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Genome Announcement

Draft genome sequence of *Streptomyces* sp. strain F1, a potential source for glycoside hydrolases isolated from Brazilian soil



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ABSTRACT

Here, we show the draft genome sequence of *Streptomyces* sp. F1, a strain isolated from soil with great potential for secretion of hydrolytic enzymes used to deconstruct cellulosic biomass. The draft genome assembly of *Streptomyces* sp. strain F1 has 69 contigs with a total genome size of 8,142,296 bp and G + C 72.65%. Preliminary genome analysis identified 175 proteins as Carbohydrate-Active Enzymes, being 85 glycoside hydrolases organized in 33 distinct families. This draft genome information provides new insights on the key genes encoding hydrolytic enzymes involved in biomass deconstruction employed by soil bacteria.

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Introduction

Streptomyces species are aerobic Gram-positive bacteria best known industrially as producers of natural antibiotics,¹ but they are also recognized for their capacity to utilize cellulosic biomass.² Phylogenetically, *Streptomyces* is the largest genus

of the Actinobacteria phylum. During their lifetime, these soil bacteria are able to differentiate, produce aerial mycelia and a wide variety of secondary metabolites.³ Although a large number of *Streptomyces* species can grow on plant biomass, understanding of key genes encoding hydrolytic enzymes involved in biomass degrading by *Streptomyces* is currently limited to a few soil-isolates.^{2,4–7} *Streptomyces* sp. strain F1

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Table 1 – Summary of genome features of *Streptomyces* sp. F1.

Features	
Source	Soil
Genome size, Mb	8.1
GC content %	0.73
tRNA	90
rRNA	3
Protein coding sequences	7262

was isolated from soil containing decomposing organic matter collected in Campinas, São Paulo, Brazil. This isolated strain showed ability to grow in culture medium containing cellulose or hemicellulose as sole carbon source, and to secrete extracellular enzymes belonging to the glycoside hydrolases (GHs) families. Glycoside hydrolases are a group of enzymes that play an important role in the conversion of lignocellulosic biomass into small chemical building blocks, which can then be used to produce biofuels and other important intermediary molecules.⁸ Here, we show the draft genome sequence of *Streptomyces* sp. F1, to identify GHs family members and to improve understanding of natural biomass utilization by soil bacteria.

Genomic DNA extraction from *Streptomyces* sp. F1 was carried out using FastDNA SPIN Kit for soil (MP Biomedicals, Irvine, CA) according to the manufacturer's instructions. The genome was sequenced by whole genome shotgun sequencing using the Illumina HiSeq 2500 System at CTBE Sequencing and Robotics NGS facility, generating 8,147,881 paired end reads (2× 100 bp). Reads were preprocessed with Trimmomatic,⁹ to remove low-quality and adapter sequences and were assembled using Spades version 3.6.¹⁰ The genome size was estimated to be 8,205,272, with approximately 100× coverage. The draft genome assembly of *Streptomyces* sp. F1 has 69 contigs, 8,142,296 bp in length with G+C content of 72.65% (Table 1), an N50 of 296,926 bp, and the largest contig was 760,841 bp. Genome completeness was evaluated using CheckM,¹¹ which revealed that the assembly is 100% complete, considering 460 marker genes from Streptomycetaceae family.

Streptomyces sp. F1 showed highest 16S rDNA sequence similarity with *Streptomyces misionensis* strain NRRL B-3230^T. In silico DNA–DNA hybridization (DDH)¹² and Average Nucleotide Identity/Alignment fraction (gANI/AF)¹³ values of *Streptomyces* sp. F1 compared to *Streptomyces misionensis* DSM 40306, were 94.2% and 99.4%/0.99, respectively, suggesting that strain F1 may be classified as *Streptomyces misionensis*.

Streptomyces sp. F1 genome was annotated using IMG-JGI Microbial Genome Annotation Pipeline (img.jgi.doe.gov). It has been predicted to include 7355 genes, being 7262 protein-coding genes, 3 rRNA (5S (1), 16S (1), 23S (1)), and 90 tRNA genes (Table 1). According to IMG functional annotation, 4453 genes were classified into COG categories, 5526 in PFAM protein families, 1542 in TIGRFAM families, and 714 in Transporter Classification. Further classification according to dbCAN showed that 175 proteins were classified as Carbohydrate-Active Enzymes, being 85 glycoside hydrolases organized in 33 distinct families. The current genome

assembly provides a preliminary landscape of the genomic and metabolic capabilities of *Streptomyces* sp. F1.

Nucleotide sequence accession number

The whole genome sequences of *Streptomyces* sp. F1 have been deposited at DDBJ/EMBL/GenBank under accession number FJJI03000000.

Conflict of interest

The authors declare no conflicts of interest.

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