

Draft Genome Sequence of *Brevibacillus* sp. Strain BAB-2500, a Strain That Might Play an Important Role in Agriculture

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A Gram-positive bacterium, *Brevibacillus* sp. strain BAB-2500, was isolated as a lab contaminant in Gandhinagar, Gujarat, India. The draft genome (5.3 Mb) of the strain possesses genes for the reduction of arsenate and aluminum. These findings might provide insights into the utilization of this strain for improving crop production.

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The genus *Brevibacillus* was established within the family *Paenibacillaceae* by Shida et al. (1). He reclassified nine species of the genus *Bacillus*, i.e., *Bacillus brevis* (2), *Bacillus laterosporus* (3) *Bacillus thermoruber* (4), *Bacillus agri* (5), *Bacillus centrosporus* (5), *Bacillus choshinensis* (6), *Bacillus borstelensis* (7), *Bacillus formosus* (7), and *Bacillus reuszeri* (7), and placed them within a new genus, *Brevibacillus* (1). Subsequently, 8 validly named species were placed taxonomically within this genus: *Brevibacillus invocatus* (8), *Brevibacillus limnophilus* (9), *Brevibacillus levickii* (10), *Brevibacillus ginsengisoli* (11), *Brevibacillus panacihumi* (12), *Brevibacillus fluminis* (13), *Brevibacillus aydinogluensis* (14), and *Brevibacillus nitrificans* (15). Members of this genus are reported to be rod-shaped, Gram-positive or Gram-variable, motile by means of peritrichous flagella, and strictly aerobic, with G+C content ranging from 42.8 to 57.4%. Earlier studies have shed light on the agricultural importance of a few members of this genus, for use as biocontrol agents (16), denitrifying bacterium (11), etc. Thus, *Brevibacillus* sp. strain BAB-2500, isolated as a lab contaminant, was subjected to whole genome sequencing for genomic study; this can add more knowledge about the agricultural as well as other potential applications of the members of this genus.

Genome sequencing of the strain was done with a high-throughput Ion Torrent Personal Genome machine with Ion Torrent Server (Torrent suite v3.2), and total data of 1,581,318 paired-end reads with 22.46 \times coverage (mean length read is 90 bp with highest read of 200 bp) were obtained. *De novo* assembly was performed using the MIRA-3 assembler (v3.1.0). The annotation of the genome was performed using the NCBI Prokaryotic Genomes Automatic Annotation Pipeline (PGAAP) (<http://www.ncbi.nlm.nih.gov/genomes/static/Pipeline.html>) utilizing GeneMark, Glimmer, and tRNAscan-SE tools (17), and using the Rapid Annotations using Subsystems Technology (RAST) server with the SEED database (18).

The total length of the genome was found to be 5,38,6487 bp, allocated into 329 contigs having >500 bp each (scaffold N₅₀; largest contigs, 48,866 bp) and 52 contigs \leq 500 bp. The G+C content was 53.5%. The draft genome of the strain BAB-2500

harbored 5,457 genes that encode 5,349 protein-coding genes, 94 transfer RNAs, and 14 ribosomal RNAs.

The genome harbored genes for the biosynthesis of vitamins B₁₂ and B₅. Transporters for multidrug resistance, potassium uptake, and arsenical pump efflux were identified within the genome. Genes for the biosynthesis of various sugars and the degradation of various aminosugars were also annotated. The loci of the CRISPR-associated endoribonuclease (Cas2) gene were present in the genome, which might play a role in providing the acquired immunity to species. The strain also exhibited an arsenate reductase enzyme that catalyzes the reduction of the toxic compound arsenate to arsenite. Cystathionine beta-lyase protein, which significantly contributes to aluminum resistance, was also predicted within the genome. These findings suggest that the strain might play a vital role in the improvement of crop production in metal-contaminated soil, as well as in acidic soil. Therefore, the draft genome of the species provides insights into the functional characterization of significant genes within the genome.

Nucleotide sequence accession number. The draft genome sequence of *Brevibacillus* sp. BAB-2500 has been deposited at GenBank under the accession no. [AOBR000000000](https://www.ncbi.nlm.nih.gov/nuccore/AOBR000000000).

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