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PROKARYOTES

Draft Genome Sequences of Two Uncultured *Armatimonadetes* Associated with a *Microcystis* sp. (*Cyanobacteria*) Isolate

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ABSTRACT Two genome sequences of the phylum *Armatimonadetes*, derived from terrestrial environments, have been previously described. Here, two additional *Armatimonadetes* genome sequences were obtained via single-molecule real-time (SMRT) sequencing of an enrichment culture of the bloom-forming cyanobacterium *Microcystis* sp. isolated from a eutrophic lake (Brandenburg, Germany). The genomes are most closely affiliated with the class *Fimbriimonadales*, although they are smaller than the 5.6-Mbp type strain genome.

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Members of the phylum *Armatimonadetes* occur in diverse environments, e.g., on human skin, in temperate soils, bioreactors, and freshwater lakes (1). To date, three strains have been isolated, *Armatimonas rosea* YO-36^T, from the roots of the aquatic plant *Phragmites australis* (2), *Chthonomonas calidirosea* T49^T, from geothermal soil (3), and *Fimbriimonas ginsengisoli* Gsoil 348^T, from soil associated with ginseng cultivars (4). The three isolates exhibit between 77 and 81% pairwise nucleotide similarity across the 16S rRNA gene. Genome analyses of *F. ginsengisoli* (5) and *C. calidirosea* (6) revealed differences in genome size, GC content, protein homology, and gene synteny, but similarities exist with regard to the utilization of complex sugars, ammonium assimilation, and the uptake of branched-chain amino acids to supplement nutrient requirements (5).

In 2011, four colony-forming *Microcystis* strains from Lake Zernsee, Potsdam, Germany, were grown in BG-11 medium (7) at 25°C and continuous illumination (16 μmol photons m^{-2} s^{-1}). Of these, one strain, *Microcystis* sp. UP-HVL2, was sequenced using the RSII platform (Pacific Biosciences) at GATC Biotech (Constance, Germany) and assembled using the SMRT Portal *de novo* workflow. Two *Armatimonadetes* genomes, those of Uphvl-Ar1 and Uphvl-Ar2, were obtained from tetranucleotide binning of the *Microcystis* sp. UP-HVL2 genome using MetaWatt version 3.5.3 (8), with default parameters. Genome completeness and contamination estimated of the genomes as assessed using CheckM (9) were 94.91% and 0.93% for Uphvl-Ar1 and 89.81% and 0.93% for Uphvl-Ar2, respectively.

Annotation was performed using the NCBI Prokaryotic Genome Annotation Pipeline. Uphvl-Ar1 comprised a single 2.99-Mbp contig, 3,131 gene features, and a GC content of 52.5%. Uphvl-Ar2 comprised a single 2.6-Mbp contig, 2,644 gene features, and a GC content of 62.1%. Uphvl-Ar1 and Uphvl-Ar2, consistent with Gsoil348^T, lacked a complete 16S-23S-5S rRNA operon. In both instances, a 0.8- to 0.84-Mbp region separated the 16S rRNA gene from the 23S-5S region. The 16S rRNA genes of Uphvl-Ar1 and Uphvl-Ar2 exhibited 90% homology with one another. The 16S rRNA genes of Uphvl-Ar1 exhibited 91% sequence homology with those from uncultured *Armatimonadetes* from bioreactors (GenBank accession numbers

KT182498, EF648093, KJ783172, and HQ864199), whereas Uphvl-Ar2 exhibited 99% homology with those from uncultured *Armatimonadetes* from freshwater (accession numbers HQ860522, GU305825, DQ501336, and FJ662688). The SINA classifier placed both strains within the family *Fimbriimonadaceae*, with ~87% identity homology with reference strains. In contrast to the terrestrial *F. ginsengisoli*, the aquatic Uphvl-Ar1 and Uphvl-Ar2 are both likely motile, possessing complete flagellum biosynthetic pathways and numerous chemotaxis receptors for simple sugars and amino acids. Uphvl-Ar1 and Uphvl-Ar2 lack the ability to take up ammonium or nitrate, instead relying on the uptake and hydrolysis of amino acids, including glutamine, to meet their nitrogen requirements.

Accession number(s). The sequences of Uphvl-Ar1 and Uphvl-Ar2 have been deposited in GenBank under the accession numbers CP021423 and CP021424, respectively.

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