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Draft Genome Sequence of *Arthrobacter gangotriensis* Strain Lz1y^T, Isolated from a Penguin Rookery Soil Sample Collected in Antarctica, near the Indian Station Dakshin Gangotri

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We report here the 4.3-Mb genome of *Arthrobacter gangotriensis* strain Lz1y^T, isolated from a penguin rookery soil sample collected in Antarctica, near the Indian station Dakshin Gangotri.

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Arthrobacter gangotriensis strain Lz1y^T is a Gram-positive, pleomorphic, and nonmotile bacterium (1). According to the 16S rRNA gene similarity, the nearest phylogenetic neighbors of *Arthrobacter gangotriensis* strain Lz1y^T are *Arthrobacter antarcticus* SPC26^T (99.36%), *Arthrobacter sulfureus* DSM 20167^T (98.64%), *Arthrobacter psychrophenolicus* AG31^T (98.36%), *Arthrobacter kerguelensis* KGN15^T (98.14%), and *Arthrobacter cryotolerans* LI3^T (97.77%).

The genome of *Arthrobacter gangotriensis* strain Lz1y^T was sequenced using Roche 454 (FLX titanium) pyrosequencing platform. The sequencing yielded 86,795,230 bases in 225,283 reads, which is a 20× coverage of the genome. The assembly of the raw data was performed using the GS *de novo* Assembler (version 2.8; F. Hoffmann-La Roche Ltd., Switzerland). Assembly yielded a genome of 4,319,900 bp in 20 contigs. All contigs were $\geq$2,394 bp, with largest contig of 656,281 bp, and an average contig length of 173,043 bp. All sequences were above the quality score of 40, with a mean quality score of 63.90. The G+C mol% of the genome of *Arthrobacter gangotriensis* strain Lz1y^T was found to be 61.40%, which is near the experimentally calculated value of 66% (1). The Prokaryotic Genome Annotation System (PROKKA) pipeline (2) was used for the annotation of the genome; tRNA was predicted by tRNAscan-SE 1.23 (3) and rRNA genes by RNAmmer 1.2 (4). The annotation has 4,082 genes, including 61 tRNAs, 4 rRNAs (5S-16S-23S), and 4,017 protein-coding genes. The annotation has 5 genes for bacterial chemotaxis and 96 genes for membrane transport, including 51 ABC transporters. The annotation also has 32 genes for resistance against antibiotics and toxic compounds, including 4 arsenic resistance genes, 7 mercury resistance genes, 12 copper homeostasis genes, and 3 cobalt-zinc-cadmium resistance genes. There are 4 genes for alkane biosynthesis in the annotation of the genome.

The sequencing of the genome of this bacterium will help in understanding the adaptation of microorganisms under extreme environmental conditions.

Nucleotide sequence accession numbers. The draft genome sequence of *Arthrobacter gangotriensis* strain Lz1y^T has been deposited in DDBJ/EMBL/GenBank under the accession AOCK00000000. The version described in this paper is the first version, AOCK01000000.

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