Draft Genome Sequence of a Sulfide-Oxidizing, Autotrophic Filamentous Anoxyoxic Phototrophic Bacterium, *Chloroflexus* sp. Strain MS-G (*Chloroflexi*)

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The draft genome sequence of the thermophilic filamentous anoxyoxic phototrophic bacterium *Chloroflexus* sp. strain MS-G (*Chloroflexi*), isolated from Mushroom Spring (Yellowstone National Park, WY, USA) was sequenced and comprises 4,784,183 bp in 251 contigs. The draft genome is predicted to encode 4,059 protein coding genes, 49 tRNA encoding genes, and 3 rRNA operons.

*Chloroflexus* sp. strain MS-G is a thermophilic, filamentous anoxyoxic bacterium of the family *Chloroflexaceae* of the phylum *Chloroflexi*. Strain MS-G was isolated from a phototrophic microbial mat in an effluent channel of Mushroom Spring, an alkaline siliceous hot spring in the Lower Geyser Basin of Yellowstone National Park (44°32′20.4″ N, 110°47′52.8″ W, WY, USA). The 16S rRNA sequence of this isolate shares >99% nucleotide identity to a 16S rRNA sequence obtained from the metagenome (IMG taxon OID 3300002510) of the green upper layer (upper ~1 mm), and both share 100% with the most abundant strain J-10-fl genome of *Chloroflexus* sp. (*Chloroflexi*) strain MS-G (*Chloroflexi*). Genome Announc. 2(5):e00872-14. doi:10.1128/genomeA.00872-14.

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The 16S rRNA sequence of this isolate shares >99% nucleotide identity to a 16S rRNA sequence obtained from the metagenome (IMG taxon OID 3300002510) of the green upper layer (upper ~1 mm), and both share 100% with the most abundant strain J-10-fl genome (*Chloroflexi*) of *Chloroflexus* sp. (*Chloroflexi*). Genome Announc. 2(5):e00872-14. doi:10.1128/genomeA.00872-14.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession JPM100000000. The version described in this paper is version JPM100000000.

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