Streptomyces sp. F-3 is a kind of thermophilic Streptomyces strain that can produce cellulolytic enzymes and diverse secondary metabolites. Here, we report the complete genome of this organism, whose genome length is 5,303,958 bp, containing 6,041 protein-coding genes, 69 tRNA operons, and three rRNA operons.

Streptomyces are a group of Gram-positive bacteria belonging to the class Actinobacteria, which are among the most numerous and ubiquitous soil bacteria (1). Streptomyces sp. F-3 is an aerobic, aerial mycelial, spore-forming bacterium that was isolated from a compost sample in Jinan City, Shandong Province, China. This strain is screened with carboxymethyl cellulose so that the growth of a microorganism with sufficient carbon and nitrogen sources (5). In addition, there were also seven putative gene clusters responsible for the production of secondary metabolites, involving genes encoding non-ribosomal peptide synthases (NRPS) and type I polyketide synthases (PKS) (6). Beyond that, metabolism of formaldehyde reveals the potential of Streptomyces sp. F-3 for converting acetaldehyde into CO2.

The genome sequence of Streptomyces sp. F-3 is considerably valuable for further functional genome study and sheds light on the understanding of the relationship between lignocellulose degradation and secondary metabolites production. Comprehensive analysis of this specific strain’s genome will be reported in the future.

ACKNOWLEDGMENTS
This work was supported by a grant from The Key Technologies R&D Program of Shandong Province (2015GSF121019) and a grant of the Fundamental Research Funds of Shandong University (2015YQ004).

The funders had no role in study design, data collection and interpretation, or the decision to submit the work for publication.

FUNDING INFORMATION
This work, including the efforts of Lushan Wang, was funded by Key Technologies R&D Program of Shandong Province (2015GSF121019). This work, including the efforts of Lushan Wang, was funded by Fundamental Research Funds of Shandong University (2015YQ004).

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