Genome Resource of *Sphingomonas carotinifaciens* L9-754^T, an Endophyte Isolated From Leaf Tissues of *Jatropha curcas*

Gengmi Li,¹ Jian Qin,¹ Tao Zhang,¹ Li Yang,¹ Qianhua Yang,¹ Yingjiang Cao,¹ Bin Tang,¹ Zhaoxiang Li,¹ Jing Luo,¹ Shumei You,¹ Xianqi Wan,¹ Ying Liu,¹ Longbiao Guo,² Kaifeng Jiang,^{1,†} and Jiakui Zheng^{1,†}

¹ Key Laboratory of Southwest Rice Biology and Genetic Breeding, Ministry of Agriculture/Luzhou Branch of National Rice Improvement Center, Rice and Sorghum Research Institute, Sichuan Academy of Agricultural Sciences, Deyang 618000, P.R. China

² State Key Laboratory of Rice Biology, China National Rice Research Institute, Chinese Academy of Agricultural Sciences, Hangzhou 310006, P.R. China

Abstract

Sphingomonas carotinifaciens strain L9-754^T (DSM 27347) is a gram-negative, chemo-heterotrophic, and rod-shaped endophyte isolated from the stem tissues of *Jatropha curcas* L. This strain has putative in vitro antagonistic ability against the plant pathogenic fungus *Magnaporthe grisea*. A draft genome of L9-754^T was obtained using the PacBio SMRT cell platform. By analyzing the genome of strain L9-754^T, a gene cluster (GQR91_18700 - GQR91_18715) related to an antioxidant enzyme was identified in the obtained draft genome. The information obtained from the draft genome is expected to reveal the putative properties helpful in biocontrol applications.

Genome Announcement

Sphingomonas carotinifaciens L9-754^T is a gram-negative, aerobic, yellow-pigmented bacterium, which was isolated from the tissues of *Jatropha curcas* L. (Madhaiyan et al. 2017). We tested and observed that L9-754^T has in vitro antagonistic activity against plant pathogenic fungus *Magnaporthe grisea*.

The strain L9-754^T (DSM 27347) was grown at 28°C in nutrient broth (NB) and its total genomic DNA was extracted following the procedure described by Madhaiyan et al. (2017). The quality of the extracted DNA was tested using the NanoDrop 2000 UV-Vis spectrophotometer (Thermo Scientific, MA, U.S.A.) and Qubit 2.0 fluorometer (Life Technologies, MA, U.S.A.). For PacBio sequencing, 1.5 µg of the sheared DNA was used to prepare the SMRTbell library with the PacBio SMRTbell Template Prep Kit 1 (Pacific Biosciences, Menlo Park, CA, U.S.A.). Whole genome sequencing was performed using the PacBio sequencing system (Pacific Biosciences). Sequence runs for the two single-molecule real-time (SMRT) cell were performed on the PacBio RS II sequencer using a 120-min movie time/SMRT cell. Postfiltered data of 500 Mb from one cell with an average read length of 7 kb were considered for further assembly.

The obtained genome was de novo assembled using the hierarchical genome assembly process (HGAP) assembly protocol, available with the SMRT Analysis packages and

Funding

This study was supported by National Natural Science Foundation of China (grant no. 31901520), Sichuan Science and Technology (grant no. 2018JY0156), and Ability Improvement Project (grants no. 2016GXTZ-007, 2016ZYPZ-031, 2018QNJJ-21).

Keywords

Sphingomonas carotinifaciens, endophyte, antagonism

[†]Corresponding authors: K. F. Jiang, jiangkf67@126.com; J. K. Zheng, zhen6102@126.com

G. M. Li and J. Qin contributed equally.

The author(s) declare no conflict of interest.

Accepted for publication 8 July 2020.

Table 1. Genome statistics of *Sphingomonas carotinifaciens* L9-754^T

Attribute	Values
Genome size (bp)	4,094,655
Number of contigs	7
DNA G+C (%)	66.90
Total genes	3,826
Protein coding genes	3,687
RNA genes	73
rRNAs	12
tRNAs	58
ncRNAs	3
Pseudo genes	66
Genes with genome islands	197
NCBI accession	WSUT00000000

assessed through the SMRT Analysis Portal version 2.1. After assembly, the postfiltered reads were mapped back to the genome and coverage across the reference was measured.

