An extremely halophilic archaeon, *Halobacterium* sp. GSL-19, was isolated from the north arm of Great Salt Lake in Utah. Single-molecule real-time (SMRT) sequencing was used to establish a GC-rich 2.3-Mbp genome composed of a circular chromosome and 2 plasmids, with 2,367 predicted genes, including 1 encoding a CTAG-methylase widely distributed among *Haloarchaea*.

Halophilic microbes capable of surviving conditions with multiple extremes are of interest for biotechnology and astrobiology (1–8). To increase our understanding of these novel microbes, an extremely halophilic archaeon, GSL-19, was isolated from brine near the shore of the north arm of the Great Salt Lake in Utah (41.4377°N, 112.6689°W), proximal to the Spiral Jetty (9).

Brine was sampled from 10 cm below the surface of the lake at 28°C, inoculated into CM+ medium (complete medium plus trace elements), and grown with shaking at 220 rpm at 37°C, as previously described (10, 11). The enrichment cultures were plated on CM+ agar plates, and the isolate, an extremely halophilic, pigmented, phase-bright haloarchaeon, was purified by 3 rounds of streaking.

Nucleic acids were extracted using standard methods for haloarchaea involving hypotonic lysis phenol extraction and ethanol precipitation, as previously described (10–12), and sequencing was performed using the PacBio Sequel platform (Pacific Biosciences, Menlo Park, CA). SMRTbell libraries were prepared from 2 μg genomic DNA sheared to 40-kbp with a Megaruptor instrument (Diagenode, Inc., Denville, NJ), New England BioLabs (NEB) reagents equivalent to the PacBio library prep kit were used (13), and the library was sequenced on a single-molecule real-time (SMRT) cell with Sequel binding kit 3.0 with 10-h collection and 2-h pre-extension times. A total of 613,574 reads were obtained (subread N50, 4,078 bp), which were filtered and assembled de novo using Hierarchical Genome Assembly Process version 4 (HGAP4) with default parameters. The final assembly comprised 3 contigs, of which all circularized automatically using HGAP4, with mean coverage of 3,924 ×.

The genome (overall GC content of 66.7%) comprises a circular chromosome (1,987,132 bp, GC content of 68%) and 2 plasmids, namely, pGSL19_284 (284,178 bp, GC content of 59.1%) and pGSL19_54.9 (54,914 bp, GC content of 61.4%). Genes were predicted in-house using GeneMark HMM (14) and analyzed with HaloWeb (https://halo.umbc.edu), tRNAscan-SE2.0, and EMBOSS version 6.6.0.0 (15–17). The genome was also deposited at NCBI, where it was independently annotated using Prokaryotic Genome Annotation Pipeline (PGAP) Build 3190 (18).

The GSL-19 genome contained 2,367 genes, including a single rRNA operon and 44 tRNA genes all carried on the chromosome. The proteome was highly acidic (19–21), with a calculated mean pI value of 4.91 (22). All 799 core haloarchaeal orthologous groups (cHOGs) were encoded in the GSL-19 genome (23). The genome contained 8 genes encoding putative transcriptional regulators.
encoding origin recognition complexes, 1 gene encoding a TATA-binding protein, and 5 genes encoding transcription factor B (24–26). A gvp gene cluster was also present, consistent with the production of gas vesicles observed as phase-bright inclinations (27, 28). Taxonomy was assigned using the 16S rRNA sequence and average nucleotide identity according to NCBI taxonomy, and the isolate has been designated *Halobacterium* sp. GSL-19 (29).

Methylated bases were determined using modification and motif analysis under the SMRTLink environment version 6.0.0.47841, revealing two methylated motifs, (m6A) GTÇÇÇAG (100%) and (m4C) ÇTAG (97.7%) (30). The CTag methyltransferase gene is widely distributed among haloarchaea, in which CTag sites are also underrepresented (31), suggesting a conserved function.

**Data availability.** The *Halobacterium* sp. GSL-19 genome sequence has been deposited in GenBank with the accession numbers CP070375.1 to CP070377.1, and raw data are available in the NCBI Sequence Read Archive with the accession number SRX10230949.

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**REFERENCES**

1. DasSarma S, DasSarma P. 2017. Halophiles. In Encyclopedia of life science. John Wiley & Sons, Ltd, Hoboken, NJ. [https://doi.org/10.1002/9780470015902.a000394.pub4](https://doi.org/10.1002/9780470015902.a000394.pub4).

