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Data in Brief

Whole genome sequences and annotation of *Micrococcus luteus* SUBG006, a novel phytopathogen of mango

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ABSTRACT

Actinobacteria, *Micrococcus luteus* SUBG006 was isolated from infected leaves of *Mangifera indica* L. var. Nylon in Rajkot, (22.30°N, 70.78°E), Gujarat, India. The genome size is 3.86 Mb with G + C content of 69.80% and contains 112 rRNA sequences (5S, 16S and 23S). The whole genome sequencing has been deposited in DDBJ/EMBL/GenBank under the accession number JOKP00000000.

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Specification	
Organism	<i>Micrococcus luteus</i>
Strain	SUBG006
Sequencer	Ion Torrent PGM
Data format	Processed
Experimental factor	Microbial strain
Experimental features	Whole genome sequencing of <i>Micrococcus luteus</i> SUBG006
Consent	N/A
Sample source location	Rajkot, Gujarat, India

1. Direct link to deposited data

<http://www.ncbi.nlm.nih.gov/bioproject/252773>

2. Experimental design, materials and methods

The genus *Micrococcus* proposed by [1] has numerous species established within the genus *Micrococcus* [2,3,4,5]. *Micrococcus luteus* was first described by [1,6]. *Micrococcus luteus* are Gram positive cocci that are 0.5 to 3.5 µm in diameter and arranged in tetrads or irregular clusters. This strain was isolated from infected leaves of *Mangifera indica* L. var. Nylon. Isolate was confirmed as phytopathogen using

pathogenicity test on healthy leaves of *Mangifera indica* L. and fulfilled Koch's postulates. DNA was extracted from isolated and reisolated organisms using protocol given by [7]. 16 s rRNA gene were sequenced using 3130 Genetic analyzer, Applied Biosystems, USA. Sequences were submitted to NCBI GenBank under accession numbers KM454981 and KM37667. The pathogen was identified as *Micrococcus luteus* strain SUBG006 using biochemical test and molecular techniques.

The whole genome sequencing of *Micrococcus luteus* SUBG006 was performed on an Ion-Torrent PGM sequencer using 314 chip and 200 bp chemistry as per the manufacturer's instructions. 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].

Data generation from the library contained 13, 78, 500 reads with an average coverage of 107.0×. The total lengths of the genome were found to be 38, 62, 811 bp, with 3169 contigs contains 2085 proteins, 2744 genes, 112 coded for rRNAs and 108 coded for tRNAs. The GC content of genome is 69.80%.

The subsystem analysis provided the insight of various genes involved in (1) cell wall and capsule, (2) virulence, disease and defense, (3) cofactors, vitamins, prosthetic groups, pigments, (4) membrane transport, (5) cell division and cell cycle, (6) fatty acids, lipids, and isoprenoids, (7) amino acids and derivatives, (8) respiration, (9) stress response, (10) nucleosides and nucleotides and (11) metabolism of

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potassium, RNA, DNA, protein, secondary metabolites, nitrogen, sulfur, phosphorus and carbohydrates.

Analysis of virulence disease and defense subsystems provide insight into *Micrococcus luteus* SUBG006 contains metal resistance genes for arsenic, cobalt, cadmium, zinc and mercuric. In addition, type II secretion system gene cluster and ABC transporters genes are also found into membrane transport subsystems. They are known to play key role in pathogenicity mechanism.

3. Nucleotide sequence accession number

The whole genome shotgun project of *Micrococcus luteus* SUBG006 has been deposited at GenBank under the accession no. JOKP00000000.

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