



Data in Brief

High-quality complete genome sequence of *Microbacterium* sp. SUBG005, a plant pathogen



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ABSTRACT

Microbacterium sp. SUBG005 is a Gram positive bacterium, isolated from infected leaf of *Mangifera indica* L. in Rajkot (22.30°N, 70.78°E), Gujarat, India. The genome sequencing of *Microbacterium* sp. SUBG005 is having type I secretion system genes of pathogenicity as well as heavy metal resistance unique genes. The genome size is 7.01 Mb with G + C content of 64.80% and contains rRNA sequences. Genome sequencing analysis provides information about the microbe role in host–pathogen interaction. The whole genome sequencing has been deposited in DDBJ/EMBL/GenBank under the accession number JNNT00000000.

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Specification

Organism	<i>Microbacterium</i> sp.
Strain	SUBG005
Sequencer	Ion Torrent PGM
Data format	Processed
Experimental factor	Microbial strain
Experimental features	Whole genome sequencing of <i>Microbacterium</i> sp. SUBG005
Consent	N/A
Sample source location	Rajkot, Gujarat, India

1. Direct link to deposited data

<http://www.ncbi.nlm.nih.gov/bioproject/248942>.

The genus *Microbacterium* was proposed by [1] which having numerous species established within the family Microbacteriaceae [1–3]. The organisms of these genera are characterized by the presence of N-glycolyl residues in the cell walls, by having major isoprenoid quinones MK-11, MK-12 and MK-13 or minor isoprenoid menaquinones MK-10 or MK-14 and by G + C contents of 65–72 mol%. The genus *Microbacterium* is known to infect human and animals most frequently, only one report on plant is found [4–6].

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2. Experimental design, materials and method

Microbacterium sp. strain SUBG005 was isolated from the infected leaves of *Mangifera indica* L. The isolate was confirmed as a phytopathogen by pathogenicity test on healthy leaves of *M. indica* L. and fulfilled Koch's postulates. Genomic DNA was extracted from young culture grown in nutrient medium using protocol given by [7].

Genome sequencing of this strain was done with high throughput ion torrent personal genome machine with ion torrent server (torrent suite v3.2), and total data of 17, 22,450 paired-end reads with 103.45X coverage were obtained. De novo assembly was performed using 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/genome/annotation_prok/) utilizing GeneMark, Glimmer, and tRNAscan-SE tools [8] and functional annotation was carried out using the Rapid Annotations using subsystems Technology (RAST) server with the seed database [9].

The total length of the genome was found to be 70, 21,676 bp, allocated into 485 contigs having >500 bp and 5740 contigs ≤500 bp. The genome of the strain SUBG005 having 6225 contigs showed 4630 protein coding sequences. Organism also contains 1879 N50 contigs, 92 rRNA (5s, 16s, 23s) and 119 tRNA. According to RAST annotation, it is interesting to note that this organism having ten genes for type I secretion systems for aggregation (Fig. 1).

Additionally, SUBG005 have 967 genes for carbohydrate metabolism, sixty seven genes for nitrogen metabolism, four genes for Arsenic resistance as well as five genes for resistance of other heavy metals like cobalt, zinc and cadmium. It also has one hundred fifty three genes related to virulence, disease and defense and 92 genes for ABC transporter as well as 26 genes for cation transporter.

Subsystem Information

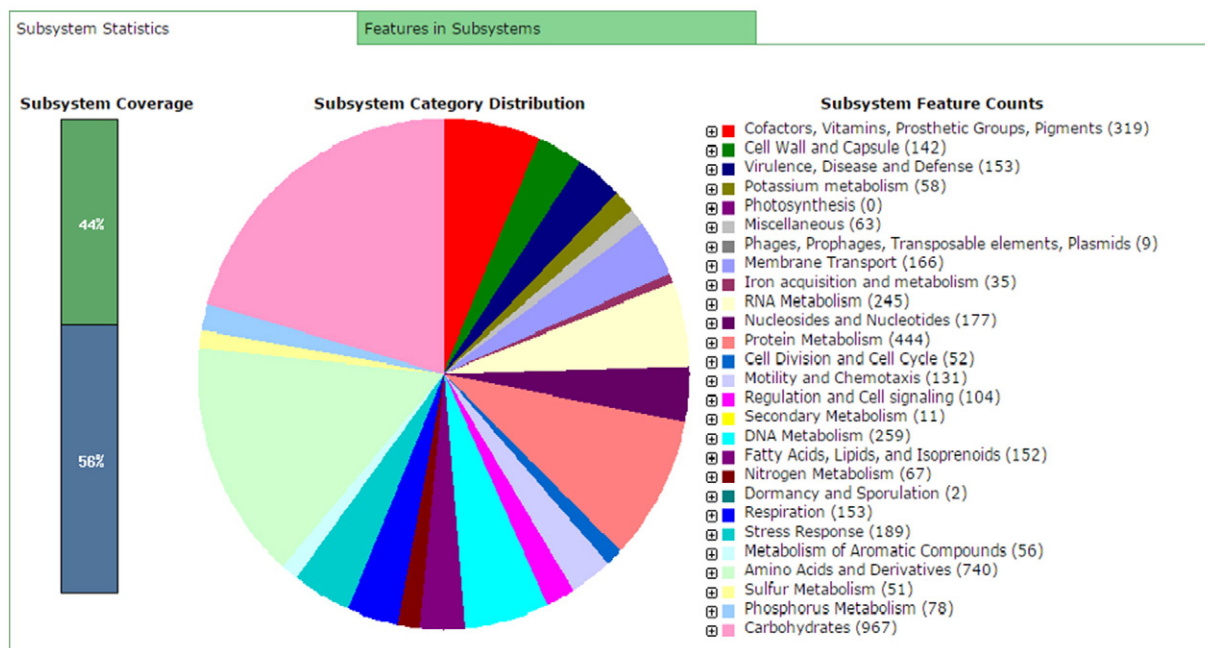


Fig. 1. Subsystem information of genome *Microbacterium* sp. SUBG005 (annotated by RAST server).

3. Nucleotide sequence accession number

The whole genome shotgun project of *Microbacterium* sp. SUBG005 has been deposited at GenBank under the accession no. JNNT00000000.

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