



Draft Genome Sequence of *Streptomyces* sp. XY006, an Endophyte Isolated from Tea (*Camellia sinensis*)

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ABSTRACT *Streptomyces* sp. XY006 is an endophytic bacterium isolated from the young leaf material of the tea plant (*Camellia sinensis*). The draft genome consists of 8.2 Mb and encodes 7,415 putative open reading frames. This strain is found to contain a high capacity for the production of natural products.

Endophytic bacteria, especially those belonging to the actinomycetes group, are an important yet underdeveloped microbial resource for novel natural products (1–4). As part of a larger research project aimed at discovering new biologically active compounds from endophytic actinomycetes, we isolated *Streptomyces* sp. XY006 from the surface-sterilized young leaf materials of the tea plant (*Camellia sinensis* cv. Tieguanynin). Based on 16S rRNA sequence analysis, strain XY006 showed close similarity to *Streptomyces levis* NRRL B-16370^T (99.9% similarity, GenBank accession no. MF496983). The methanol extracts from *Streptomyces* sp. XY006 fermentation were found to be active against several plant fungal pathogens, including *Fusarium graminearum*, *Fusarium oxysporum* f. sp. *lycopersici*, *Fusarium oxysporum* f. sp. *cubense*, and *Colletotrichum* spp. (our unpublished data).

Streptomyces sp. XY006 was cultivated on Difco ISP4 agar at 30°C until sporulation. Genomic DNA was extracted using a DNeasy UltraClean microbial kit (Qiagen, USA) following the manufacturer's protocol. The draft genome was sequenced from an Illumina paired-end library with an average insert size of 350 bp, using an Illumina HiSeq X Ten instrument with a 2 × 150-bp configuration at the Beijing Novogene Bioinformatics Technology Co., Ltd. (Beijing, China). The sequencing of strain XY006 generated 1,891 Mb of data. After adapter filtering and quality trimming, *de novo* assembly of the reads was performed using SOAPdenovo (5) and resulted in 74 scaffolds with an N_{50} value of 218,181 bp. The draft genome contains 8,251,847 bp, with a G+C content of 72.33%.

Gene prediction and annotation were performed with the Rapid Annotations using Subsystems Technology (RAST) server (6). A total of 7,415 putative protein-coding genes and 75 RNA genes were identified. Functional annotation of genes revealed that strain XY006 holds potential genes associated with plant growth promotion, including genes involved in indole-3-acetic acid (IAA) synthesis, such as tryptophan 2-monooxygenase and indole-3-acetamide hydrolase (7); the *acdS* gene encoding 1-aminocyclopropane-1-carboxylate deaminase (ACC deaminase); genes involved in mineral phosphate solubilization, transport, and assimilation, such as exopolyphosphatase, inorganic pyrophosphatase, alkaline phosphatase, and some genes in the Pho regulon (8); and genes involved in fungal cell-wall degradation, such as family 19 chitinases (9).

Analysis of the *Streptomyces* sp. XY006 genome with antiSMASH version 4.0 (10) identified 27 putative secondary metabolite biosynthetic gene clusters. Five shared

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complete identity with previously reported clusters for antimycin, melanin, informati-peptin, albaflavenone, and roseoflavin biosynthesis. The remaining clusters included five nonribosomal peptide synthetases (NRPSs), one type III polyketide synthase (PKS), four PKS-NRPS hybrids, seven terpenes, one NRPS-terpene hybrid, and one bacteriocin.

This work reveals the presence of a wealth of genes related to plant growth promotion and secondary metabolite production in the genome of strain XY006, which merits further studies.

Accession number(s). This whole-genome shotgun project has been deposited at DDBJ/ENA/GenBank under the accession number [NOKT0000000](https://doi.org/10.1093/nar/gkv437). The version described in this paper is the first version, NOKT01000000.

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