

Draft Genome Sequence of the Marine Actinomycete *Streptomyces sulphureus* L180, Isolated from Marine Sediment

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Marine-derived actinobacteria are rich sources of valuable natural products and industrial enzymes for biotechnology applications. The marine-derived *Streptomyces sulphureus* strain L180 was isolated from the marine sediment in a sea cucumber farm at a depth of about 10 m in Dalian, China, and its 16S rRNA gene sequence was determined to have the highest identity to that of *Streptomyces sulphureus* NRRL B-1627^T (99.65%). Here, we report the draft genome sequence of this strain.

Marine-derived actinobacteria are gaining the interest of many researchers for the discovery of novel natural products and industrial enzymes. During our previous studies on marine actinobacteria, a marine-derived *Streptomyces* was isolated from the marine sediment in a sea cucumber farm at a depth of about 10 m in Dalian, China, and its 16S rRNA gene sequence was determined to have the highest identity to that of *Streptomyces sulphureus* NRRL B-1627^T (99.65%) and the second highest to that of *Streptomyces luteireticuli* NBRC 13422^T (96.99%) (2). Here, we report the draft genome sequence of this strain.

The nucleotide sequencing was performed by Beijing Genome Institute (BGI) in Shenzhen, China, using Illumina sequencing. The paired-end reads generated by Illumina sequencer were assembled by using SOAPdenovo1.05 (4). Coding sequences were predicted by using Prodigal (3). Functional assignment of coding genes was obtained by performing a sequence similarity search with BLAST (<http://blast.ncbi.nlm.nih.gov/Blast.cgi>) against the Clusters of Orthologous Groups (COG) (<http://www.ncbi.nlm.nih.gov/COG/>) reference database, and functional gene annotation was based on BLASTP with the KEGG databases.

The *S. sulphureus* L180 draft genome contains 5,665,377 bp with a GC content of 72.27%. The assembly consists of 385 contigs (>500 bp) with an N50 size of ~31 kb. The genome consists of one linear chromosome with 6,114 protein-coding genes (coding sequences [CDSs]), and the average gene length is 926 bp. Sequence analysis identified three gene clusters that are related to the biosynthesis of polyketide compounds, and two gene clusters for the biosynthesis of nonribosomal peptide antibiotics are also observed. Interestingly, one gene cluster containing genes showing the highest identity to those involved in microbisporicin biosynthesis (43.75% to 65.05% sequence identity) in *Microbispora coralline* was also revealed (1), suggesting that strain L180 is a potential antibiotic producer.

A portion of genes involved in the biodegradation of xenobiotics (about 6.7% of the whole genome, more than 400 genes) were also located in the L180 genome from the results of KEGG pathway classification, and the xenobiotic agents include naphthalene, 1- and 2-methylnaphthalene, benzoate, anthracene, 1- and 2-chloroacrylic acid, atrazine, and 2,4-dichlorobenzoate. The L180 genome also contains many genes that showed low identity (40% to 50%) to the homologous genes in the GenBank database, and the function of these genes is proposed to be involved in gene regulation, as well as transport of amino acid or drug molecules,

which implies that novel regulatory systems may exist in this strain. Putative genes of glycoside hydrolase, monooxygenase, glycosyl transferase, hydrolase, oxidoreductase, and cytochrome P450 were identified in the L180 genome, and many of these genes show low identity with those of the known ones, which indicates that the species is a potential producer of novel enzymes.

The strain most closely related to L180 identified by the 16S rRNA gene sequence is *S. sulphureus* NRRL B-1627^T (99.65% identity), whose genomic sequence is not yet available. So far, the biological aspects and biotechnological applications of *S. sulphureus* NRRL B-1627^T and its related strains are very poorly studied. The genomic sequence of strain L180 not only provides a basis for the exploration of this strain for biotechnology applications but also is valuable for systematic studies of related strains and species.

Nucleotide sequence accession numbers. The genome sequence has been deposited at DDBJ/EMBL/GenBank under accession no. AJTQ00000000. The version described in this paper is the first version, AJTQ00000000.

ACKNOWLEDGMENTS

We appreciate the financial support of Open Project of State Key Laboratory of Microbial Technology, Shandong University (grant M2011-01) and Open Project of Key Laboratory of Marine Bio-resources Sustainable Utilization, Chinese Academy of Sciences (grant LMB111002).

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Received 25 May 2012 Accepted 6 June 2012

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doi:10.1128/JB.00900-12