closest neighbors (identified by phylogenetic reconstruction of all available genomes of *Gammaproteobacteria* type strains) was estimated with the enveomics collection toolbox using default parameters (12). SS-5 did not get a higher AAI value than 55.67% with other *Chromatiaceae* members (the best score was with *Allochromatium vinosum* DSM 180; GenBank accession number NC_013851). As a newly identified member of the *Gammaproteobacteria*, this strain will provide a valuable resource for further characterizing the metabolic potential of this group. For instance, the genes necessary for magnetosome formation were found to be present in the genome of SS-5 (13). Thus, this closed genome will provide the opportunity to further elucidate the origin and evolution of magnetotaxis.

Data availability. The SS-5 genome sequence has been deposited in GenBank under BioProject number PRJNA491989 and BioSample number SAMN10093509. The genomic raw sequencing reads are available in the Sequence Read Archive (SRA) database under accession number CP032508.1.

ACKNOWLEDGMENTS

This work was supported by a U.S. NSF grant (EAR-1423939) and by the French National Research Agency (SIGMAG, ANR-18-CE31-0003, and PHOSTORE, ANR-19-CE01-0005-02). The financial support from the Brazilian agencies CNPq, CAPES, and FAPERJ is acknowledged.

REFERENCES

1. Blakemore R. 1975. Magnetotactic bacteria. Science 190:377–379. https://doi.org/10.1126/science.170679.
2. Uebe R, Schüler D. 2016. Magnetosome biogenesis in magnetotactic bacteria. Nat Rev Microbiol 14:621–637. https://doi.org/10.1038/nrmicro.2016.99.
3. Bazylinski DA, Frankel RB. 2004. Magnetosome formation in prokaryotes. Nat Rev Microbiol 2:217–230. https://doi.org/10.1038/nrmicro842.
4. Klumpp S, Lefèvre CT, Bennet M, Faivre D. 2019. Swimming with magnets: from biological organisms to synthetic devices. Phys Rep 789:1–54. https://doi.org/10.1016/j.physrep.2018.10.007.
5. Lefèvre CT, Bazylinski DA. 2013. Ecology, diversity, and evolution of magnetotactic bacteria. Microbiol Mol Biol Rev 77:497–526. https://doi.org/10.1128/MMBR.00021-13.
6. Amor M, Mathon FP, Monteil CL, Busigny V, Lefevre CT. 2020. Iron-biomineralizing organelle in magnetotactic bacteria: function, synthesis and preservation in ancient rock samples. Environ Microbiol 22:3611–3632. https://doi.org/10.1111/1462-2920.15098.
7. Lefèvre CT, Viloria N, Schmidt ML, Pósfai M, Frankel RB, Bazylinski DA. 2012. Novel magnetite-producing magnetotactic bacteria belonging to the Gammaproteobacteria. ISME J 6:440–450. https://doi.org/10.1038/ismej.2011.97.
8. Teal TK, Schmidt TM. 2010. Identifying and removing artificial replicates from 454 pyrosequencing data. Cold Spring Harb Protoc 2010:pdb.prot5409. https://doi.org/10.1101/pdb.prot5409.
9. Margulies M, Egholm M, Altman WE, Attiya S, Bader JS, Bemben LA, Berka J, Braverman MS, Chen Y-J, Chen Z, Dewell SB, Du L, Fierro JM, Gomes XV, Godwin BC, He W, Helgesen S, Ho CH, Ho CH, Irzyk GP, Jando SC, Alenquer MLI, Jarvie TP, Jirage KB, Kim J-B, Knight JR, Lanza JR, Leamon JH, Lefkowitz SM, Lei M, Li J, Lohman KL, Lu H, Makhijani VB, McDade KE, McKenna MP, Myers EW, Nickerson E, Nobile JR, Plant R, Puc BP, Ronan MT, Roth GT, Sarkis GJ, Simons JF, Simpson JW, Srinivasan M, Tartaro KR, Tomasz A, Vogt KA, et al. 2005. Genome sequencing in microfabricated high-density picolitre reactors. Nature 437:376–380. https://doi.org/10.1038/nature03959.
10. Lima NCB, Tanmoy AM, Westeel E, de Almeida LGP, Rajoharison A, Islam M, Endtz HP, Saha SK, de Vasconcelos ATR, Komurian-Pradel F. 2019. Analysis of isolates from Bangladesh highlights multiple ways to carry resistance genes in Salmonella Typhi. BMC Genomics 20:530. https://doi.org/10.1186/s12864-019-5916-6.
11. 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.
12. Rodriguez-R LM, Konstantinidis KT. 2016. The enveomics collection: a toolbox for specialized analyses of microbial genomes and metagenomes. PeerJ Prepr 4:e1900v1. https://doi.org/10.7287/peerj.preprints.1900v1.
13. Lefèvre CT, Wu LF. 2013. Evolution of the bacterial organelle responsible for magnetotaxis. Trends Microbiol 21:534–543. https://doi.org/10.1016/j.tim.2013.07.005.

Downloaded from https://journals.asm.org/journal/mra on 09 September 2021 by 147.94.135.30.