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GENOME SEQUENCES

High-Quality Draft Genome Sequence of *Fischerella thermalis* JSC-11, a Siderophilic Cyanobacterium with Bioremediation Potential

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ABSTRACT Here, we report the draft genome sequence of the siderophilic cyanobacterium *Fischerella thermalis* JSC-11, which was isolated from an iron-depositing hot spring. JSC-11 has bioremediation potential because it is capable of both extracellular absorption and intracellular mineralization of colloidal iron. This genomic information will facilitate the exploration of JSC-11 for bioremediation.

We report the high-quality draft genome sequence of the cyanobacterium JSC-11, which was isolated from an iron-depositing mat from Chocolate Pots Hot Springs (Yellowstone National Park, WY, USA) (temperature of 55°C, pH of 5.6, and total soluble iron concentration of ~20 μM) (1). Single-colony isolation was performed as described previously (2, 3). Because optimal growth occurred at 45 to 55°C and 0.4 to 0.6 mM iron, JSC-11 has been characterized as a thermophilic and siderophilic species (4). Its 16S rRNA sequence (GenBank accession number HM636645.1) shares 100% identity with those of several *Fischerella thermalis* strains, and it shares their characteristic true-branching morphology (5, 6). Therefore, it was classified as *F. thermalis* strain JSC-11 (CCMEE 7001). This strain absorbs iron oxides on its exopolymers and produces intracellular iron deposits (Fig. 1), making it a potential candidate for bioremediation (7).

Genomic DNA of JSC-11 was isolated using the UltraClean microbial DNA isolation kit (MoBio Laboratories, USA), following cultivation in DH medium as described previously (8). The draft genome of JSC-11 was generated at the U.S. Department of Energy (DOE) Joint Genome Institute (JGI) using a combination of four next-generation sequencing (NGS) libraries from the same DNA extract. An Illumina GAIIx (9) library was created using the KAPA-Illumina library creation kit (Kapa Biosystems), yielding 31,933,200 reads of 76-bp average length. One 454 Titanium library was created using the GS FLX Titanium rapid library preparation kit (Roche), generating 267,779 reads of 395-bp average length; two paired-end 454 libraries, with average insert sizes of 4 kb and 8 kb, were created according to the method described by Peng et al. (10), generating 602,963 reads of 160- and 188-bp average length, respectively. Kits were used according to the manufacturers' instructions.

The 454 data were assembled with Newbler v2.3 (9), the Illumina data were assembled with Velvet v1.0.13 (11), and the contigs were computationally shredded into 2-kb and 1.5-kb overlapping fake reads (shreds), which were integrated with the 454 paired-end library reads using parallel Phrap v1.080812 (High Performance Software, LLC). POLISHER (12) was used to correct base errors. Misassemblies were corrected by using Gap Resolution (13), Dupfinisher (14), or sequencing of cloned bridging PCR

