genomeA
Journals.ASM.org

Draft Genome Sequence of the Terrestrial Cyanobacterium *Scytonema millei* VB511283, Isolated from Eastern India

Diya Sen,[a] Mathu Malar Chandrababunaidu,[a] Deeksha Singh,[a] Neha Sanghi,[a] Arpita Ghorai,[a] Gyan Prakash Mishra,[a] Madhavi Madduluri,[a] Siba Prasad Adhikary,[b] Sucheta Tripathy[a]

Structural Biology and Bioinformatics Division, Council of Scientific and Industrial Research, Indian Institute of Chemical Biology, Kolkata, West Bengal, India[a]; Fakir Mohan University, Vyasa Vihar, Nuapadhi, Balasore, Odisha, India[b]

We report here the draft genome sequence of *Scytonema millei* VB511283, a cyanobacterium isolated from biofilms on the exterior of stone monuments in Santiniketan, eastern India. The draft genome is 11,627,246 bp long (11.63 Mb), with 118 scaffolds. About 9,011 protein-coding genes, 117 tRNAs, and 12 rRNAs are predicted from this assembly.

Received 6 January 2015 **Accepted** 16 January 2015 **Published** 5 March 2015

Citation Sen D, Chandrababunaidu MM, Singh D, Sanghi N, Ghorai A, Mishra GP, Madduluri M, Adhikary SP, Tripathy S. 2015. Draft genome sequence of the terrestrial cyanobacterium *Scytonema millei* VB511283, isolated from eastern India. Genome Announc 3(2):e00009-15. doi:10.1128/genomeA.00009-15.

Copyright © 2015 Sen et al. This is an open-access article distributed under the terms of the Creative Commons Attribution 3.0 Unported license.

Address correspondence to Siba Prasad Adhikary, adhikarysp@gmail.com, or Sucheta Tripathy, tsucheta@gmail.com.

Cyanobacteria are photosynthetic Gram-negative bacteria that are found in marine water and freshwater, as well as under diverse terrestrial habitats. They can naturally produce a wide range of compounds ranging from pigments, antibiotics, and food supplements to biofuels and biodegradable plastics (1). Current research is aimed at genetically increasing the yields of biofuels, such as ethylene, alkane, 1-butanol (2), and fatty alcohols (3), so as to make them economically more feasible. Scytoscalarol is an antimicrobial terpene containing several different cyclic peptides functioning as protease inhibitors isolated from *Scytonema* sp. strain UTEX 1163 (4, 5). Another strain of *Scytonema* has been shown to produce an extracellular sheath pigment called scytonemin that absorbs UV radiation and allows the organism to survive in high-energy solar radiation (6). This compound can be used in the production of marketable sunscreen products (7). Despite having useful applications in drug and cosmetic development, *Scytonema* is a genus that is unexplored for its bioprospecting potential.

Syctonema millei VB511283, a terrestrial cyanobacterium, was isolated from biofilms growing on the exterior of stone monuments in Santiniketan, eastern India (8). It was maintained in BG11 medium at room temperature (approximately 26°C) in a cycle of 16 h of light/8 h of darkness, without shaking. The culture formed dark green mats on solid slants but was ribbon-like in liquid medium.

Genomic DNA was isolated with the UniFlex bacterial DNA isolation kit (Genei, USA). A total of 404 ng of DNA was used for sequencing. Sequencing was carried out on an Illumina HiSeq platform (Genotypic Technologies, India) using paired-end and mate-pair libraries. The paired-end library consisted of an approximately 300-bp insert, with a read length of 151 bp and coverage of 291×, resulting in 44 million reads. The mate-pair library consisted of an approximately 3,000-bp insert, with a read length of 101 bp and 20× coverage, yielding 4.4 million reads. The raw reads were cleaned by SGA and TagDust (9). Genome assembly was carried out on cleaned reads from both libraries using AllPaths-LG (10). This resulted in 118 scaffolds, with an N_{50} of 2,155,310. The largest scaffold was 3,887,589 bp long, and the smallest was 3,012 bp long; the draft genome is 11,627,246 bp and has a G+C content of 51%.

