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Draft Genome Sequence of Thiostrepton-Producing *Streptomyces azureus* ATCC 14921

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***Streptomyces azureus* ATCC 14921 belongs to the *Streptomyces cyaneus* cluster and is known to be a thiostrepton producer. Here, we report a draft genome sequence for this strain, consisting of 350 contigs containing a total of 8,790,525 bp, 8,164 predicted coding sequences, and a G+C content of 70.9%.**

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Streptomyces species are Gram-positive aerobic mycelial bacteria belonging to the phylum *Actinobacteria*. They are useful for their capacity to produce large numbers of secondary metabolites and are also interesting subjects for the study of morphological differentiation (1). Pock formation involving conjugative plasmids is a typical physiological characteristic of the morphological differentiation of *Streptomyces* species (2, 3).

Streptomyces azureus ATCC 14921 is categorized in the blue-spore *Streptomyces cyaneus* cluster and is known to be a thiostrepton producer (4). The thiostrepton resistance gene (*tsr*), which is a selective marker often used in the genetic engineering of actinomycetes, was isolated from the strain (5, 6). *S. azureus* contains the pock-forming conjugative plasmid pSA1.1 (7), and spontaneous development of pocks in the strain is caused by the action of the plasmid and lysogenic phage SAt2 (8). The genome sequence of *S. azureus* may shed light on the mechanism of pock formation and may also be useful in comparative studies of morphological and metabolic differentiation among blue-spore *Streptomyces* species.

A sample was prepared for sequencing by growing *S. azureus* ATCC 14921 aerobically overnight at 28°C in tryptic soy broth (TSB) (Oxoid). The genomic DNA was then extracted and purified as we described previously (9). The prepared genome was sequenced using MiSeq (Illumina) and Ion PGM (Thermo) and assembled using the Microbial Genome Annotation Pipeline (MiGAP) (http://www.migap.org/) (10).

The genomic DNA included a total of 8,790,525 bp and was sequenced using the whole-genome shotgun strategy, which generated 3,669,353 reads and achieved approximately 62-fold coverage. Assembly of all the reads resulted in 156 contigs (>100 bp), with an N_{50} contig size of 85,729 bp. Genome annotation of the obtained scaffolds was performed using MetaGeneAnnotator version 1.0 and NCBI BLAST version 2.2.18 against a nonredundant protein sequence database. The genome of *S. azureus* ATCC 14921 has a G+C content of 70.9%, and annotation using the COG, RefSeq, and TrEMBL databases with tRNAscan-SE version 1.23 (11) and additional manual inspection revealed 8,164 predicted coding regions, 68 tRNA genes, and 3 rRNA genes.

The gene cluster for thiostrepton biosynthesis was annotated within contig SAZU364 and showed strong similarity to the thiostrepton biosynthesis cluster of *Streptomyces laurentii* ATCC 31255 (12). The *tsr* gene is located between the ABC transporter genes and two-component response system genes within contig SAZU036. Plasmid pSA1.1 was integrated adjacent to the $tRNA^{Ile}$ gene in contig SAZU077. We suggest pock formation is caused by competitive inhibition between products of the *spi* gene in pSA1.1 and the *spoIIIE*- or *ftsK*- like gene products (13). However, no genes homologous to *spoIIIE*- or *ftsK* have been annotated in the genome. An alternative mechanism for pock formation in *S. azureus* should therefore be considered. Within contig SAZU025, a gene cluster encoding phage-related proteins, including the tail protein, capsid and scaffold proteins, terminase, and integrase, was annotated. It appears these genes encoding defective phage SAt2 might produce a lytic zone in spontaneously developing pocks.

Nucleotide sequence accession number. The *S. azureus* ATCC 14921 genome sequence and annotation data have been deposited in the DDBJ/EMBL/GenBank under the accession no. BBYS00000000.

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