The draft genome of L9-754^T was found to contain seven contigs corresponding to 4,094,655 base pairs. The completeness this genome was found to be 98.78% after running the CheckM (Parks et al. 2015) with a sequencing depth of around 78x. Coding sequences (CDS), tRNAs, and rRNAs were predicted using the RAST (rapid annotation using subsystem technology) annotation server (Overbeek et al. 2014). The Kyoto Encyclopedia of Genes and Genomes (KEGG) and Clusters of Orthologous Groups (COGs) were used to classify the predicted genes and pathways (Kanehisa and Goto 2000; Tatusov et al. 2000). Genomic islands (GIs) were detected using Island Viewer (Langille and Brinkman 2009). Gene clusters involved in secondary metabolite production were predicted by comparing the genome sequences with the antiSMASH database (Weber et al. 2015). In total, 3,687 coding sequences were predicted. Additional features of this genome are shown in Table 1. Interestingly, a gene cluster (GQR91_18700 to GQR91_18715) related to an antioxidant enzyme was uniquely observed in L9-754^T. Several reports have suggested that this gene cluster enhances the activity of antioxidant enzymes, increasing stress tolerance, and thus the biocontrol efficacy (Chi et al. 2015; Rais et al. 2017). Overall, the sequence provides insights into the physiology of this poorly studied bacterium, facilitating its potential application in biocontrol.

Data availability. The data obtained in this Whole-Genome Shotgun project have been deposited in GenBank under the accession number WSUT00000000. The version described in this paper is version WSUT00000000.1.

Literature Cited

- Chi, M., Li, G., Liu, Y., Liu, G., Li, M., Zhang, X., Sun, Z., Sui, Y., and Liu, J. 2015. Increase in antioxidant enzyme activity, stress tolerance and biocontrol efficacy of *Pichia kudriavzevii* with the transition from a yeast-like to biofilm morphology. *Biol. Control* 90:113-119.
- Kanehisa, M., and Goto, S. 2000. KEGG: Kyoto encyclopedia of genes and genomes. *Nucleic Acids Res.* 28:27-30.
- Langille, M. G. I., and Brinkman, F. S. L. 2009. IslandViewer: an integrated interface for computational identification and visualization of genomic islands. *Bioinformatics* 25:664-665.
- Madhaiyan, M., Alex, T. H. H., Cho, H., Kim, S.-J., Weon, H.-Y., Kwon, S.-W., Whitman, W. B., and Ji, L. 2017. *Sphingomonas jatrophae* sp. nov. and *Sphingomonas carotinifaciens* sp. nov., two yellow-pigmented endophytes isolated from stem tissues of *Jatropha curcas* L. *Int. J. Syst. Evol. Microbiol.* 67:5150-5158.
- Overbeek, R., Olson, R., Pusch, G. D., Olsen, G. J., Davis, J. J., Disz, T., Edwards, R. A., Gerdes, S., Parrello, B., Shukla, M., Vonstein, V., Wattam, A. R., Xia, F., and Stevens, R. 2014. The SEED and the rapid annotation of microbial genomes using subsystems technology (RAST). *Nucleic Acids Res.* 42: D206-D214.
- Parks, D. H., Imelfort, M., Skennerton, C. T., Hugenholtz, P., and Tyson, G. W. 2015. CheckM: assessing the quality of microbial genomes recovered from isolates, single cells, and metagenomes. *Genome Res.* 25:1043-1055.
- Rais, A., Jabeen, Z., Shair, F., Hafeez, F. Y., and Hassan, M. N. 2017. *Bacillus* spp., a bio-control agent enhances the activity of antioxidant defense enzymes in rice against *Pyricularia oryzae*. *PLoS One* 12:e0187412.
- Tatusov, R. L., Galperin, M. Y., Natale, D. A., and Koonin, E. V. 2000. The COG database: a tool for genome-scale analysis of protein functions and evolution. *Nucleic Acids Res.* 28:33-36.
- Weber, T., Blin, K., Duddela, S., Krug, D., Kim, H. U., Brucocoleri, R., Lee, S. Y., Fischbach, M. A., Müller, R., and Wohlleben, W. 2015. antiSMASH 3.0—a comprehensive resource for the genome mining of biosynthetic gene clusters. *Nucleic Acids Res.* 43:W237-W243.