AMERICAN SOCIETY FOR MICROBIOLOGY | Microbiology Resource Announcements

GENOME SEQUENCES

Draft Genome Sequence of *Streptomyces* Strain SJ1-7, a Soil Bacterial Isolate

Won-Jae Chi,[a] Da Som Kim,[a] Soonok Kim,[a] Eu Ddeum Choi,[b] Sook-Young Park[b]

[a]Genetic Resources Assessment Division, National Institute of Biological Resources, Incheon, South Korea
[b]Department of Plant Medicine, Sunchon National University, Suncheon, South Korea

ABSTRACT The draft genome sequence of *Streptomyces* strain SJ1-7, a bacterial strain isolated from the rhizosphere of a *Pinus densiflora* plant, is reported. The whole-genome assembly comprised 7.9 Mbp, with a GC content of 71.80% and 4,262 predicted protein-coding genes.

The genus *Streptomyces* belongs to the order *Actinomycetales*, phylum *Actinobacteria*, and consists of diverse aerobic, Gram-positive filamentous bacteria abundant in soil. It is well known that *Streptomyces* spp. produce numerous valuable biologically active secondary metabolites (SMs), including antifungals (1), antibacterials (2), antivirals (3), antitumor agents (4), immunosuppressants (5), and plant growth-promoting factors (6). *Streptomyces* spp. have been reported to produce almost 8,000 SMs (7, 8). Considering that we have not fully explored its diversity and biochemical capabilities, the genus will likely offer more pharmaceuticals as well as compounds that can help agricultural industries (9–11).

Streptomyces strain SJ1-7 was isolated by single-colony isolation on starch-casein agar (SCA) medium from rhizospheric soils surrounding the roots of a *Pinus densiflora* plant in Sangju, South Korea (36°26′41.0″N, 128°15′16.9″E), in 2018. For long-term preservation, the purified colonies were scraped from agar plates using a scraper with 15% glycerol buffer solution, transferred to a sterile cryovial, and then stored at −80°C. The strain was incubated in SCA medium for 7 days at 28°C, and a single colony was incubated in casein-starch-peptone-yeast extract-malt extract (CSPY-ME) broth with shaking at 120 rpm at 28°C for 7 days (12). Genomic DNA from SJ1-7 was extracted using a MagAttract high-molecular-weight DNA kit (Qiagen, Hilden, Germany) as instructed by the manufacturer. The extracted genomic DNA was cleaned using a phenol-chloroform-isoamyl alcohol (25:24:1) extraction protocol (13). Purified genomic DNA (15 μg) was size selected (15 to 20 kb) using a Covaris g-TUBE device and checked for concentration (Qubit). For genome sequencing, a single-molecule real-time (SMRT) cell library was prepared according to the Pacific Bioscience sample preparation protocol (https://www.pacb.com/wp-content/uploads/2015/09/User-Bulletin-Guidelines-for-Preparing-20-kb-SMRTbell-Templates.pdf), and sequencing was performed using the PacBio RS II platform by DNALink, Inc. (Seoul, South Korea). Sequencing generated 150,292 reads with a mean read length of 4,353 bp. The raw reads were trimmed, filtered, and assembled using the Hierarchical Genome Assembly Process (HGAP) v. 3.0 pipeline with default parameters as embedded in the PacBio SMRT Link software. The genome assembly yielded two contigs with 7,764,317 bp and 157,044 bp, representing 54.29-fold coverage and a 71.5% GC ratio. A total of 8,622 coding sequences (CDSs) and the genes for 18 rRNAs and 76 tRNAs were predicted by the Prokka v. 1.13.3 annotation pipeline with default parameters (14). Further analysis of the genome sequence, including functional and biochemical analyses, will reveal its secondary metabolism-associated genes. This draft genome sequence will also serve as a reference for comparative genomics with other *Streptomyces* spp.

Citation Chi W-J, Kim DS, Kim S, Choi ED, Park S-Y. 2021. Draft genome sequence of *Streptomyces* strain SJ1-7, a soil bacterial isolate. Microbiol Resour Announc 10:e01283-20. https://doi.org/10.1128/MRA.01283-20.

Editor David A. Baltrus, University of Arizona

Address correspondence to Sook-Young Park, spark@scnu.ac.kr.

