Draft Genome Sequence of
_Selenotrophomonas bentonitica_ BII-R7T, a Selenite-Reducing Bacterium Isolated from Spanish Bentonites

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**ABSTRACT** The Gram-negative bacterium _Selenotrophomonas bentonitica_ BII-R7T was isolated from bentonite formations. Like other species within the genus _Selenotrophomonas_, strain BII-R7T possesses high tolerance to numerous heavy metals, suggesting potential for bioremediation purposes. The draft genome sequence reported here comprises 4.37 Mb with a G+C content of 66.5% and 3,796 predicted protein-coding sequences.

_Selenotrophomonas bentonitica_ BII-R7T (= LMG 29893T = CECT 9180T = DSM 103927T) is a recently described Gram-negative bacterial strain that was isolated from bentonite formations located in southern Spain (1). The genus _Selenotrophomonas_ has hitherto comprised 14 established species, isolated from a large variety of environments (2–14), that are resistant to certain antibiotics and metals (15). In this sense, _S. bentonitica_ has shown high uranium (1) and selenium (M. A. Ruiz-Fresneda, unpublished data) tolerance due to different interaction mechanisms, suggesting potential applicability for bioremediation purposes. Indeed, the biotechnological use of _Selenotrophomonas_ spp. has already been proposed (16–21). Research on all but one of the 14 known _Selenotrophomonas_ spp., _S. tumulicola_ (13), counts on freely available genome sequences of the corresponding species (22). Here, we report the draft genome sequence of _S. bentonitica_ strain BII-R7T.

After cultivation on LB medium, genomic DNA of _S. bentonitica_ BII-R7T was extracted as described by Martín-Platero et al. (23). A genomic library with an insert size of 350 bp was sequenced using the Illumina HiSeq 2000 platform at Macrogen, Inc. (Seoul, Republic of Korea).

A total of 53,608,108 paired-end 101-bp reads were obtained (>1,000 × coverage). The quality of the reads was assessed using FastQC (24), and the Q20 and Q30 indices were 95.34% and 87.69%, respectively. Multiple de novo genome assemblies were performed using ABySS version 1.5.1 (25) with k-mer sizes between 19 and 95. The assemblies were merged, filtered, and further assembled into scaffolds using TransABySS (26) and GS de novo assembler software (Roche). We obtained 191 scaffolds with an N50 of 35,432 and an L50 of 38. The mean size of these scaffolds was 22,890 bp with the largest comprising 187,875 bp and the smallest comprising 2,262 bp. The size of the entire sequence was 4,371,992 bp with a 66.5% G+C content, which are values in accordance with described _Selenotrophomonas_ spp.

Gene prediction and annotation were performed using the Rapid Annotations using Subsystems Technology server (27) and the Prokaryotic Genome Annotation Pipeline (28). The genomic features of _S. bentonitica_ BII-R7T included a total of 3,786 coding sequences (CDSs), 1 complete rRNA cluster, 44 tRNAs, 4 ncRNAs, and 158 pseudogenes. The coding sequences were classified into 431 subsystems, the most abundant of which were for the metabolism of amino acid derivatives (n = 352 CDSs); carbohydrates (n =...
protein metabolism (n = 205); metabolism of cofactors, vitamins, prosthetic groups, and pigments (n = 204); membrane transport (n = 160); and RNA metabolism (n = 147). Additionally, 115 of these coding sequences were related to stress responses, such as osmotic and oxidative stress, cold and heat shock stress, or uptake of selenate and selenite. Genes related to degradation or resistance to a variety of toxic compounds (e.g., ethidium bromide) and heavy metals (e.g., cobalt, zinc, cadmium, tellurium, copper, arsenic, or mercury) were also identified in the present draft genome. Moreover, the draft genome contains specific enzymes, such as alkaline and acid phosphatases or gluthionine reductases, which could, respectively, be involved in the high levels of tolerance that S. bentonitica BII-R7T (1, 17) has to uranium and selenium.

Accession number(s). This whole-genome shotgun project has been deposited at GenBank/ENA/DDJB under the accession number MKCZ00000000. The version described in this paper is the first version, MKCZ01000000.

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