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Data in Brief

Genomic analysis of novel phytopathogenic *Georgenia* sp. strain SUB25

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ABSTRACT

A Gram positive bacterium, *Georgenia* sp. SUB25 was isolated from infected leaves of *Solanum lycopersicum* L. in Rajkot (22.30°N, 70.78°E), Gujarat, India. We sequenced and analyzed *Georgenia* sp. SUB25 that is novel plant pathogen using next generation sequencing platform and assembly yielded contigs representing a size of 4.84 Mb with 81 tRNAs and 88 rRNAs. The whole genome sequencing has been deposited in DDBJ/EMBL/GenBank under the accession number JNFL00000000. This genome sequence contains Type II secretion system genes, which involved in pathogenicity mechanism that may help to understand plant microbial interaction.

Specifications	
Organism	*Georgenia* sp.
Strain	SUB25
Sequencer	Ion Torrent PGM
Data format	Processed
Experimental factor	Microbial strain
Experimental features	Whole genome sequencing of *Georgenia* sp. SUB25
Consent	N/A
Sample source location	Rajkot, Gujarat, India

1. Direct link to deposited data

http://www.ncbi.nlm.nih.gov/bioproject/224116.

The genus *Georgenia* was established within the family Bogoriellaceae subdivided into genera *Bogorilla* [1] and *Georgenia* [2]. Members of genus *Georgenia* are reported to be Gram-positive, motile or non-motile, non-endospore forming, aerobic or facultative anaerobic, oxidase and catalase positive *actinobacteria*. They are also identified on the basis of chemotaxonomic properties such as fatty acid profiling, polar lipids, amino acids, peptidoglycan as well as isoprenoid quinones with MK-8(H(4)) as the predominant menaquinone and less frequently by polyamines. They are having unique characteristics containing anteiso-$C_{15:0}$ as a predominant fatty acid and DNA G + C contents range from 69.7 to 72.9 mol%. At the time of writing the genus comprises ten different recognized species namely *Georgenia muralis* [2], *Georgenia ruanii* [3], *Georgenia thermotolerans* [4], *Georgenia soli* [5], *Georgenia halophila* [6], *Georgenia daeguensis* [7], *Georgenia satyanarayani* [8], *Georgenia sediminis* [9], *Georgenia deserti* and *Georgenia ferrireducens*; however, no one amongst them is reported as plant pathogen.

2. Experimental designs, materials and methods

Georgenia sp. strain SUB25 was isolated from infected leaves of *Solanum lycopersicum* L. Pure culture was maintained on nutrient agar containing 0.5% salt concentration with beef extract. The isolate was confirmed as phytopathogen by pathogenicity test on healthy leaves of *S. lycopersicum* L. and fulfilled Koch's postulates. Genomic DNA was extracted from 24 h old culture using protocol given by [10]. Phytopathogen was identified based on biochemical test and 16s rDNA sequencing.

Genome sequencing of this strain was performed with high throughput ion torrent personal genome machine with ion torrent server (torrent suite v3.2). 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.nim.nih.gov/genome/annotation_prok/) utilizing GeneMark, Glimmer, and tRNAscan-SE tools [11] and using the Rapid Annotations using subsystems Technology (RAST) server with the seed database [12]. Annotated sequences were submitted to NCBI GenBank under Whole genome sequencing projects.

Georgenia sp. strain SUB25 was Gram positive actinobacteria, rod in shape and about 0.8–1.2 μm in diameter; colonies were observed in yellow color, non-spore forming, oxidase and catalase positive. It also has capacity to utilize many monosaccharide and disaccharides.

