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Complete Genome Sequence of *Streptomyces* sp. Sge12, Which Produces Antibacterial and Fungicidal Activities

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ABSTRACT *Streptomyces* sp. Sge12 was isolated from forest soil and exhibited remarkable antimicrobial activities against selected fungi and Gram-positive bacteria. Here, we report the complete genome sequence of this strain, which contains 37 putative secondary metabolite gene clusters.

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Streptomyces is the largest genus of *Actinobacteria*, and its members are the major targets of genome mining for the discovery of bioactive secondary metabolites (1). *Streptomyces* sp. strain Sge12 was isolated from the forest soil of Shengnongjia, Northwest Hubei Province, China, and was preserved at the China Center for Type Culture Collection (CCTCC AA92011). *Streptomyces* sp. Sge12 cultured on YBP agar (2) exhibited strong growth-inhibitory activities against selected Gram-positive bacteria, including *Staphylococcus aureus*, *Mycobacterium smegmatis* mc^{2}155, and *Bacillus mycoides*, and fungi such as *Gibberella zeae* and *Thanatephorus cucumeris*. Here, we report the sequenced genome of *Streptomyces* sp. Sge12 in order to analyze its potential for the mining of novel bioactive secondary metabolites.

The whole genome of *Streptomyces* sp. Sge12 was sequenced by using a combined strategy of paired-end Illumina HiSeq 4000 (688.0-Mb sequences, 84.8-fold coverage) and single-molecule real-time PacBio RSII (1,127.1-Mb sequences, 139.0-fold coverage) sequencing. The reads from the Illumina HiSeq 4000 and PacBio RSII sequencing were assembled using Meraculous version 2.0 software (3) and RS_HGAP Assembly version 3.0 software (4), respectively. Subsequently, the final assembly of the whole genome was finished by using Illumina/PacBio hybrid assembly approaches (5). The total size of the genome is 8,110,698 bp, with a G+C content of 72.17%, and contains a linear chromosome (7,983,613 bp) and a circular plasmid (pSGE, 127,085 bp). Next, open reading frames of the genome were predicted by Glimmer version 3.02, and the predicted genes were annotated using the NR, COG, GO, Swiss-Prot, and KEGG databases. In general, the whole genome encompasses 7,491 protein-coding genes (with 126 of them located on pSGE), 71 tRNA operons, and 21 rRNA operons.

The genome sequence of *Streptomyces* sp. Sge12 was examined using antiSMASH version 3.0 (6), leading to the identification of 37 putative biosynthetic gene clusters (BGCs) for various types of secondary metabolites, including 6 terpenes, 5 nonribosomal peptides, 5 polyketides, 3 nonribosomal peptide-polyketide hybrids, and 3 ribosomally synthesized and posttranslationally modified peptides (RiPPs), which may be involved in the observed antimicrobial activities. Only four exhibited 100% similarity with known gene clusters, which were responsible for the biosynthesis of the odorous metabolite 2-methylisoborneol (7), the siderophore desferrioxamine B (8), the morphogen SapB (9), and the compatible solute ectoine (10). An additional four gene clusters showed >50% similarity with the BGCs of hopene (11, 12), gray spore pigment (13), lactazole A (14), and alkylresorcinol (15). None of the above eight compounds has been reported to exhibit strong antimicrobial activity. Further experimental studies of the

Streptomyces sp. Sge12 BGCs may lead to the discovery of antimicrobial metabolites and provide insights into their production.

Accession number(s). The genome sequence of *Streptomyces* sp. Sge12 has been deposited in the DDBJ/ENA/GenBank database under the GenBank accession numbers CP020555 for the linear chromosome and CP020556 for the circular plasmid pSGE (two entries).

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