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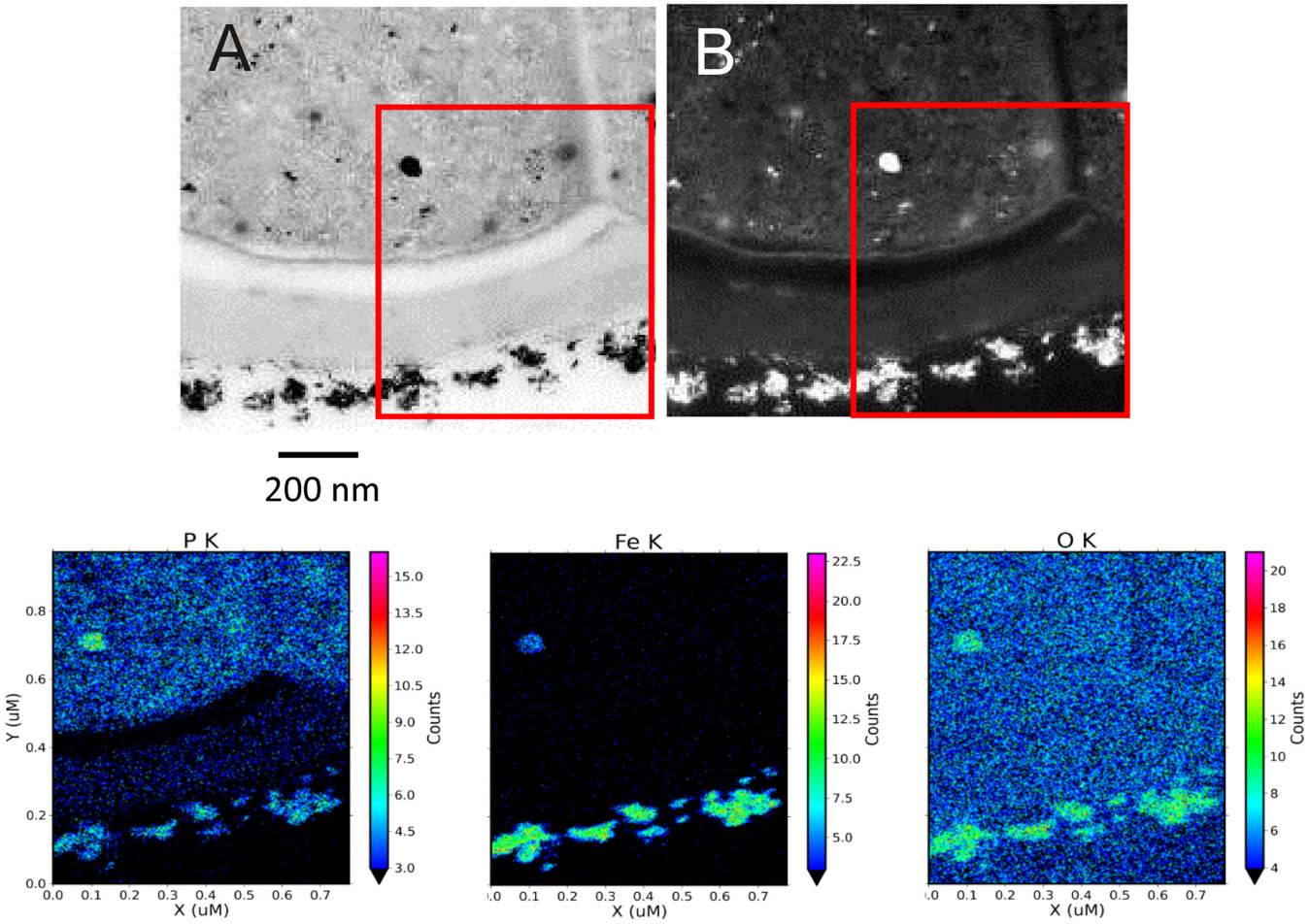

FIG 1 Scanning transmission electron microscopy (STEM) views of extracellular and intracellular iron-rich particles found in JSC-11 cells incubated with 600 μM $FeCl_3 \cdot 6H_2O$ and 0.04 mM $Na_2HPO_4 \cdot 7H_2O$. (Upper, left) Bright-field STEM photograph of a JSC-11 cell encrusted with external Fe-bearing precipitates and containing an electron-dense, internal, Fe-rich particle ~100 nm in size. (Upper, right) Dark-field STEM photograph to localize Fe-rich aggregates. (Lower) Quantitative element maps for internal and external particles, showing distribution patterns for phosphorus (P), Fe, and oxygen (O). The electron-dense particles within the JSC-11 cytoplasm contain substantial amounts of P, Fe, and O.

fragments with subcloning. Gaps were closed manually using Consed (15, 16) and 168 PCR and Bubble PCR primer walks.

Annotation was performed with the Oak Ridge National Laboratory annotation pipeline using Prodigal v1.4 (17), followed by manual curation using the JGI GenePRIMP pipeline (18). The JSC-11 genome is 5,380,000 bp long, with a G+C content of 41.0%, and has 99.76% completeness and 0.0% contamination according to CheckM v1.1.3 (19). It contains 4,367 coding genes, 1 rRNA operon, and 43 tRNA genes.

The JSC-11 genome may shed light on specific mechanisms of iron homeostasis in siderophilic cyanobacteria, because it encodes proteins predicted to be involved in iron transport (21 total) or maintaining a balance between intracellular Fe^{2+} and Fe^{3+} (5 total). Genomic analysis also revealed that JSC-11 may be capable of far-red-light photoacclimation (20).

Data availability. The GenBank accession number for the 16S rRNA gene is HM636645.1. The GenBank assembly accession number is GCA_000231365.2. The NCBI RefSeq assembly accession number is GCF_000231365.1. The BioProject accession number is PRJNA61093. The nucleotide GenBank accession number is AGIZ00000000.1. The SRA accession numbers for the raw sequences are SRR21655585, SRR21655586, SRR21655587, and SRR3927276.

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