



HAL
open science

Draft Whole-Genome Shotgun Sequence of *Streptomyces* sp. Strain ETH9427

Annabelle Thibessard, Cláudia M Vicente, Claire Bertrand, Bertrand Aigle,
Pierre Leblond

► **To cite this version:**

Annabelle Thibessard, Cláudia M Vicente, Claire Bertrand, Bertrand Aigle, Pierre Leblond. Draft Whole-Genome Shotgun Sequence of *Streptomyces* sp. Strain ETH9427. *Microbiology Resource Announcements*, 2018, 7 (12), pp.e01197. 10.1128/MRA.01197-18 . hal-01887322

HAL Id: hal-01887322

<https://hal.univ-lorraine.fr/hal-01887322>

Submitted on 4 Oct 2018

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.



Distributed under a Creative Commons Attribution - ShareAlike 4.0 International License



Draft Whole-Genome Shotgun Sequence of *Streptomyces* sp. Strain ETH9427

Annabelle Thibessard,^a Cláudia M. Vicente,^a Claire Bertrand,^a Bertrand Aigle,^a Pierre Leblond^a

^aUniversité de Lorraine, Inra, DynAMic, Nancy, France

ABSTRACT The draft genome of *Streptomyces* sp. strain ETH9427 was sequenced and assembled into three large scaffolds, a 7.745-Mb linear chromosome with terminal inverted repeats of 201 kb and two probable extrachromosomal elements. Thirty-two biosynthetic gene clusters (BGCs) were identified, out of which four are duplicated in the terminal inverted repeats.

We report here the draft genome sequence of *Streptomyces* sp. ETH9427, a strain initially reported as *Streptomyces ambofaciens* ETH9427 (1). The strain was obtained from Ralf Hütter (1) and has been maintained at the DynAMic lab since then. The sequencing project was aimed at unveiling the biosynthetic gene clusters (BGCs) and comparing the BGC content of the genomes of closely related *Streptomyces* isolates and comparing their genome organizations.

After growth in liquid Hickey-Tresner medium (2) at 30°C for 30 h and DNA purification (2), two libraries, a mate pair (~8 kb) and a paired-end (~300 bp) library, were created (MiSeq reagent kit version 3; 600 cycles), from which 3,329,310 and 405,558 reads (average size, 301 bp), respectively, were generated using a Genome Analyzer (Illumina). The reads were assembled with Velvet version 1.2.10 (default settings, option -scaffolding, "yes"; k-mer, 95) into a total of 68 scaffolds (N_{50} , 1.33 Mb) comprising 739 contigs (N_{50} , 19,192 bp), for a total estimated genome size of 7.8 Mb (genome coverage, 144×). Contig order was validated by reference to closely related strains using the Artemis Comparison Tool (3). Coding sequence prediction and annotation were performed using the NCBI Prokaryotic Genome Annotation Pipeline (4).

The genome sequence of *Streptomyces* sp. strain ETH9427 consists of a linear chromosome of 7,745,357 bp with long terminal inverted repeats of 201,878 bp and an average GC content of 72.07%. Six rRNA operons, 68 tRNAs, and 7,140 protein-coding genes were found on the chromosome. The following two probable extrachromosomal elements were characterized: (i) pETH1, a linear plasmid of 106,771 bp (GC content, 71.7%) having, at the chromosome's end, typical palindromic telomere sequences and possessing two complete CRISPR loci, as predicted by CRISPRfinder (5; see also <http://crispr.i2bc.paris-saclay.fr/>); and (ii) pETH2, a 125,903-bp plasmid (GC content, 71.3%), which was also predicted to be linear. The PHAge Search Tool (PHAST) (6) predicted that this latter molecule contains or constitutes a whole bacteriophage.

Assessment of the phylogenetic relationship of the species using average nucleotide identity (ANI) values (7; see also <http://enve-omics.ce.gatech.edu/ani>) determined that the closest species whose genome is available is *Streptomyces* sp. strain 4F with an ANIb value of 94% (GenBank accession number CP013142). Despite its first assignment (1), the ANIb value (~81%) was too low to support its assignment to the species *S. ambofaciens*; it does, however, support the organism being renamed *Streptomyces* sp. The isolates *Streptomyces* sp. strain ETH9427, *Streptomyces* sp. strain 4F, and *S. ambofaciens* strain ATCC 23877 (8) constitute, however, a group of related strains, since the divergence of their 16S rRNA genes does not exceed 1%.

A preliminary analysis of the *Streptomyces* sp. strain ETH9427 sequence using

Received 28 August 2018 Accepted 31 August 2018 Published 27 September 2018

Citation Thibessard A, Vicente CM, Bertrand C, Aigle B, Leblond P. 2018. Draft whole-genome shotgun sequence of *Streptomyces* sp. strain ETH9427. Microbiol Resour Announc 7:e01197-18. <https://doi.org/10.1128/MRA.01197-18>.

