

Whole-Genome Shotgun Sequencing of the Extremophile *Alkalibacillus haloalkaliphilus* C-5, of Indian Origin

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***Alkalibacillus haloalkaliphilus* C-5 is a haloalkaliphilic bacterium that was isolated from a soil sample from the salty Sambhar Lake, Rajasthan, India. The organism is capable of alkaline protease production under conditions of pH 10 and 10% (wt/vol) salt. We sequenced and have reported the whole genome of *Alkalibacillus haloalkaliphilus* C-5, of Indian origin, for the first time.**

Haloalkaliphilic bacteria, a group of organisms with twin extremities of pH and salinity, have been investigated after isolation from a variety of habitats (2, 3, 4, 5). The limited studies on the unique applications of extremophiles indicate that the unique “survival strategies” available for these organisms can be a great source of novel commercial applications. Their robust biocatalysts and unique metabolic capabilities are the major points of attractions of the organisms for developing processes for bioremediation and other biotechnological applications. Such important molecules from these microbes from unexplored and extreme habitats have recently prompted interest among scientific communities and industry (6). Most of the studies (4) on haloalkaliphilic bacteria, however, have so far focused on phylogenetic analyses of the organisms, and only limited information is available on their genomics and other potential biotechnology applications.

Alkalibacillus haloalkaliphilus C-5 was isolated from a saline soil sample from Sambhar Lake, Rajasthan, India. It is an aerobic, Gram-positive, rod-shaped organism. It shows optimal growth at pH 10, 10% (wt/vol) NaCl, and 37°C. It produces a thermophilic serine protease. The genome sequence for *Alkalibacillus haloalkaliphilus* C-5 was determined to help us understand its physiology and enzymatic potentials.

The whole-genome sequencing of *Alkalibacillus haloalkaliphilus* C-5 was performed using an Ion Torrent PGM sequencer. The data generated from the genomic library contained 419,990 reads and 46,141,879 nucleotide bases, with an average read length of 110 bases. Assembly using Newbler version 2.6 generated a 2,913,611-bp single chromosome. The genome annotation and comparative analysis of the genome were performed using the RAST program (rapid annotation using subsystem technology) (1). The organism has a GC content of 37.1%, with 3,160 predicted coding regions and 55 RNA genes. Of the 55 RNA genes, 52 code for tRNA, 2 for rRNA, and 1 is for 5S rRNA. For metabolic reconstruction, metabolic subsystems were assembled to create a metabolic reaction network for *Alkalibacillus haloalkaliphilus* C-5.

The subsystem analysis revealed various genes involved in (i) metabolic pathways of cofactors, vitamins, prosthetic groups, and pigments, (ii) cell wall and capsule, (iii) virulence, disease, and defense, (iv) potassium metabolism, (v) membrane transport, (vi) iron acquisition and metabolism, (vii) RNA and protein metabo-

lism, (viii) cell division and regulation, (ix) cell signaling, (x) DNA metabolism, (xi) nitrogen metabolism, (xii) sporulation, (xiii) stress responses, (xiv) metabolism of aromatic compounds, amino acids, and derivatives, and (xv) sulfur, phosphorous, and carbohydrate metabolism. The presence of genes related to osmotic stress, oxidative stress, heat shock, and other sources of stress explain the organism’s possible survival strategy in such a hypersaline environment.

Nucleotide sequence accession number. The complete sequence of the *Alkalibacillus haloalkaliphilus* C-5 genome can be accessed under GenBank accession number [AKIF00000000](https://www.ncbi.nlm.nih.gov/nuclseq/ALIF00000000).

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