

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

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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.

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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.

Scytonema 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/multi-drug 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](https://www.ncbi.nlm.nih.gov/nuccore/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.

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