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Draft Genome Sequence of *Azospira* sp. Strain I13, a Nitrous Oxide-Reducing Bacterium Harboring Clade II Type *nosZ*

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ABSTRACT We report here a draft genome sequence of *Azospira* sp. strain I13 in the class *Betaproteobacteria*, a facultative anaerobic bacterium responsible for nitrous oxide (N_2O) reduction. Deciphering this genome would pave the way for the use of *Azospira* sp. strain I13 to facilitate N_2O consumption in a nitrogen-removing bioreactor emitting N_2O.

Nitrous oxide (N_2O), a highly potent greenhouse gas causing ozone depletion, is utilized by microorganisms as an electron accepter in natural ecosystems and engineered systems, serving as a N_2O sink (1, 2). It was recently reported that N_2O-reducing bacteria are classified into two clade types based on sequences of a functional gene (*nosZ*) encoding N_2O reductase (3, 4). Furthermore, distinct *nos* gene clusters with the two clades display divergent traits in terms of the gene expression, electron transfer, and N_2O-reducing activity (4–6). The complete genome of *Azospira suillum* strain PS, a perchlorate-reducing bacterium, was previously reported (7, 8). Nevertheless, genome and physiological data about members of the genus *Azospira* remain scarce, especially regarding their role in nitrogen transformations. Recently, we isolated three strains of N_2O-reducing bacteria by inoculating activated sludge in a municipal wastewater treatment plant with an enrichment reactor fed with sodium acetate and N_2O as an electron donor and acceptor, respectively (T. Suenaga, T. Hori, S. Riya, M. Hosomi, B. F. Smets, and A. Terada, unpublished data). One of the isolates, *Azospira* sp. strain I13, has a high affinity for N_2O and exhibits rapid recovery of N_2O reduction activity from oxygen exposure-derived deterioration (9). The physiological traits are of promise for engineering applications in mitigating N_2O emissions (9). We present here the draft genome sequence of *Azospira* sp. strain I13.

Azospira sp. strain I13 was aerobically grown using sodium acetate as a sole electron donor. Total nucleic acids were extracted by a phenol extraction method with chemical cell lysis and subsequently purified with cetyltrimethylammonium bromide. Then, DNA was purified by RNA decomposition with RNaseA (TaKaRa Bio, Inc., Japan). A paired-end DNA library (insert size, 250 to 500 bp) was prepared as previously reported (10). The library was sequenced using a MiSeq platform (Illumina, USA) and read with 700-fold genome coverage (10,672,103 250-bp paired-end reads). The acquired sequence, consisting of 26 scaffolds in total, was assembled using SOAPdenovo version 2.04 (11). The draft genome size of strain I13 was 3.79 Mb with a G+C content of 64.0%. The largest scaffold was 557 kb.

Fifty of the tRNA-encoding genes and three of the rRNA-encoding genes were identified by tRNAscan-SE version 1.3.1 (12) and RNAmmer version 1.2 (13), respectively. The draft genome sequence was annotated using the DDBJ Fast Annotation and Submission Tool (DFAST) (14), which yielded a total of 3,413 protein-coding DNA sequences. *Azospira* sp. strain I13 codes a clade II type *nosZ* gene. In addition, the strain possesses nitrogen metabolism-related genes for nitrate (dissimilatory NapAB), nitrite

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(cd_1-containing NirS), nitric oxide, dissimilatory nitrite reduction, and nitrogen fixation. The draft genome sequence of *Azospira* sp. strain I13 will contribute to a comprehensive understanding of nitrogen metabolisms in natural environments and engineered systems.

Accession number(s). The draft genome of *Azospira* sp. strain I13 has been deposited as 26 scaffolds in DDBJ/EMBL/GenBank under the accession number BFBP00000000 (BFBP01000001 to BFBP01000026). The version described in this paper is the first version.

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