2. DasSarma P, Coker JA, Huse V, DasSarma S. 2009. Microorganisms, halophiles, industrial applications, p 2769–2777. In Flickinger MC (ed), Wiley encyclopedia of industrial biotechnology, bioprocess, bioseparation, and cell technology. John Wiley and Sons, New York, NY.

3. DasSarma S, Schwietmer EW. 2021. Early evolution of purple retinal pigments on Earth and implications for exoplanet biosignatures. Int J Astrobiol 20:241–250. [https://doi.org/10.1017/S1473550418000423](https://doi.org/10.1017/S1473550418000423).

4. DasSarma P, Simões MF, Antunes A, DasSarma S. 2020. Earth’s stratosphere and microbial life. Curr Issues Mol Biol 38:197–244. [https://doi.org/10.21775/cimob.38.09.1](https://doi.org/10.21775/cimob.38.09.1).

5. DasSarma P, DasSarma S. 2018. Survival of microbes in Earth’s stratosphere. Curr Opin Microbiol 43:24–30. [https://doi.org/10.1016/j.copmi.2017.11.002](https://doi.org/10.1016/j.copmi.2017.11.002).

6. DasSarma P, Simões MF, Antunes A, DasSarma S. 2020. Earth’s stratosphere and microbial life. In Antunes A (ed), Astrobiology: current, evolving and emerging perspectives. Caister Academic Press, Norfolk, UK.

7. DasSarma S, DasSarma P, Laye VJ, Schwietmer EW. 2020. Extremophilic models for astrobiology: halarchaeal survival strategies and pigments for remote sensing. Extremophiles 24:31–41. [https://doi.org/10.1007/s00792-019-01126-3](https://doi.org/10.1007/s00792-019-01126-3).

8. Carrier BL, Beaty DW, Meyer MA, Blank JG, Chou L, DasSarma S, Des Marais DJ, Carrier BL, Beaty DW, Meyer MA, Blank JG, Chou L, DasSarma S, Des Marais DJ, S00792-019-01126-3. DasSarma S, DasSarma P, Laye VJ, Schwieterman EW. 2020. Extremophiles, industrial applications, p 2769–2777. In Flickinger MC (ed), Wiley encyclopedia of industrial biotechnology, bioprocess, bioseparation, and cell technology. John Wiley and Sons, New York, NY.

9. DasSarma S, DasSarma P, DasSarma S. 2015. Halophiles and their enzymes: negativity put to next? Conference report. Astrobiology 20:785. [https://doi.org/10.1089/ast.2015.2237](https://doi.org/10.1089/ast.2015.2237).

10. Chianese R. 2013. How green is Earth art? Spiral Jetty. Am Sci 101:20–21. [https://doi.org/10.1177/0003130X13510143](https://doi.org/10.1177/0003130X13510143).

11. Becker BR, Müller JA, DasSarma S. 2006. Genetic systems for halophilic archaea. Methods Microbiol 35:649–680.

12. Ng WL, Yang CF, Halladay JT, Arora P, DasSarma S. 1995. Protocol 25. Isolation of genomic and plasmid DNAs from *Halobacterium halobium*, p 179–184. In DasSarma S, Fleischman EM (ed), Archaea, a laboratory manual: halophiles. Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY.

13. DasSarma S, Fomenkov A, DasSarma SL, Vincee T, DasSarma P, Roberts RJ. 2019. Methylyomes of two extremely halophilic archaea species, *Haloarcula marismortui* and *Halofexis mediterranei*. Microbiol Res Announc 8e00577-19. [https://doi.org/10.1128/MRA.00577-19](https://doi.org/10.1128/MRA.00577-19).

14. Lefoulon E, Vaisman N, Frydman HM, Sun L, Voland L, Foster JM, Slatko BE. 2019. Large enriched fragment targeted sequencing (LEFT-SEQ) applied to capture of Wolbachia genomes. Sci Rep 9:5939. [https://doi.org/10.1038/s41598-019-42454-w](https://doi.org/10.1038/s41598-019-42454-w).

15. Besemer J, Lomsadze A, Borodovsky M. 2001. GeneMarkS, a self-training method for prediction of gene starts in microbial genomes. Implications for finding sequence motifs in regulatory regions. Nucleic Acids Res 29:2607–2618. [https://doi.org/10.1093/nar/29.12.2607](https://doi.org/10.1093/nar/29.12.2607).

