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# Draft Genome Sequence of *Calothrix* Strain 336/3, a Novel H<sub>2</sub>-Producing Cyanobacterium Isolated from a Finnish Lake

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**We announce the draft genome sequence of *Calothrix* strain 336/3, an N<sub>2</sub>-fixing heterocystous filamentous cyanobacterium isolated from a natural habitat. *Calothrix* 336/3 produces higher levels of hydrogen than *Nostoc punctiforme* PCC 73102 and *Anabaena* strain PCC 7120 and, therefore, is of interest for potential technological applications.**

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To diversify a potential to exploit naturally occurring photosynthetic organisms for sustainable biofuel production, we investigated strains from the University of Helsinki Culture Collection (UHCC) for their capability to produce H<sub>2</sub> (1). The preliminary screening process involved 400 different cyanobacterial species utilizing four different conditions, including aerobic, anaerobic, light, and dark conditions. The promising strains were then compared against the H<sub>2</sub> photoproduction capacities of reference strains *Nostoc punctiforme* PCC 73102 and *Anabaena* PCC 7120 cyanobacteria. After optimization of the production system and exclusion of strains that had a toxic nature or have been too light sensitive, two strains, *Calothrix* 336/3 and *Calothrix* XPORK 5E, have been found to be the best H<sub>2</sub>-producing cyanobacteria among investigated species (1, 2).

*Calothrix* 336/3 is an N<sub>2</sub>-fixing heterocystous filamentous cyanobacterium isolated from the Enäjärvi lake, Laukilahti, Finland (3). DNA preparations were obtained as described by Neilan et al. (4) and sent for commercial sequencing at the Beijing Genome Institute (BGI), where two *Calothrix* 336/3 DNA libraries containing short ~500-bp inserts and mate-pair ~2,000-bp inserts were constructed. Sequencing was performed on the HiSeq 2000 Illumina platform. A total of 13,333,340 raw paired-end reads were produced, resulting in ~100-fold genome coverage. The reads were assembled with SOAPdenovo (5) into 43 scaffolds larger than 100 bp. The following GC-content analysis showed the presence of the two scaffold groups. The GC content of 41% to 50% was determined for 27 scaffolds, while 16 scaffolds had a GC content of 30% to 34%. The taxonomic analysis with MEGAN v. 5.5.4 (6) revealed that the first group of 27 scaffolds contained proteins that were found in other cyanobacterial species, while the second group belonged to an unknown *Bacteroides*-like genus, which resulted, most probably, from strain contamination. The latter group of 16 contaminated scaffolds was discarded from further analysis. The 27 scaffolds with the higher GC content were combined by PCR using synthetic primers selected from regions

near scaffold ends, resulting in 4 scaffolds, with a total of 6,419,212 bp.

The draft genome was automatically annotated with the NCBI Prokaryotic Annotation Pipeline (PGAP); (<http://www.ncbi.nlm.nih.gov/genomes/static/Pipeline.html>), using the Rapid Annotations based on Subsystem Technology (RAST) server (7, 8) and the DOE-JGI Microbial Annotation Pipeline (9). The resulting *Calothrix* 336/3 genome comprises 4,946 genes with 4,834 coding sequences, 42 pseudogenes, 6 ribosomal RNAs, and 63 transfer RNAs. The overall GC content percentage is 41.41%. Based on 16S rRNA gene sequence similarity, *Calothrix* 336/3 is 93.73%, 92.45%, and 91.98% identical to the *Calothrix* strains PCC 7507 (CP003943), PCC 6303 (CO003610), and PCC 7103 (ALVJ00000000), respectively.

Genome annotation revealed that the *Calothrix* 336/3 genome contains *nif* (*nifHDK1*) and *hup* (*hupLS*) operons encoding nitrogenase and uptake hydrogenase enzymes but lacks *hoxEFUYH* genes encoding bidirectional hydrogenase and sets of *nifHDK2* and *vnfDGGK* genes encoding alternative nitrogenases, in line with the results obtained by Leino et al. with enzyme activity and Southern hybridization analyses (2). The strain demonstrated a high stability and prolonged H<sub>2</sub> photoproduction capacity after immobilization in thin alginate films (10, 11). Investigation of the *Calothrix* 336/3 genome opens new opportunities for potential technological applications in the development of biohydrogen production.

**Nucleotide sequence accession number.** The draft genome sequence of *Calothrix* strain 336/3 has been deposited at GenBank under the accession number [JPKF00000000](https://www.ncbi.nlm.nih.gov/nuccore/JPKF00000000).

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