Data in Brief

Genomic analysis of novel phytopathogenic Georgenia sp. strain SUB25

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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 JNFL0000000. This genome sequence contains Type II secretion system genes, which involved in pathogenicity mechanism that may help to understand plant microbial interaction.

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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 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.

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 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.

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 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.

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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 48,504,495 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].

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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References

[1] E. Stackebrandt, P. Schumann, Description of Bogoriellaceae fam. nov., Dermacoccaceae fam. nov., Rarobacteraceae fam. nov. and Sanguibacteraceae fam. nov. and emendation of some families of the suborder Micrococccineae. Int. J. Syst. Evol. Microbiol. 50 (2000) 1279–1285.
[2] P.P. Altenburger, P. Kasmpfer, P. Schumann, D. Vybiral, W. Lubitz, H.S. Busse, *Georgenia muralis* gen. nov., sp. nov., a novel actinobacterium isolated from a medieval wall. Int. J. Syst. Evol. Microbiol. 52 (2002) 875–881.
[3] W. Li, P. Xu, P. Schumann, Y. Zhang, R. Pukall, L. Xu, E. Stackebrandt, C. Jiang, *Georgenia ruanii* sp. nov., a novel actinobacterium isolated from forest soil in Yunnan (China), and emended description of the genus *Georgenia*. Int. J. Syst. Evol. Microbiol. 57 (2007) 1424–1428.
[4] M. Hamada, T. Tamura, Y. Ishida, K. Suzuki, Georgenia thermotolerans sp. nov., an actinobacterium isolated from forest soil. Int. J. Syst. Evol. Microbiol. 59 (2009) 1875–1879.

[5] P. Kampfer, A.B. Arun, H.J. Busse, S. Langer, C.C. Young, W.M. Chen, P. Schumann, A.A. Syed, P.D. Rekha, Georgenia soli sp. nov., isolated from iron-ore-contaminated soil in India. Int. J. Syst. Evol. Microbiol. 60 (2010) 1027–1030.

[6] S. Tang, Y. Wang, J. Lee, K. Lou, D. Park, C. Kim, W. Li, Georgenia halophilica sp. nov., a halophilic actinobacterium isolated from a salt lake. Int. J. Syst. Evol. Microbiol. 60 (2010) 1317–1321.

[7] S.G. Woo, Y. Cui, M.S. Kang, L. Jin, K.K. Kim, S.T. Lee, M. Lee, J. Park, Georgenia daeguensis sp. nov., isolated from 4-chlorophenol enrichment culture. Int. J. Syst. Evol. Microbiol. 62 (2012) 1703–1709.

[8] A. Srinivas, K. Rahul, C. Sasikala, Y. Subhash, E.V.V. Ramaprasad, V.C. Ramana, Georgenia satyanarayani sp. nov., an alkaliphilic and thermotolerant amylase-producing actinobacterium isolated from a soda lake. Int. J. Syst. Evol. Microbiol. 62 (2012) 2405–2409.

[9] Z. You, J. Li, S. Qin, X. Tian, F. Wang, S. Zhang, Georgenia sediminis sp. nov., a moderately thermophilic actinobacterium isolated from sediment. Int. J. Syst. Evol. Microbiol. 63 (2013) 4243–4247.

[10] K.S. Chudasama, V.S. Thaker, Screening of potential antimicrobial compounds against Xanthomonas campestris from 100 essential oils of aromatic plants used in India: an ecofriendly approach. Arch. Phytopathol. Plant Protect. 45 (2012) 783–795.

[11] T. Disz, S. Akhter, D. Cuevas, R. Olson, R. Overbeek, V. Vonstein, R. Stevens, R.A. Edwards, Accessing the SEED genome databases via Web services API: tools for programmers. BMC Bioinf. 11 (2010) 319.

[12] R.K. Aziz, D. Bartels, A.A. Best, M. DeJongh, T. Disz, R.A. Edwards, et al., The RAST server: rapid annotations using subsystems technology. BMC Genomics 9 (2008) 75.

[13] S.C. Kachlany, P.J. Planet, R. DeSalle, D.H. Fineand, D.H. Figurski, Genes for tight adherence of Actinobacillus actinomycetemcomitans: from plaque to pond scum. Trends Microbiol. 9 (2001) 429–437.

[14] H.C. Schreiner, K. Sinatra, J.B. Kaplan, D. Furgang, S.C. Kachlany, P.J. Planet, B.A. Perez, D.H. Figurski, D.H. Fine, Tight-adherence genes of Actinobacillus actinomycetemcomitans are required for virulence in a rat model. Proc. Natl. Acad. Sci. U. S. A. 100 (12) (2003) 7295–7300.

[15] P.J. Planet, S.C. Kachlany, D.H. Fine, R. DeSalle, D.H. Figurski, The widespread colonization island of Actinobacillus actinomycetemcomitans. Nat. Genet. 34 (2) (2003) 193–198.