

Genomic analysis of a pure culture of magnetotactic bacterium *Terasakiella* sp. SH-1*

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Abstract Magnetotactic bacteria (MTB) display magnetotaxis ability because of biomineralization of intracellular nanometer-sized, membrane-bound organelles termed magnetosomes. Despite having been discovered more than half a century, only a few representatives of MTB have been isolated and cultured in the laboratory. In this study, we report the genomic characterization of a novel marine magnetotactic spirillum strain SH-1 belonging to the genus *Terasakiella* that was recently isolated. A gene encoding haloalkane dehalogenase, which is involved in the degradation of chlorocyclohexane, chlorobenzene, chloroalkane, and chloroalkene, was identified. SH-1 genome contained *cysCHI* and *soxBZYX* genes, thus potentially capable of assimilatory sulfate reduction to H₂S and using thiosulfate as electron donors and oxidizing it to sulfate. Genome of SH-1 also contained genes encoding periplasmic dissimilatory nitrate reductases (*napAB*), assimilatory nitrate reductase (*nasA*) and assimilatory nitrite reductases (*nasB*), suggesting that it is capable of gaining energy by converting nitrate to ammonia. The pure culture of *Terasakiella* sp. SH-1 together with its genomic results offers new opportunities to examine biology, physiology, and biomineralization mechanisms of MTB.

Keyword: magnetotactic bacteria; magnetotaxis; pure culture; comparative genomic analysis

1 INTRODUCTION

Magnetotactic bacteria (MTB) are prokaryotes that orient and migrate along the geomagnetic field lines, a behavior referred to as magnetotaxis or microbial magnetoreception. MTB share the capacity to synthesize magnetosomes, which are magnetic crystals of magnetite (Fe₃O₄) and/or greigite (Fe₃S₄) and enveloped by a phospholipid bilayer membrane (Blakemore, 1982; Bazylinski et al., 1995; Bazylinski and Frankel, 2004). Many morphotypes of MTB,

including coccoid, ovoid, rod, vibrio, spirillum, and multicellular forms have been observed worldwide across from freshwater, brackish, and marine waters to waterlogged soils (Maratea and Blakemore, 1981; Hanzlik et al., 2002; Sakaguchi et al., 2002; Lefèvre

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