Draft Genome Sequence of Streptomyces olivochromogenes NBRC 3561, a Bioactive Peptide-Producing Actinobacterium

メタデータ	言語: eng
	出版者:
	公開日: 2017-12-25
	キーワード (Ja):
	キーワード (En):
	作成者: Dohra, Hideo, Miyake, Yuto, Kodani, Shinya
	メールアドレス:
	所属:
URL	http://hdl.handle.net/10297/00024379

Draft Genome Sequence of *Streptomyces olivochromogenes* NBRC 3561, a Bioactive Peptide-Producing Actinobacterium

Hideo Dohra,[a,b] Yuto Miyake,[c] Shinya Kodani[c]

Instrumental Research Support Office, Research Institute of Green Science and Technology, Shizuoka University, Suruga-ku, Shizuoka, Japan[a]; Department of Biological Science, Graduate School of Integrated Science and Technology, Shizuoka University, Suruga-ku, Shizuoka, Japan[b]; Department of Applied Biological Chemistry, Graduate School of Integrated Science and Technology, Shizuoka University, Suruga-ku, Shizuoka, Japan[c]

ABSTRACT   Recently, we found that *Streptomyces olivochromogenes* NBRC 3561 produced a bioactive peptide, so we sequenced its genome to clarify its biosynthesis. We report here the draft genome sequence of *S. olivochromogenes* NBRC 3561, in which 40 potential secondary metabolite gene clusters were predicted by antiSMASH.

*S*treptomyces is the largest genus in the phylum *Actinobacteria*, and its members are prolific producers of bioactive secondary metabolites, as has been well studied (1). *Streptomyces olivochromogenes* produces useful enzymes, such as xylose isomerase. However, there have been few reports on low-molecular-weight compounds of *S. olivochromogenes*. Recently, our chemical investigation revealed that *S. olivochromogenes* NBRC 3561 produced a bioactive peptide. The draft genome sequence of *S. olivochromogenes* NBRC 3561 was determined and searched for a gene cluster possibly involved in the production of the bioactive peptide.

S. olivochromogenes strain NBRC 3561 was acquired from the NITE Biological Resource Center, Japan. Genomic DNA of *S. olivochromogenes* NBRC 3561 was extracted using the DNeasy blood and tissue kit and fragmented using the Covaris Acoustic Solubilizer. A paired-end library constructed by the TruSeq DNA PCR-free library preparation kit was sequenced using the Illumina MiSeq platform (301-bp paired ends). The raw read sequences were cleaned up using Trimmomatic (2) by trimming adapter sequences, low-quality ends (quality score, <15), the last 301 bases, and reads less than 150 bp. The filtered reads were additionally processed using khmer version 2.0 (3) by filtering reads with a low *k*-mer coverage (<3) to remove sequencing errors and contaminated sequences. The resultant 3,567,049 high-quality reads totaling 764 Mb, which corresponds to an approximately 66-fold coverage of the genome, were assembled using SPAdes version 3.10.0 (4) with a *k*-mer size of 21, 33, 55, 77, 99, and 127 bp and the options --careful, --only-assembler, and --cov-cutoff auto, and contigs less than 200 bp were eliminated.

The draft genome of *S. olivochromogenes* NBRC 3561 contains 131 contigs consisting of 11,639,641 bp with a G+C content of 70.22%. The draft genome was annotated using the DFAST Legacy server (5) based on Prokka (6) with a RefSeq database. The *S. olivochromogenes* NBRC 3561 genome contains 10,550 protein-coding sequences and 88 tRNAs. The proteins encoded by the genome were additionally annotated with the COG (Clusters of Orthologous Groups) database (7). Among 10,550 proteins, 6,621 (62.8%) were assigned to COG functional categories, including 82 proteins involved in the ABC-type multidrug transport system (COG0842, COG1131, and COG1132) and 31 proteins involved in the ABC-type antimicrobial peptide transport system (COG0577

and COG1136). This result suggests that *S. olivochromogenes* NBRC 3561 has developed transport systems for bioactive peptides such as antimicrobial peptides.

