

Draft Genome Sequence of a Selenite- and Tellurite-Reducing Marine Bacterium, *Lysinibacillus* sp. Strain ZYM-1

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***Lysinibacillus* sp. ZYM-1, a Gram-positive strain isolated from marine sediments, reduces selenite and tellurite efficiently. Meanwhile, it also exhibits high resistance to Zn²⁺ and Mn²⁺. Here, we report the draft genome sequence of strain ZYM-1, which contains genes related to selenite and tellurite reduction and also metal resistance.**

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Lysinibacillus is a Gram-positive, rod-shaped, and round-spore-forming bacterial genus in the family *Bacillaceae* (1). More recently, several reports have indicated that *Lysinibacillus* spp. are potential candidates for heavy metal bioremediation. *L. fusiformis* ZC1 can reduce 1 mM hexavalent chromium within 12 h, and 25 strains of *L. sphaericus* can grow in arsenate, hexavalent chromium, and/or lead (2, 3). Strain ZYM-1 was isolated from marine sediments using 1 mM selenite as selection pressure. This strain has been deposited in the China General Microbiological Culture Collection Center (accession number: CGMCC 1.15346). The 16S rRNA sequences of strain ZYM-1 (GenBank accession number: KT263530) revealed that it belongs to the genus *Lysinibacillus*. Besides the widely reported heavy metal resistance of *Lysinibacillus* spp., strain ZYM-1 also exhibits high selenate (MIC 10 mM), selenite (MIC 100 mM), and tellurite (MIC 2 mM) resistance. Red selenium and black tellurium nanoparticles were formed as reduction products of selenite and tellurite, which have potential application in heavy metal adsorption, photocatalysis, and energy storage (4–6). As no selenite/tellurite reduction capacity has been reported among the *Lysinibacillus* spp., and most strains of *Lysinibacillus* have been isolated from soils, the genome sequence of strain ZYM-1 may provide fundamental information of selenite/tellurite reduction genes in this species.

The genome of strain ZYM-1 was sequenced using Illumina HiSeq-2500 by PE125 strategy. The obtained reads were assembled into 84 large contigs using SOAPdenovo software (<http://soap.genomics.org.cn/soapdenovo.html>). Then, gene prediction was performed using the GeneMarkS server (<http://opal.biology.gatech.edu>). The genome sequence of ZYM-1 is 4,862,873 bp in length with G+C content of 37.86%. There are 5,006 predicted coding sequences, accounting for 85.01% of the total sequences.

A rich set of 247 annotated genes are related to inorganic ion transport and metabolism according to the COG function classification (7). As mentioned previously, strain ZYM-1 could tolerate selenite up to 10 mM, but failed to reduce this oxyanion. This is consistent with the absence of any reported genes encoding

selenate reductases (*serABC*, *srdBCA*, *ynfE*, and *ygfK*) in the genome. In addition, the genes encoding NirS-type nitrite reductases are also not found (8). However, five thioredoxin reductases encoding genes are identified, which may have mediated the selenite reduction in strain ZYM-1 (9, 10). Also, two genes (*dedA* and *cysA*) encoding the possible uptake proteins selenite and selenate were found. On the other hand, we also found several genes involved in tellurite resistance and reduction, including *terC*, *terD*, *yceH*, and *yceF* (11). In addition, there are several genes involved in heavy metal resistance, such as ABC-type Mn²⁺/Zn²⁺ transport systems (*ytgA*, *ytgB*, *ytgC*, and *ytgD*) and the Zn²⁺ responsive regulator *zur*, which may relate to the Mn²⁺/Zn²⁺ resistance of strain ZYM-1. The genome sequence information indicates that strain ZYM-1 can provide a platform for selenite/tellurite detoxification and production of selenium/tellurium nanoparticles.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under accession number [LKPY00000000](https://www.ncbi.nlm.nih.gov/nuccore/LKPY00000000). The version described in this paper is the first version, LKPY01000000.

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