# Draft Genome Sequences of Four *Microcystis aeruginosa* Strains (NIES-3787, NIES-3804, NIES-3806, and NIES-3807) Isolated from Lake Kasumigaura, Japan

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**ABSTRACT** *Microcystis aeruginosa* is a bloom-forming cyanobacterium found in freshwater environments. The draft genomes of the *M. aeruginosa* strains NIES-3787, NIES-3804, NIES-3806, and NIES-3807, which were isolated from Lake Kasumigaura, Japan, were sequenced. The genome sizes of NIES-3787, NIES-3804, NIES-3806, and NIES-3807 were 4,524,637, 4,522,701, 4,370,004, and 4,378,226 bp, respectively.

Cyanobacterial blooms occur widely in freshwater environments worldwide (1). *Microcystis aeruginosa* is the most well-known bloom-forming cyanobacterium, and it is distributed in eutrophic freshwater environments. The most serious problem associated with this species is the production of hepatotoxic cyanotoxins called microcystins (2, 3). *M. aeruginosa* isolates are genetically divided into at least 12 phylogenetic groups (groups A to K and X) based on multilocus phylogenetic analyses (2, 3). The strains in groups A and X, as well as some B strains, produce microcystins (3, 4). In the current study, we sequenced *M. aeruginosa* strains NIES-3787, NIES-3804, NIES-3806, and NIES-3807, isolated from Lake Kasumigaura, Japan.

Axenic cultures of *M. aeruginosa* NIES-3787, NIES-3804, NIES-3806, and NIES-3807 were obtained from the microbial culture collection of the National Institute for Environmental Studies (https://mcc.nies.go.jp/index.html). These strains were established by using a micropipette under an inverted microscope. The strains were cultured in 10 ml of *Microcystis aeruginosa* medium at 22°C under light at 25 $\mu$mol photons m$^{-2}$ s$^{-1}$ with a 12:12-h light/dark cycle. Genomic DNA was extracted from 10-ml cultures of these strains using Agencourt Chloropure (Beckman Coulter) following the manufacturer's protocol. The resultant DNAs were fragmented to approximately 550 bp using an M220 ultrasonicator (Covaris). Genomic libraries of paired-end reads were constructed using a NEBNext Ultra II DNA library prep kit for Illumina (New England Biolabs). Next-generation sequencing was performed with the MiSeq platform (Illumina) using a 500-cycle MiSeq reagent kit version 2. The resultant paired-end reads for NIES-3787, NIES-3804, NIES-3806, and NIES-3807 were 151,461,029 bp, 643,439,906 bp, 395,828,445 bp, and 197,435,680 bp, respectively. The raw reads were trimmed using Trimmomatic version 0.38 (5), and then *de novo* assembly was performed using SPAdes version 3.11.1 (6) in Shovill version 1.0.4 (https://github.com/tseemann/shovill). Next, the assembled scaffolds were polished using Pilon version 1.22 (7). After the removal of short reads (<200 bp), functional annotation was performed using the DFAST legacy server (8) with CyanoBase (9) as a database. We used CheckM version 1.0.11 to estimate genome completeness (10). Default parameters were used for all software. Group identification analysis of each strain was carried out based on *ftsZ*, one of seven multilocus sequence typing loci (2, 3).

The genome assembly results are detailed in Table 1. As the result of group identification analysis, NIES-3787, NIES-3806, and NIES-3807 were identified as group G, and NIES-3804 was not assigned to any known group. These four strains did not possess

**TABLE 1** Characteristics and accession numbers of four *Microcystis aeruginosa* genomes

| Strain name | Assembly size (bp) | No. of contigs | $N_{50}$ (bp) | Genome completeness (%) | CheckM contamination (%) | GC content (%) | No. of coding sequences | Accession no. of whole-genome shotgun submissions | SRA accession no. | GenBank assembly accession no. |
|---|---|---|---|---|---|---|---|---|---|---|
| NIES-3787 | 4,378,226 | 214 | 73,037 | 99.89 | 0.66 | 43.0 | 4,126 | BJCH01000001–BJCH01000214 | DRR205020 | GCA_009811815 |
| NIES-3804 | 4,524,637 | 238 | 45,562 | 99.89 | 0.37 | 43.0 | 4,226 | BJCI01000001–BJCI01000238 | DRR205021 | GCA_009811835 |
| NIES-3806 | 4,522,702 | 235 | 67,327 | 99.89 | 0.37 | 43.0 | 4,180 | BJCJ01000001–BJCJ01000235 | DRR205022 | GCA_009811855 |
| NIES-3807 | 4,370,004 | 214 | 46,356 | 99.89 | 0.95 | 43.0 | 4,066 | BJCK01000001–BJCK01000228 | DRR205023 | GCA_009811875 |

a microcystin biosynthetic gene cluster (11). However, some secondary metabolite gene clusters, including aeruginosin (NIES-3787, NIES-3806, and NIES-3807) (12), anabaenopeptin (NIES-3806) (13), microcyclamide (NIES-3804) (14), and micropeptin (NIES-3787 and NIES-3806) (15), were predicted using antiSMASH version 5.0.0 (16). Additional genomic information about *M. aeruginosa* would be useful for monitoring algal blooms and managing freshwater ecosystems.

**Data availability.** The draft genomic sequences of *Microcystis aeruginosa* NIES-3787, NIES-3804, NIES-3806, and NIES-3807 have been deposited in DDBJ/EMBL/GenBank under the accession numbers BJCH01000001 to BJCH01000214, BJCI01000001 to BJCI01000238, BJCJ01000001 to BJCJ01000235, and BJCK01000001 to BJCK01000228, respectively. The raw genomic reads of the strains are available in DDBJ/EMBL/GenBank under the accession numbers DRR205020, DRR205021, DRR205022, and DRR205023, respectively.

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