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GENOME SEQUENCES

Draft Genome Sequence of *Bacillus safensis* RP10, Isolated from Soil in the Atacama Desert, Chile

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ABSTRACT Genome analysis of *Bacillus safensis* RP10, a strain from the soil of Atacama Desert in northern Chile, reflects a bacterium adapted to live in soil containing high levels of heavy metals, high salt conditions, and low carbon and energy sources.

The Atacama Desert of Chile is the driest desert in the world (1, 2) and has soils naturally enriched in heavy metals and salts, which affects local agricultural activities (3). These soils also harbor species of the genus *Bacillus* (4, 5). This genus is adapted to live in many different environments (6, 7), and it has been used for biocontrol of agricultural plagues (8), for phytoremediation (9, 10), and as a probiotic (11). With the aim of understanding how *Bacillus* species have adapted to conditions in the Atacama Desert, we isolated *Bacillus* strains by mixing 1 g of soil with 9 ml of NaCl 0.8% and incubating at 50°C for 1 h. The solution was decanted, and 1 ml of the supernatant was spread on Luria broth (LB) agar and incubated at 37°C for 4 days under aerobic conditions. One of the colonies recovered was named RP10, and its genome was sequenced. The genomic DNA was purified using a QuickExtract bacterial DNA extraction kit (Epibio), and the library was constructed using a Nextera XT kit (Illumina). Whole-genome shotgun sequencing was performed using 2 × 250- bp (paired-end) reads on an Illumina MiSeq platform. A total of 14.2 million reads was obtained. Reads were filtered for a Phred quality score of at least 20 and assembled using the A5 pipeline (2015 Linux, default parameters) (12). Open reading frame prediction and annotation were performed using Prokka software version 1.11 (13).

Bacillus species identification was achieved by using the JSpeciesWS server online with BLAST (14) average nucleotide identity (ANIb) and MUMmer average nucleotide identity (ANIm) analysis (15–17). The RP10 strain was identified as a member of the species *Bacillus safensis*, and the highest identities were with *B. safensis* FO-36b (16S rRNA, 99.2%; ANIb, 98.83%; ANIm, 99.07%) and *B. safensis* JPL-MERTA-8-2 (ANIb, 98.7%; ANIm, 99.00%). Both strains were isolated from clean rooms at the Jet Propulsion Laboratory at NASA (Pasadena, CA). (18–19). A genome comparison between these three strains by Mauve software (20) and the Rapid Annotation using Subsystem Technology (RAST)-National Microbial Pathogen Database Resource (NMPDR) server with SEED view indicated that the RP10 genome contained an island enriched in phage-related genes (60 kb), an arsenic resistance operon, and other uncharacterized metabolic operons not found in the other two genomes.

The draft genome of *Bacillus safensis* RP10 consists of 3,813,379 bp distributed in 102 contigs, with an average GC content of 41.7%. The draft genome comprises 75 tRNAs and 20 T box leader sequences that are probably involved in a riboswitch mechanism described for Gram-positive bacteria (21). The RAST-NMPDR server with SEED view

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indicates that this strain carries genes and operons for resistance to arsenic (*arsRRBC*), lead (*epsABCDEFFHIKLMN* and *cadA*), copper (*copZA*), and manganese (*mntP*, *mnH*, and *mntABC*) and an operon with potential antimicrobial activity and 34% identity with the bacteriocin operon AS-48 of *Enterococcus faecalis*. Finally, the genome encodes diverse capabilities for synthesizing several vitamins, siderophores, and aromatic compounds, including tryptophan (*trpEDCFBA*) and several multidrug efflux pumps, which are potentially associated with the ability to survive under saline soil conditions with a low content of energy and carbon sources.

Data availability. This whole-genome shotgun project has been deposited at DDBJ/ENA/GenBank under the accession number MKXN00000000 with contigs under accession numbers MKXN01000001 to MKXN01000102, and the raw reads are available in the SRA under the accession number PRJNA345377.

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