Genome Sequence Announcement of *Bacillus paranthracis* Strain ICIS-279, Isolated from Human Intestine

Oleg V. Bukharin,a Natalia B. Perunova,a Sergey V. Andryuschenko,a Elena V. Ivanova,a Taisia A. Bondarenko,a Irina N. Chainikova

aOrenburg Federal Research Center of the Ural Branch of the Russian Academy of Sciences, Institute for Cellular and Intracellular Symbiosis, Orenburg, Russia

**ABSTRACT** This report describes the genome sequence of *Bacillus paranthracis* strain ICIS-279, isolated from human feces. It demonstrates a tumor necrosis factor alpha (TNF-α) inhibitory activity up to 0.1 ng/ml. The genome size is 5,180,499 bp, with a G+C content of 35.4%. Annotation revealed 5,168 coding sequences, including 5,168 proteins and 43 rRNA, 102 tRNA, and 5 noncoding RNA (ncRNA) genes.

The *Bacillus cereus* group comprises 21 closely related species of environmentally ubiquitous spore-forming Gram-positive bacteria (1). Some of them are opportunistic pathogens (2, 3). Due to their diverse lifestyles and differences in gene content, some strains of the *B. cereus* group are considered to be probiotics (4). Bacillus-based probiotics have a specific advantage, namely, the inherent resistance of *Bacillus* spores (5) to different environmental conditions.

*Bacillus paranthracis* strain ICIS-279 was initially isolated on a Schaedler agar plate (HiMedia Laboratories Pvt. Limited) from a human feces sample diluted in a 0.9% NaCl solution to 10⁵-fold by mass. Taxonomic belonging of this strain was verified by the 16S rRNA gene sequence.

In order to apply the DNA isolation procedure, a single colony of ICIS-279 agar culture (HiMedia Laboratories Pvt. Limited) from a human feces sample diluted in a 0.9% NaCl solution to 10⁵-fold by mass. Taxonomic belonging of this strain was verified by the 16S rRNA gene sequence.

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The genomic DNA of *B. paranthracis* strain ICIS-279 was used to prepare a DNA library with the Nextera XT DNA sample preparation kit (Illumina). The library was sequenced in a 2×300-nucleotide run by using the MiSeq reagent kit version 3 and MiSeq desktop sequencer (Illumina). The 2,339,050 sequence reads generated were quality trimmed by using the sliding window mode of the Trimmmomatic program version 0.36 (8). De novo genome assembly was performed by using the SPAdes genome assembler (St. Petersburg genome assembler; version 3.10.1) (9). The assembly yielded 109 contigs covering a total of 5,180,499 bp, with an N₅₀ value of 115,047 bp, a G+C content of 35.4%, and an average coverage of 30.6×. The genome sequence was annotated using the National Center for Biotechnology Information (NCBI) Prokaryotic Genome Annotation Pipeline (PGAP) (10), which revealed 5,510 gene sequences, including 5,168 proteins, 192 pseudogenes, 43 rRNA genes (5S, 16S, and...
23S), 102 tRNA genes, and 5 noncoding RNA (ncRNA) genes. Software was used with the default settings and parameters unless otherwise specified.

The revealed properties of *B. paranthracis* ICIS-279 (TNF-α inhibitory activity) may be useful for probiotic development. This strain can serve as one of the models for host-microbiota interaction studies.

**Data availability.** This whole-genome shotgun project has been deposited at DDBJ/ENA/GenBank under the accession number SWDD00000000. The version described in this paper is the first version, SWDD01000000. The BioProject database accession number of the sequenced strain is PRJNA412558. The Sequence Read Archive information for this project is available under the accession number SRP185385.

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