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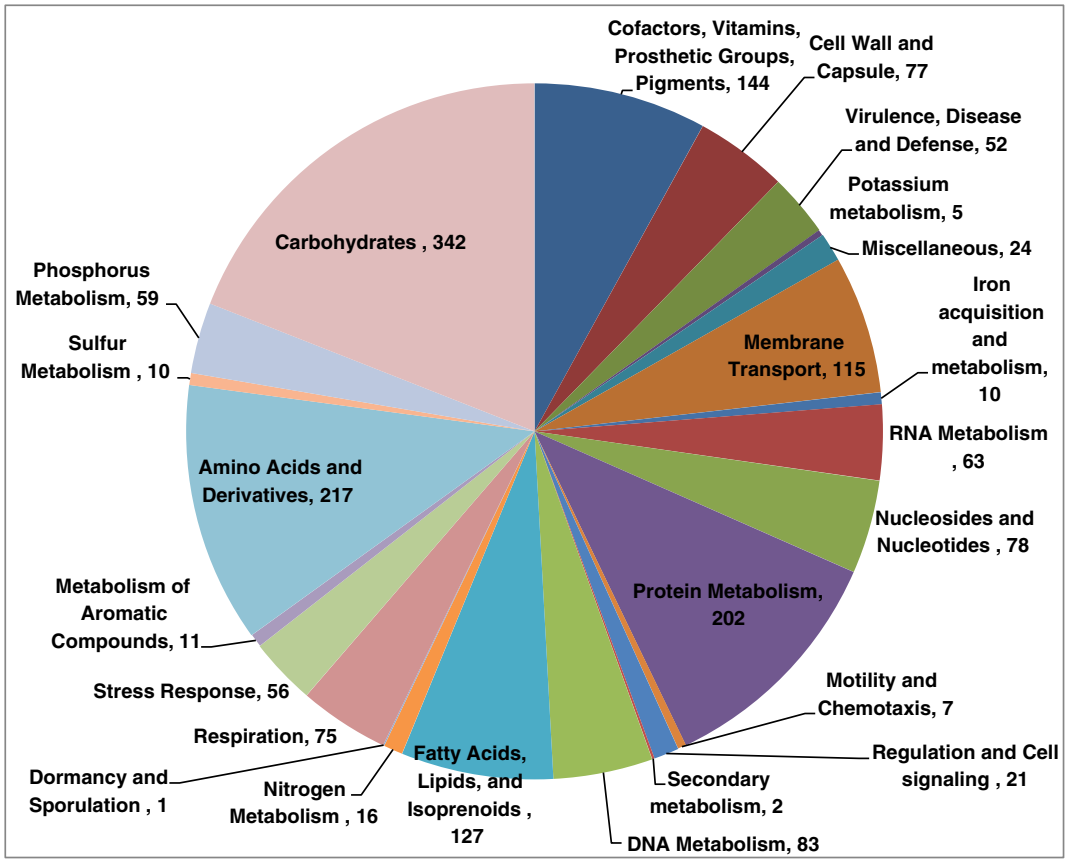

Fig. 1. Genes present in *Georgenia* sp. SUB25 (NZ_JNFL00000000) based on RAST annotation server.

Optimum growth and pH was observed at 37 °C temperature and at 7.0 pH. On the basis of 16S rRNA gene sequencing analysis the isolated organism was resembled to genus *Georgenia*.

The total length of the genome was found to be 48, 50, 495 base pairs, allocated into 796 contigs having >500 bp and 1852 contigs ≤500 bp with 88.5X coverage. Total 2648 contigs showed 4030 protein coding sequences, and 88 ribosomal RNAs. The G + C content is 71.80 mol%.

Prokaryotes use various secretion systems to infect plants. Pathogenicity is not reported till date in any member of genus *Georgenia*. According to RAST annotated, *Georgenia* sp. SUB25 having genes of Type II secretion system (T2SS). Type II secretion system is mediated by conserved, multi-component secretion system, which span both inner and outer membranes and proteins are transported. This secretion system encodes a novel genomic island, which encompasses the Tad (tight adherence) gene cluster, shown to be essential for colonization of surfaces by a human pathogen *Actinobacillus actinomycetemcomitans* [13,14]. The majority of tad genes were shown to be essential for tenacious biofilm formation and synthesis of bundled Flp pili (fibrils) that mediated adherence. The pilin subunit Flp remains inside the cell in various tad-mutants, indicating that they encode a secretion system for export and assembly of fibrils. Homologous gene clusters have been detected in a wide range of bacterial and archaeal species, and their sequence characteristics indicate possible horizontal transfer [15]. *Georgenia* sp. strain SUB25 having genes related to wide spread colonization and Type II/IV secretion system protein TadC, ATPase TadZ/CpaE, is associated with Flp pilus assembly and ATP hydrolase TadA/VirB11/CpaF, TadA subfamily genes.

In addition to these, five genes for potassium metabolism, sixteen genes for nitrogen metabolism, ten genes for iron metabolism, 59 genes for phosphorous metabolism along with 342 genes for carbohydrate metabolism, 127 genes for fatty acid metabolism and 202 genes for protein metabolism are also present. It also contains seven genes that are resistance towards cobalt–zinc–cadmium (Fig. 1).

3. Nucleotide sequence accession number

The whole genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession no. JNFL00000000; with reference sequence number NZ_ JNFL00000000.

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