Genome annotation was performed with the Prokaryotic Genome Annotation Pipeline (PGAP) at NCBI (http://www.ncbi.nlm.nih.gov/genome/annotation_prok/). There are 9,011 protein-coding genes, 1,300 pseudogenes, 2 clustered regularly interspaced short palindromic repeat (CRISPR) arrays, 117 tRNAs, 12 rRNAs, and 2 noncoding RNAs (ncRNAs). tBLASTn carried out against cyanobacterial core orthologs (11) revealed the presence of 382 of the 384 core orthologs. Besides the core orthologs, the genome of *S. millei* encodes several types of multidrug resistance systems, such as macrolide/bacitracin/multidrug ABC transporters, the acriflavin resistance gene (*acrB*), and β-lactamases. A polyketide synthase gene bearing 66% identity at the amino acid level to its homolog in *Nostoc punctiforme* PCC 73102 (accession no. WP_012409829.1) was identified. This strain can thus be explored for the production of pharmacologically important polyketides.

Nucleotide sequence accession number. The whole-genome sequence and annotation data for *S. millei* VB511283 have been submitted to GenBank under the accession no. JTJC00000000.

ACKNOWLEDGMENTS

S.T. received funds from DBT-RLS and CSIR Genesis, and ICAR AMAAS for the completion of this work. D.S. and M.M.C. received fellowships from CSIR and DST, respectively.

REFERENCES

1. **Abed RMM, Dobretsov S, Sudesh K.** 2009. Applications of cyanobacteria in biotechnology. J Appl Microbiol **106:**1–12. http://dx.doi.org/10.1111/j.1365-2672.2008.03918.x.
2. **Ducat DC, Way JC, Silver PA.** 2011. Engineering cyanobacteria to generate high-value products. Trends Biotechnol **29:**95–103.
3. **Ruffing AM.** 2014. Improved free fatty acid production in cyanobacteria with *Synechococcus* sp. PCC 7002 as host. Front Bioeng Biotechnol **2:**17. http://dx.doi.org/10.3389/fbioe.2014.00017.
4. **Mo S, Krunic A, Pegan SD, Franzblau SG, Orjala J.** 2009. An antimicrobial

guanidine-bearing sesterterpene from the cultured cyanobacterium *Scytonema* sp. J Nat Prod **72:**2043–2045. http://dx.doi.org/10.1021/np900288x.
5. **Krunic A, Vallat A, Mo S, Lantvit DD, Swanson SM, Orjala J.** 2010. Scytonemides A and B, cyclic peptides with 20S proteasome inhibitory activity from the cultured cyanobacterium *Scytonema hofmanii*. J Nat Prod **73:**1927–1932. http://dx.doi.org/10.1021/np100600z.
6. **Dillon JG, Castenholz RW.** 1999. Scytonemin, a cyanobacterial sheath pigment, protects against UVC radiation: implications for early photosynthetic life. J Phycol **35:**673–681. http://dx.doi.org/10.1046/j.1529-8817.1999.3540673.x.
7. **Proteau PJ, Gerwick WH, Garcia-Pichel F, Castenholz RW.** 1993. The structure of scytonemin, an ultraviolet sunscreen pigment from the sheaths of cyanobacteria. Experientia **49:**825–829. http://dx.doi.org/10.1007/BF01923559.
8. **Keshari N, Adhikary SP.** 2013. Characterization of cyanobacteria isolated from biofilms on stone monuments at Santiniketan, India. Biofouling **29:**525–536. http://dx.doi.org/10.1080/08927014.2013.794224.
9. **Coil D, Jospin G, Darling AE.** 2014. A5-miseq: an updated pipeline to assemble microbial genomes from Illumina MiSeq data. Bioinformatics, in press. http://dx.doi.org/10.1093/bioinformatics/btu661.
10. **Butler J, MacCallum I, Kleber M, Shlyakhter IA, Belmonte MK, Lander ES, Nusbaum C, Jaffe DB.** 2008. ALLPATHS: *de novo* assembly of whole-genome shotgun microreads. Genome Res **18:**810–820. http://dx.doi.org/10.1101/gr.7337908.
11. **Larsson J, Nylander JA, Bergman B.** 2011. Genome fluctuations in cyanobacteria reflect evolutionary, developmental and adaptive traits. BMC Evol Biol **11:**187. http://dx.doi.org/10.1186/1471-2148-11-187.