16. DasSarma SL, Capes MD, DasSarma P, DasSarma S. 2010. Haloweb: the halarchaeal genomes database. Saline Syst 6:12. [https://doi.org/10.1186/1746-1448-6-12](https://doi.org/10.1186/1746-1448-6-12).

17. Madeira F, Park YM, Lee J, Boso N, Gur T, Madhusoodanan N, Basutkar P, Tivey ARN, Potter SC, Finn RD, Lopez R. 2019. The EMBL-EBI search and sequence analysis tools APIs in 2019. Nucleic Acids Res 47:W636–W641. [https://doi.org/10.1093/nar/gkz226](https://doi.org/10.1093/nar/gkz226).

18. Tatusova T, DiCuccio M, Badetdin A, Chevtieva V, Navrocki EP, Zaslavsky L, Lomsadze A, Pruitt KD, Borodovsky M, Ostertell J. 2016. NCBI Prokaryotic Genome Annotation Pipeline. Nucleic Acids Res 44:6614–6624. [https://doi.org/10.1093/nar/gkw569](https://doi.org/10.1093/nar/gkw569).

19. DasSarma S. 2004. Genome sequence of an extremely halophilic archaeon, p 383–399. In Fraser CM, Read T, Nelson KE (ed), Microbial genomes. Humana Press, Inc, Totowa, NJ.

20. DasSarma S, DasSarma P. 2015. Halophiles and their enzymes: negativity put to good use. Curr Opin Microbiol 25:120–126. [https://doi.org/10.1016/j.mib.2015.05.009](https://doi.org/10.1016/j.mib.2015.05.009).

21. Kozlowski LP. 2016. IPC—Isoelectric point calculator. Biol Direct 11:55. [https://doi.org/10.1186/s13062-016-0159-9](https://doi.org/10.1186/s13062-016-0159-9).

22. Capes MD, DasSarma P, DasSarma S. 2012. The core and unique proteins of halooarchaea. BMC Genomics 13:39. [https://doi.org/10.1186/1471-2164-13-39](https://doi.org/10.1186/1471-2164-13-39).

23. DasSarma S, Capes M, DasSarma P. 2009. Chapter 1: haloarchaeal mega-plasmids, p 3–30. In Schwartz E (ed), Microbial megaplasmids, vol 11. Springer-Verlag, Berlin, Germany.

24. Kennedy SP, Ng WV, Salzberg SL, Hood L, DasSarma S. 2001. Understanding the adaptation of *Halobacterium* species NFC-1 to its extreme
environment through computational analysis of its genome sequence. Genome Res 11:1641–1650. https://doi.org/10.1101/gr.190201.

26. Capes MD, Coker JA, Gessler R, Grinblat-Huse V, DasSarma SL, Jacob CG, Kim J-M, DasSarma P, DasSarma S. 2011. The information transfer system of halophilic archaea. Plasmid 65:77–101. https://doi.org/10.1016/j.plasmid.2010.11.005.

27. DasSarma S, DasSarma P. 2015. Gas vesicle nanoparticles for antigen display. Vaccines (Basel) 3:686–702. https://doi.org/10.3390/vaccines3030686.

28. DasSarma P, DasSarma S. 2021. Gas vesicle nanoparticles, p 1–14. In Encyclopedia of life sciences, vol 2. John Wiley & Sons, Ltd, Hoboken, NJ. https://doi.org/10.1002/9780470015902.a0029044.

29. Schoch CL, Ciufo S, Domrachev M, Hotton CL, Kannan S, Khovanskaya R, Leipe D, Mcveigh R, O'Neill K, Robbertse B, Sharma S, Soussov V, Sullivan JP, Sun L, Turner S, Karsch-Mizrachi I. 2020. NCBI taxonomy: a comprehensive update on curation, resources and tools. Database 2020:baaa062. https://doi.org/10.1093/database/baaa062.

30. Roberts RJ, Vincze T, Posfai J, Macelis D. 2015. REBASE—a database for DNA restriction and modification: enzymes, genes and genomes. Nucleic Acids Res 43:D298–D299. https://doi.org/10.1093/nar/gku1046.

31. Blow MJ, Clark TA, Daum CG, Deutschbauer AM, Fomenkov A, Fries R, Froula J, Kang DD, Malmstrom RR, Morgan RD, Posfai J, Singh K, Visel A, Wetmore K, Zhao Z, Rubin EM, Korlach J, Pennacchio LA, Roberts RJ. 2016. The epigenomic landscape of prokaryotes. PLoS Genet 12:e1005854. https://doi.org/10.1371/journal.pgen.1005854.