Complete Genome Sequence Data of Rare Actinomycetes Strain *Saccharothrix texasensis* 6-C, a Biological Control Agent for Potato Late Blight

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Abstract

A rare actinomycetes strain of *Saccharothrix texasensis*, strain 6-C, has been isolated from the potato rhizosphere and it was shown to act as a biological control agent to potato late blight. It is also the first report on *Saccharothrix* spp. inhibiting *Phytophthora infestans*. Here, we present the complete genome data of *S. texasensis* strain 6-C, assembled by sequencing reads obtained by both PacBio and Illumina technologies with annotation. The final assembled genome length is 9,045,220 bp, without gaps and plasmid, and its GC content is 72.39%. Nine nonribosomal peptides synthetase, five type I polyketide synthase, four terpene, and three lanthipeptide gene clusters were identified in the genome, which would be likely to encode lots of antimicrobial active substances to help host plants against disease. This genome sequence could contribute to investigations of the molecular basis underlying the biocontrol activity of this *Saccharothrix* strain.

Keywords

biocontrol, genomics, rare actinomycetes, rhizosphere, *Saccharothrix* sp.

Genome Announcement

Actinobacteria are widely distributed in both terrestrial and aquatic ecosystems (Barka et al. 2016), and have been major storehouse microorganisms for the discovery of natural products that are highly effective against bacterial, fungal, and oomycete diseases (Choi et al. 2015; De Vrieze et al. 2018; Huang et al. 2007; Zhang et al. 2020). Although many of the discovered natural products have been successfully isolated from the most dominant actinomycetes genus, *Streptomyces*, novel natural products are increasingly coming from the non-*Streptomyces* family, known as rare actinomycetes (Choi et al. 2015; Tiwari and Gupta 2012). In actinomycetes, the number of antibiotics or bioactive molecules found thus far corresponds to approximately 10% or less of potential total number estimated by their biosynthetic genes, meaning that these genes are not expressed under typical laboratory culture conditions (Ding et al. 2019; Tiwari and Gupta 2012; Worsley et al. 2020). Accordingly, genome mining has become a widely practiced alternative way to identify potentially valuable cryptic natural products from actinomycetes. However, relatively few genome mining cases are available in rare actinomycetes, especially in genus *Saccharothrix*. At present, available records of 4,149 *Streptomyces* and 36 *Saccharothrix* genome assemblies can be searched at

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Table 1. Statistical table of secondary metabolite synthesis gene clusters^a

Cluster ID	Type	Similar cluster	Similarity (%)	Gene number
Cluster 1	Terpene	Lividomycin biosynthetic gene cluster, saccharide	6	20
Cluster 2	Lantipeptide	Erythraepectin biosynthetic gene cluster, RiPP	75	23
Cluster 3	Terpene	Isorenieratene biosynthetic gene cluster, terpene	42	23
Cluster 4	Bacteriocin	–	–	12
Cluster 5	Terpene	Isorenieratene biosynthetic gene cluster, terpene	85	24
Cluster 6	T3PKS	Herboxidiene biosynthetic gene cluster, polyketide	2	44
Cluster 7	Others	–	–	41
Cluster 8	NRPS	Erythrochelin biosynthetic gene cluster, NRPS	85	58
Cluster 9	NRPS-ladderane	Skylamycin biosynthetic gene cluster, NRPS	22	92
Cluster 10	Thiopeptide-T2PKS-NRPS	Sch47554/Sch47555 biosynthetic gene cluster, polyketide	21	115
Cluster 11	T1PKS	Akaeolide biosynthetic gene cluster, polyketide	32	34
Cluster 12	T1PKS	Meridamycin biosynthetic gene cluster, hybrid	10	41
Cluster 13	T1PKS-NRPS	Lobosamide biosynthetic gene cluster, T1PKS	8	67
Cluster 14	Others	Leinamycin biosynthetic gene cluster, hybrid	4	41
Cluster 15	NRPS	Salinomycin biosynthetic gene cluster, polyketide	12	50
Cluster 16	Oligosaccharide-others-T1PKS-NRPS	Streptazone E biosynthetic gene cluster, T1PKS	75	116
Cluster 17	T1PKS	Salinilactam biosynthetic gene cluster, polyketide	84	49
Cluster 18	T1PKS	Tiacumicin B biosynthetic gene cluster, polyketide	12	29
Cluster 19	Oligosaccharide	–	–	62
Cluster 20	NRPS	Kedarcidin biosynthetic gene cluster, polyketide	2	42
Cluster 21	Indole	Fortimicin biosynthetic gene cluster, saccharide	6	20
Cluster 22	Transatpks-T1PKS-NRPS	Teicoplanin biosynthetic gene cluster, NRPS	9	45
Cluster 23	Terpene	Brasilicardin A biosynthetic gene cluster, terpene	45	24
Cluster 24	T1PKS	Kedarcidin biosynthetic gene cluster, polyketide	9	42
Cluster 25	Terpene	SF2575 biosynthetic gene cluster, polyketide	6	16
Cluster 26	Siderophore	–	–	17
Cluster 27	Lantipeptide	Meridamycin biosynthetic gene cluster, hybrid	13	21
Cluster 28	Others	–	–	46
Cluster 29	Lantipeptide	–	–	21

^a Secondary metabolite synthesis gene clusters were predicted by comparing the genome sequences with antiSMASH. NRPS = nonribosomal peptides synthetase and PKS = polyketide synthase.

the GenBank database. Only two complete genomes (assembly levels) of *Saccharothrix* were reported: *Saccharothrix espanaensis* (GCA_000328705.1) (Strobel et al. 2012) and *S. syringae* (GCA_009498035.1) (Mo and Yang 2020). No complete genome of *S. texasensis* has been reported.