Editor J. Cameron Thrash, Louisiana State University

Copyright © 2018 Thibessard et al. This is an open-access article distributed under the terms of the [Creative Commons Attribution 4.0 International license](https://creativecommons.org/licenses/by/4.0/).

Address correspondence to Pierre Leblond, pierre.leblond@univ-lorraine.fr.

A.T. and C.M.V. contributed equally to this work.

antiSMASH (9, 10) allowed the identification of a total of 32 BGCs, out of which 4 were found to be duplicates since they lay in the terminal inverted repeats. Strains *Streptomyces* sp. ETH9427, *Streptomyces* sp. 4F, and *S. ambofaciens* ATCC 23877 shared nine BGCs, while three additional BGCs were conserved between *Streptomyces* sp. strains ETH9427 and 4F, confirming the phylogenetic relationship inferred by the ANiB analysis.

Data availability. The whole-genome sequence reported here has been deposited in GenBank under the accession numbers [CP029624](#), [CP029625](#), and [CP029626](#). Raw sequence reads (Illumina) have been deposited in the NCBI Sequence Read Archive under the accession number [SRP158364](#).

ACKNOWLEDGMENTS

This work was funded by the French National Research Agency through two programs (ANR Streptoflux ANR-07-BLAN-0096 and ANR MiGenS) and by the French National Institute for Agricultural Research (INRA), Région Lorraine and the Laboratory of Excellence ARBRE (ANR-11-LABX-0002-01). C. M. Vicente was also supported by the AgreeSkillsPlus Program (FP7-609398.0000).

We acknowledge support of DynAMic by the “Impact Biomolecules” project of the Lorraine Université d’Excellence (Investissements d’avenir–ANR).

REFERENCES

- Hütter R. 1967. Systematik der Streptomyceten. Karger Verlag, Basel.
- Kieser T, Bibb M, Buttner M, Chater K, Hopwood D. 2000. Practical *Streptomyces* genetics. John Innes Foundation, Norwich, United Kingdom.
- Carver T, Berriman M, Tivey A, Patel C, Böhme U, Barrell BG, Parkhill J, Rajandream M-A. 2008. Artemis and ACT: viewing, annotating and comparing sequences stored in a relational database. *Bioinformatics* 24: 2672–2676. <https://doi.org/10.1093/bioinformatics/btn529>.
- Tatusova T, DiCuccio M, Badretdin A, Chetvernin V, Nawrocki EP, Zaslavsky L, Lomsadze A, Pruitt KD, Borodovsky M, Ostell J. 2016. NCBI Prokaryotic Genome Annotation Pipeline. *Nucleic Acids Res* 44: 6614–6624. <https://doi.org/10.1093/nar/gkw569>.
- Grissa I, Vergnaud G, Pourcel C. 2007. CRISPRFinder: a Web tool to identify clustered regularly interspaced short palindromic repeats. *Nucleic Acids Res* 35:W52–W57. <https://doi.org/10.1093/nar/gkm360>.
- Zhou Y, Liang Y, Lynch KH, Dennis JJ, Wishart DS. 2011. PHAST: a fast phage search tool. *Nucleic Acids Res* 39:W347–W352. <https://doi.org/10.1093/nar/gkr485>.
- Goris J, Konstantinidis KT, Klappenbach JA, Coenye T, Vandamme P, Tiedje JM. 2007. DNA–DNA hybridization values and their relationship to whole-genome sequence similarities. *Int J Syst Evol Microbiol* 57:81–91. <https://doi.org/10.1099/ijs.0.64483-0>.
- Thibessard A, Haas D, Gerbaud C, Aigle B, Lautru S, Pernodet J-L, Leblond P. 2015. Complete genome sequence of *Streptomyces ambofaciens* ATCC 23877, the spiramycin producer. *J Biotechnol* 214:117–118. <https://doi.org/10.1016/j.jbiotec.2015.09.020>.
- Medema MH, Blin K, Cimermancic P, de Jager V, Zakrzewski P, Fischbach MA, Weber T, Breitling R, Takano E. 2011. antiSMASH: rapid identification, annotation and analysis of secondary metabolite biosynthesis gene clusters in bacterial and fungal genome sequences. *Nucleic Acids Res* 39:W339–W346. <https://doi.org/10.1093/nar/gkr466>.
- Blin K, Medema MH, Kazempour D, Fischbach MA, Breitling R, Takano E, Weber T. 2013. antiSMASH 2.0—a versatile platform for genome mining of secondary metabolite producers. *Nucleic Acids Res* 41:W204–W212. <https://doi.org/10.1093/nar/gkt449>.