Prediction of secondary metabolite biosynthesis gene clusters by antiSMASH version 3.0.5 (8) suggested that the *S. olivochromogenes* NBRC 3561 genome contained 40 potential biosynthetic gene clusters, including 7 polyketide synthases (PKSs), 4 nonribosomal peptide synthetases (NRPSs), 4 bacteriocins, 4 terpenes, 3 siderophores, 2 lantipeptides, and a lassopeptide. Among 40 gene clusters, 5 were predicted to be hybrid clusters, such as an NRPS-PKS hybrid and a lantipeptide-terpene hybrid.

The genome information and predicted secondary metabolite biosynthesis gene clusters of *S. olivochromogenes* NBRC 3561 will contribute to studies on the structure and function of bioactive compounds and their biosynthetic pathways and transport systems.

Accession number(s). The draft genome sequence of *S. olivochromogenes* NBRC 3561 was deposited in DDBJ/EMBL/GenBank under accession no. BDQI00000000. The version described in this paper is the first version, BDQI01000000.

REFERENCES

1. Bérdy J. 2005. Bioactive microbial metabolites. J Antibiot 58:1–26. https://doi.org/10.1038/ja.2005.1.
2. Bolger AM, Lohse M, Usadel B. 2014. Trimmomatic: a flexible trimmer for Illumina sequence data. Bioinformatics 30:2114–2120. https://doi.org/10.1093/bioinformatics/btu170.
3. Crusoe MR, Alameldin HF, Awad S, Boucher E, Caldwell A, Cartwright R, Charbonneau A, Constantinides B, Edvenson G, Fay S, Fenton J, Fenzl T, Fish J, Garcia-Gutierrez L, Garland P, Gluck J, Gonzalez I, Guermond S, Guo J, Gupta A, Herr JR, Howe A, Hyer A, Harpfer A, Irber L, Kidd R, Lin D, Lippi J, Mansour T, McA'Nulty P, McDonald E, Mizzi J, Murray KD, Nahum JR, Nanlohy K, Nederbragt AJ, Ortiz-Zuazaga H, Ory J, Pell J, Pepe-Ranney C, Russ ZN, Schwarz E, Scott C, Seaman J, Sievert S, Simpson J, Skennerton CT, Spencer J, Srinivasan R, Standage D, Stapleton JA, Steinman SR, Stein J, Taylor B, Trimble W, Wiencko HL, Wright M, Wyss B, Zhang Q, Zyme E, Brown CT. 2015. The khmer software package: enabling efficient nucleotide sequence analysis. F1000Res 4:900. https://doi.org/10.12688/f1000research.6924.1.
4. Bankevich A, Nurk S, Antipov D, Gurevich AA, Dvorkin M, Kulikov AS, Lesin VM, Nikolenko SI, Pham S, Prjibelski AD, Pyshkin AV, Sirotkin AV, Vyahhi N, Tesler G, Alekseyev MA, Pevzner PA. 2012. SPAdes: a new genome assembly algorithm and its applications to single-cell sequencing. J Comput Biol 19:455–477. https://doi.org/10.1089/cmb.2012.0021.
5. Tanizawa Y, Fujisawa T, Kaminuma E, Nakamura Y, Arita M. 2016. DFAST and DAGA: Web-based integrated genome annotation tools and resources. Biosci Microbiota Food Health 35:173–184. https://doi.org/10.12938/bmfh.16-003.
6. Seemann T. 2014. Prokka: rapid prokaryotic genome annotation. Bioinformatics 30:2068–2069. https://doi.org/10.1093/bioinformatics/btu153.
7. Galperin MY, Makarova KS, Wolf YI, Koonin EV. 2015. Expanded microbial genome coverage and improved protein family annotation in the COG database. Nucleic Acids Res 43:D261–D269. https://doi.org/10.1093/nar/gku1223.
8. Weber T, Blin K, Duddela S, Krug D, Kim HU, Bruccoleri R, Lee SY, Fischbach MA, Müller R, Wohlleben W, Breitling R, Takano E, Medema MH. 2015. antiSMASH 3.0—a comprehensive resource for the genome mining of biosynthetic gene clusters. Nucleic Acids Res 43:W237–W243. https://doi.org/10.1093/nar/gkv437.