

Complete Genome Sequence of *Cyanobium* sp. NIES-981, a Marine Strain Potentially Useful for Ecotoxicological Bioassays

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***Cyanobium* sp. NIES-981 is a marine cyanobacterium isolated from tidal flat sands in Okinawa, Japan. Here, we report the complete 3.0-Mbp genome sequence of NIES-981, which is composed of a single chromosome, and its annotation. This sequence information may provide a basis for developing an ecotoxicological bioassay using this strain.**

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Ecotoxicological bioassay is a widely used method for ecological risk assessment of environmental pollution. For freshwater environments, there are several standard methods using freshwater algal species to evaluate the ecotoxicity of chemicals; however, such methods are not well established for marine environments (1). To improve this situation, we are developing a method using a marine cyanobacterial strain of *Cyanobium* sp. NIES-981 because this strain demonstrates adequate growth rate and cell viability after cryopreservation. *Cyanobium* sp. NIES-981 is a unicellular, shortly rod-shaped cyanobacterium, isolated from tidal flat sands in Iriomotejima Island, Okinawa, Japan. Here, we report the complete genome sequence of *Cyanobium* sp. NIES-981, a marine strain potentially useful for ecotoxicological bioassays.

A 1-liter sample of the axenic culture was used for DNA extraction using NucleoBond AXG Columns with Buffer Set III (Macherey-Nagel). DNA sequencing was performed on the PacBio RS II sequencer (Pacific Biosciences). A 20-kb fragmented library was constructed, followed by size selection using the electrophoresis unit BluePippin (Sage Science) at 15 kb. A single library was prepared and then sequenced in a single-molecule real-time cell with P6 DNA polymerase and C4 chemistry, yielding a total of 67,150 reads. *De novo* assembly was performed by the Hierarchical Genome Assembly Process version 2.3 (2). The resulting genome comprised a single circular chromosome of 3,021,545 bp with an average genome coverage of approximately 220×. The complete genome of NIES-981 was annotated with the MicroScope platform (3), and then 3,268 protein-coding sequences, 46 tRNA genes, and three sets of rRNA genes were predicted. The G+C content of the genome was 68.62%.

The sequence of 16S rRNA was compared with that of *Cyanobium gracile* PCC 6307 and *Cyanobium* sp. PCC 7001, of which two genome sequences are available in the GenBank database (<http://www.ncbi.nlm.nih.gov/Genbank/index.html>), resulting in 97.31% and 98.72% similarity, respectively. The genome shares 2,194 (74%) and 2,214 (75%) of 2,965 gene families with PCC 6307 and PCC 7001, respectively.

As candidates of marine pollutants, several heavy metals de-

rived from seabed drilling will be assumed. Thus, we subjected protein sequences of NIES-981 to a BLAST search against those of *Synechocystis* sp. PCC 6803, which is a well-studied cyanobacterium in terms of functional genes of heavy metal homeostasis and resistance (4, 5). The obtained results revealed the following genes of NIES-981 that are homologous to those of *Synechocystis* sp. PCC 6803: P₁-type ATPases CtaA (encoded by open reading frame *slr1950*) and PacS (*sll1920*) (42% and 53% identity, respectively) for copper import; RND protein CopA (*slr6043*; 59% identity) for a copper efflux system; CopRS two-component system (*sll0789* and *sll0790*; 51% and 38% identity, respectively) for copper resistance; and ABC-type transporter MntCAB (*sll1598*, *sll1599*, and *sll1600*; 54%, 59%, and 61% identity, respectively) for high-affinity transport of manganese ions.

Nucleotide sequence accession number. This whole-genome shotgun project has been deposited in EMBL under the accession number **LT578417**. The version described in this paper is the first version.

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