Received 9 November 2020
Accepted 11 February 2021
Published 11 March 2021

Data availability. The whole-genome shotgun data set was deposited at GenBank under whole-genome sequencing project number JABFHJ000000000, BioProject accession number PRJNA623260, and BioSample accession number SAMN14543207. The version described in this article is the first version (JABFHJ010000000).

ACKNOWLEDGMENT

This work was supported by a grant from the National Institute of Biological Resources, funded by the Ministry of Environment of the Republic of Korea (grant number NIBR202020101).

REFERENCES

1. Vezina C, Kudelski A, Sehgal SN. 1975. Rapamycin (AY-22,989), a new antifungal antibiotic. I. Taxonomy of the producing streptomycete and isolation of the active principle. J Antibiot (Tokyo) 28:721–726. https://doi.org/10.7164/antibiotics.28.721.
2. Mellouli L, Ben Ameur-Mehdi R, Sioud S, Salem M, Bejar S. 2003. Isolation, purification and partial characterization of antibacterial activities produced by a newly isolated *Streptomyces* sp. US24 strain. Res Microbiol 154:345–352. https://doi.org/10.1016/S0923-2508(03)00077-9.
3. Mohamed HS, Galal AM. 2005. Identification and antiviral activities of some halotolerant streptomycetes isolated from Qaroon Lake. Int J Agric Biol 7:747–753.
4. Mao Y, Varoglu M, Sherman DH. 1999. Molecular characterization and analysis of the biosynthetic gene cluster for the antitumor antibiotic mitomycin C from *Streptomyces lavendulae* NRRL 2564. Chem Biol 6:251–263. https://doi.org/10.1016/S1074-5521(99)80040-4.
5. Pahl A, Keller U. 1992. FK-506-binding proteins from streptomycetes producing immunosuppressive macrolactones of the FK-506 type. J Bacteriol 174:5888–5894. https://doi.org/10.1128/jb.174.18.5888-5894.1992.
6. Doumbou CL, Salove MKH, Crawford DL, Beaulieu C. 2005. Actinomycetes, promising tools to control plant diseases and to promote plant growth. Phytoprotection 82:85–102. https://doi.org/10.7202/706219ar.
7. Berdy J. 2005. Bioactive microbial metabolites. J Antibiot (Tokyo) 58:1–26. https://doi.org/10.1038/ja.2005.1.
8. Pagmadulam B, Tserendulam D, Rentsenkhand T, Igarashi M, Sawa R, Nihei C-I, Nishikawa Y. 2020. Isolation and characterization of antiprotozoal compound-producing *Streptomyces* species from Mongolian soils. Parasitol Int 74:101961. https://doi.org/10.1016/j.parint.2019.101961.
9. Anderson AS, Wellington EM. 2001. The taxonomy of *Streptomyces* and related genera. Int J Syst Evol Microbiol 51:797–814. https://doi.org/10.1099/00207713-51-3-797.
10. Nguyen HT, Pokhrel AR, Nguyen CT, Pham VTT, Dhakal D, Lim HN, Jung HJ, Kim T-S, Yamaguchi T, Sohng JK. 2020. *Streptomyces* sp. VN1, a producer of diverse metabolites including non-natural furan-type anticancer compound. Sci Rep 10:1756. https://doi.org/10.1038/s41598-020-58623-1.
11. El Sayed OH, Asker MMS, Swelim MA, Abbas IH, Attwa AI, El Awady ME. 2016. Production of hydroxy marilone C as a bioactive compound from *Streptomyces badius*. J Genet Eng Biotechnol 14:161–168. https://doi.org/10.1016/j.jgeb.2016.04.001.
12. Singh LS, Sharma H, Sahoo D. 2019. Actinomycetes from soil of Lachung, a pristine high altitude region of Sikkim Himalaya, their antimicrobial potentiality and production of industrially important enzymes. Adv Microbiol 9:750–773. https://doi.org/10.4236/aim.2019.98046.
13. Green MR, Sambrook J. 2012. Molecular cloning: a laboratory manual, 4th ed. Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York.
14. Seemann T. 2014. Prokka: rapid prokaryotic genome annotation. Bioinformatics 30:2068–2069. https://doi.org/10.1093/bioinformatics/btu153.