S. texasensis strain 6-C was isolated from the potato rhizosphere and its cell-free fermentation broth has a significant growth inhibitory effect on *Phytophthora infestans* (unpublished data). Potato late blight induced by *P. infestans* is one of the 10 major oomycete diseases (Kamoun et al. 2015). There are few reports on the inhibition of oomycosis by *Saccharothrix* spp. Therefore, mining the genome information of *S. texasensis* strain 6-C is of great significance for understanding its biocontrol mechanism and discovering new natural products. It might provide new insights for the prevention and control of oomycete diseases.

In this study, genomic DNA of *S. texasensis* strain 6-C was extracted using the Bacteria DNA Kit (Omega Bio-Tek Co., Ltd., Guangzhou, China). The genome of *S. texasensis* strain 6-C was sequenced using a combination of Illumina short-read and PacBio long-read sequencing technologies, and sequencing was performed at the Shanghai Majorbio Bio-pharm Technology Co., Ltd. (Shanghai, China). Sequence runs for single-molecule real-time (SMRT) cells were carried out on a PacBio RS II sequencer. SMRT Analysis Portal version 2.1 was used for read filtering and adapter trimming, with default parameters (Cui et al. 2020; Li et al. 2020). Illumina Hiseq x-ten read sequences comprising raw reads (>100×) were used to correct base errors of the assembled sequence obtained by the long-read sequences (>100×). The genome was de novo assembled using the HGAP assembly protocol (Chin et al. 2013). The coding sequence in the genome was predicted by Glimmer, GeneMarkS, and Prodigal software. The transfer RNA (tRNA) and ribosomal RNA (rRNA) were predicted by tRNAscan-SE v2.0 and Barrnap. These databases were used for functional annotation of predicted protein-coding genes, including the gene ontology (GO) (Ashburner et al. 2000), Kyoto Encyclopedia of Genes and Genomes (KEGG) (Aoki-Kinoshita 2006), EuKaryotic

Orthologous Groups (KOG) (Koonin et al. 2004), GenBank nonredundant (NR) (Koonin et al. 2004), and Swiss-Prot databases (Stutz et al. 2006). In addition, gene clusters involved in secondary metabolite production, antibiotic resistance, toxin synthesis, and carbohydrate-active enzymes (CAZymes) were predicted by comparing the genome sequences with the CAZymes database and antiSMASH (Cui et al. 2020; Yin et al. 2012).

The final assembled genome is a single circular chromosome (9,045,220 bp), without gaps and plasmid, and a GC content of 72.39%. In all, 12 rRNAs and 53 tRNAs were predicted. There were, in total, 8,077 protein-coding genes. Among these genes, 6,390 (79%) were classified using the KOG database, 4,010 (50%) were mapped to the Swiss-Prot database, 4,625 (57%) were assigned GO terms, 1,902 (24%) were mapped to the KEGG database, and 7,705 (95%) were mapped to the NR database. Genome analysis using the CAZymes database predicted the existence of 221 glycoside hydrolases, 74 carbohydrate esterases, 69 glycosyl transferases, 20 polysaccharide lyases, 12 carbohydrate-binding modules, and 33 auxiliary activities, which are reported to participate in a diversity of key biological processes such as energy uptake or cell wall degradation (Compain 2020; Gilbert 2010). Genome analysis using antiSMASH predicted the existence of 29 gene clusters involved in secondary metabolite production (Table 1). The top four gene clusters were nonribosomal peptides synthetase (nine clusters), type I polyketide synthase (five clusters), terpene (four clusters), and lanthipeptide (three clusters), and some of the enzymes encoded by such clusters are reported to be involved in the biosynthesis of antimicrobials or antagonistic activity of particular biocontrol bacteria (Li et al. 2014; Malmierca et al. 2013; Repka et al. 2017).

This genome sequence could contribute to the understanding of genetic and genomic diversities of *Saccharothrix* spp. It could also provide opportunities to analyze the molecular basis of its biocontrol activity. The complete whole-genome sequence of *S. texasensis* strain 6-C has been deposited at GenBank database under the accession number CP064192 (BioProject: PRJNA671555, BioSample: SAMN16534143).

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Author-Recommended Internet Resources

antiSMASH: <https://antismash.secondarymetabolites.org/#/start>

Barnmap: <https://github.com/tseemann/barnmap>

Glimmer: <http://ccb.jhu.edu/software/glimmer/index.shtml>

tRNAscan-SE v2.0: <http://trna.ucsc.edu/software>

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